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(54) Title: NOVEL HUMAN GENES AND GENE EXPRESSION PRODUCTS

(57) Abstract: The invention provides novel polynucleotides. The invention further provides novel members of protein families, and polynucleotides that are differentially expressed in cancer cells relative to normal cells, and in metastatic cancer cells relative to normal cells or non-metastatic cancer cells.

NOVEL HUMAN GENES AND GENE EXPRESSION PRODUCTS

FIELD OF THE INVENTION

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The present invention relates to novel polynucleotides of human origin and the encoded gene products.

5 BACKGROUND OF THE INVENTION

Identification of novel polynucleotides, particularly those that encode an expressed gene product, is important in the advancement of drug discovery, diagnostic technologies, and the understanding of the progression and nature of complex diseases such as cancer. Identification of genes expressed in different cell types isolated from sources that differ in disease state or stage, developmental stage, exposure to various environmental factors, the tissue of origin, the species from which the tissue was isolated, and the like is key to identifying the genetic factors that are responsible for the phenotypes associated with these various differences.

This invention provides novel human polynucleotides, the polypeptides encoded by these polynucleotides, and the genes and proteins corresponding to these novel polynucleotides.

SUMMARY OF THE INVENTION

This invention relates to novel human polynucleotides and variants thereof, their encoded polypeptides and variants thereof, to genes corresponding to these polynucleotides and to proteins expressed by the genes. The invention also relates to diagnostics and therapeutics comprising such novel human polynucleotides, their corresponding genes or gene products, including probes, antisense nucleotides, and antibodies. The polynucleotides of the invention correspond to a polynucleotide comprising the sequence information of at least one of SEQ ID NOs: 1-3351.

Various aspects and embodiments of the invention will be readily apparent to the ordinarily skilled artisan upon reading the description provided herein.

DETAILED DESCRIPTION OF THE INVENTION

The invention relates to polynucleotides comprising the disclosed nucleotide sequences, to full length cDNA, mRNA genomic sequences, and genes

corresponding to these sequences and degenerate variants thereof, and to polypeptides encoded by the polynucleotides of the invention and polypeptide variants.

Polypeptide variants differ from wild type protein in having one or more amino acid substitutions that either enhance, add, or diminish a biological activity of the wild type protein.

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Six of the polypeptides disclosed herein encode new members of the MKK kinase family; the coding region is found within the nucleotide region in parentheses: SEQ ID NO:29 (nucleotides 295-421); SEQ ID NO:31 (298-397); SEQ ID NO:196 (37-322); SEQ ID NO:3175 (nucleotides 14-164); SEQ ID NO:3190 (229-390); and SEQ ID NO:3281 (15-182). Twenty-four of the polypeptides encode new members of the family of transcription factor proteins having a basic region plus leucine zipper: SEQ ID NO:410 (42-191); SEQ ID NO:552 (116-288); SEQ ID NO:768 (116-288); SEQ ID NO:822 (108-262); SEQ ID NO:836 (158-353); SEQ ID NO:1288 (73-234); SEQ ID NO:1365 (69-257); SEQ ID NO:1540 (289-471); SEQ ID NO:1549 (200-391); SEQ ID NO:1556 (163-354); SEQ ID NO:1630 (100-291); SEQ ID NO:1563 (107-298); SEQ ID NO:1622 (180-365); SEQ ID NO:1630 (100-291); SEQ ID NO:1704 (184-372); SEQ ID NO:1808 (36-161); SEQ ID NO:1454 (49-209); SEQ ID NO:2363 (48-211); SEQ ID NO:2424 (43-194); SEQ ID NO:3147 (190-369); SEQ ID NO:3152 (129-320); SEQ ID NO:3158 (167-334); and SEQ ID NO:3208 (34-256).

SEQ ID NOs:186 (175-395); 2591 (60-165); 3307 (43-321); and 3339 (94-342) encode polypeptides having an SH2 domain, and SEQ ID NOs:234 (23-121), 1832 (18-173), and 1835 (57-206) encode polypeptides having an SH3 domain. Nine polypeptides encode new members of the family of proteins having Ank repeat regions: SEQ ID NO:187 (358-432); SEQ ID NO:1268 (238-315); SEQ ID NO:1804 (301-378); SEQ ID NO:1819 (278-355); SEQ ID NO:1839 (224-307); SEQ ID NO:1830 (184-267); SEQ ID NO:2562 (18-101); SEQ ID NO:3015 (131-214); and SEQ ID NO:3267 (97-180).

The following eleven polynucleotides encode polypeptides having a C2H2 type zinc finger: SEQ ID NOs:308 (110-172); 807 (339-392); 1324 (294-356); 1503 (154-216); 1527 (156-212); 1674 (196-258); 1779 (64-126); 1801 (295-351); 3081 (190-252); 3193 (293-355); and 3306 (161-223). Eight polynucleotides encode polypeptides of the family of ATPases: SEQ ID NOs:431 (71-428); 639 (157-561); 2135 (2-401); 2684 (9-461); 2859 (100-320); 3178 (45-386); 3197 (281-343) and 3266 (8-139). Polypeptides having a fibronectin type III domain are encoded by SEQ ID NO:746 (209-427) and 1192 (186-416). Polypeptides having an EF-hand domain are encoded by SEQ ID NO:820 (341-

406); 1755 (281-367) and 3285(16-102). Six polypeptides of the protein kinase family are encoded by SEQ ID NOs:1157 (41-444); 1478 (54-437), 1496 (241-520); 2286 (12-182); 2969 (5-387); and 3190 (118-390).

LIM domain-containing polypeptides are encoded by SEQ ID NO:1269 (79-240); 1309 (248-404); 1360 (222-377); and 1386 (243-398). Two polypeptides of the family having a C2 domain (protein kinase C-like) are encoded by SEQ ID NO:1325 (1-234) and 2282(183-353). Polypeptides having a WD domain, G-beta repeat motif are encoded by SEQ ID NOs:1336 (66-164); 1380 (42-140); 1711 (263-361); 1762 (236-334); 1909 (160-258); 2218 (127-225); 3047 (191-292); 3108 (275-367) and 3292 (208-300).

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SEQ ID NO:1410 (222-350) encodes a member of the trypsin family. SEQ ID NOs:1417 (8-354); 2281 (20-387) and 2310 (20-371) encode members of the protein tyrosine phosphatase family. SEQ ID NOs:1464 (4-180) and 1514 (2-252) encode members of the family having an RNA recognition motif (also known as RRM, RBD, or RNP domain). SEQ ID NOs:1496 (241-520) and 3297(7-153) encode helicases having a conserved C-terminal domain. SEQ ID NO:1538 (9-635) encodes a member of the wnt family of developmental signaling proteins.

Three polynucleotides encode polypeptides having a homeobox domain: SEQ ID NOs:1676 (9-86); 1820 (123-299); and 1821 (127-303). A novel thioredoxin is encoded by SEQ ID NO:1677 (316-369). Two novel members of the ras family are encoded by SEQ ID NO:1688(109-410) and 3258(138-394). A novel polypeptide having a phosphatidylinositol-specific phospholipase C Y-domain is encoded by SEQ ID NO:1707 (92-439). A novel serine carboxypeptidase is encoded by SEQ ID NO:1744 (238-433). A novel polypeptide having N-terminal homology in the Ets domain is encoded by SEQ ID NO:1811 (184-315). A novel polypeptide having a bromodomain is encoded by SEQ ID NO:1814 (127-294). A novel polypeptide having a double-stranded RNA binding motif is encoded by SEQ ID NO:1818 (9-146). A novel polypeptide having a G-protein alpha subunit is encoded by SEQ ID NO:1846 (12-398).

SEQ ID NOs:1911 (35-151) and 1980 (60-197) encode polypeptides having a C3HC4 type zinc finger domain (RING finger). SEQ ID NO:2065 (253-306) encodes a polypeptide having a CCHC zinc finger domain. SEQ ID NO:2216 (90-179) encodes a polypeptide having a WW/rsp5/WWP domain. SEQ ID NO:2428 (25-350) encodes a polypeptide member of the dual specificity phosphatase family, having a catalytic domain.

SEQ ID NOs:2577 (0-311); 3183 (14-215); and 3195 (0-215) encode members of the 4 transmembrane segment integral membrane protein family. SEQ ID

NOs:2826 (116-400) and 2871 (198-392) encode polypeptides of the DEAD and DEAH box helicase family. SEQ ID NO:2944 (18-281) encodes a polypeptide having a calpain large subunit, domain III.

SEQ ID NO:3274 (11-187) encodes a eukaryotic transcription factor with a fork head domain. SEQ ID NO:3345 (65-271) encodes a polypeptide having a PDZ domain, and SEQ ID NO:3351 (124-270) encodes a polypeptide in the family of phorbol esters/glycerol binding proteins.

Described below are polynucleotide compositions encompassed by the invention, methods for obtaining cDNA or genomic DNA encoding a full-length gene product, expression of these polynucleotides and genes, identification of structural motifs of the polynucleotides and genes, identification of the function of a gene product encoded by a gene corresponding to a polynucleotide of the invention, use of the provided polynucleotides as probes and in mapping and in tissue profiling, use of the corresponding polypeptides and other gene products to raise antibodies, and use of the polynucleotides and their encoded gene products for therapeutic and diagnostic purposes.

Polynucleotide Compositions

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The scope of the invention with respect to polynucleotide compositions includes, but is not necessarily limited to, polynucleotides having a sequence set forth in any one of SEQ ID NOs:1-3351; polynucleotides obtained from the biological materials described herein or other biological sources (particularly human sources) by hybridization under stringent conditions (particularly conditions of high stringency); genes corresponding to the provided polynucleotides; variants of the provided polynucleotides and their corresponding genes, particularly those variants that retain a biological activity of the encoded gene product (e.g., a biological activity ascribed to a gene product corresponding to the provided polynucleotides as a result of the assignment of the gene product to a protein family(ies) and/or identification of a functional domain present in the gene product). Other nucleic acid compositions contemplated by and within the scope of the present invention will be readily apparent to one of ordinary skill in the art when provided with the disclosure here. "Polynucleotide" and "nucleic acid" as used herein with reference to nucleic acids of the composition is not intended to be limiting as to the length or structure of the nucleic acid unless specifically indicated.

The invention features polynucleotides that are expressed in human tissue, specifically human colon, breast, and/or lung tissue. Novel nucleic acid

compositions of the invention comprise a sequence set forth in any one of SEQ ID NOs:1-3351 or an identifying sequence thereof. An "identifying sequence" is a contiguous sequence of residues at least about 10 nt to about 20 nt in length, usually at least about 50 nt to about 100 nt in length, that uniquely identifies a polynucleotide sequence, e.g., exhibits less than 90%, usually less than about 80% to about 85% sequence identity to any contiguous nucleotide sequence of more than about 20 nt. Thus, the subject novel nucleic acid compositions include full length cDNAs or mRNAs that encompass an identifying sequence of contiguous nucleotides from any one of SEQ ID NOs:1-3351.

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The polynucleotides of the invention also include polynucleotides having sequence similarity or sequence identity. Nucleic acids having sequence similarity are detected by hybridization under low stringency conditions, for example, at 50°C and 10XSSC (0.9 M saline/0.09 M sodium citrate) and remain bound when subjected to washing at 55°C in 1XSSC. Sequence identity can be determined by hybridization under stringent conditions, for example, at 50°C or higher and 0.1XSSC (9 mM saline/0.9 mM sodium citrate). Hybridization methods and conditions are well known in the art, see, e.g., U.S. Patent No. 5,707,829. Nucleic acids that are substantially identical to the provided polynucleotide sequences, e.g., allelic variants, genetically altered versions of the gene, etc., bind to the provided polynucleotide sequences (SEQ ID NOs:1-3351) under stringent hybridization conditions. By using probes, particularly labeled probes of DNA sequences, one can isolate homologous or related genes. The source of homologous genes can be any species, e.g., primate species, particularly human; rodents, such as rats and mice; canines, felines, bovines, ovines, equines, yeast, nematodes, etc.

Preferably, hybridization is performed using at least 15 contiguous nucleotides (nt) of at least one of SEQ ID NOs:1-3351. That is, when at least 15 contiguous nt of one of the disclosed SEQ ID NOs. is used as a probe, the probe will preferentially hybridize with a nucleic acid comprising the complementary sequence, allowing the identification and retrieval of the nucleic acids that uniquely hybridize to the selected probe. Probes from more than one SEQ ID NO. can hybridize with the same nucleic acid if the cDNA from which they were derived corresponds to one mRNA. Probes of more than 15 nt can be used, e.g., probes of from about 18 nt to about 100 nt, but 15 nt represents sufficient sequence for unique identification.

The polynucleotides of the invention also include naturally occurring variants of the nucleotide sequences (e.g., degenerate variants, allelic variants).

Variants of the polynucleotides of the invention are identified by hybridization of putative variants with nucleotide sequences disclosed herein, preferably by hybridization under stringent conditions. For example, by using appropriate wash conditions, variants of the polynucleotides of the invention can be identified where the allelic variant exhibits at most about 25-30% base pair (bp) mismatches relative to the selected polynucleotide probe. In general, allelic variants contain 15-25% bp mismatches, and can contain as little as even 5-15%, or 2-5%, or 1-2% bp mismatches, as well as a single bp mismatch.

The invention also encompasses homologs corresponding to the polynucleotides of SEQ ID NOs:1-3351, where the source of homologous genes can be any mammalian species, e.g., primate species, particularly human; rodents, such as rats; canines, felines, bovines, ovines, equines, yeast, nematodes, etc. Between mammalian species, e.g., human and mouse, homologs generally have substantial sequence similarity, e.g., at least 75% sequence identity, usually at least 90%, more usually at least 95% between nucleotide sequences. Sequence similarity is calculated based on a reference sequence, which may be a subset of a larger sequence, such as a conserved motif, coding region, flanking region, etc. A reference sequence will usually be at least about 18 contiguous nt long, more usually at least about 30 nt long, and may extend to the complete sequence that is being compared. Algorithms for sequence analysis are known in the art, such as BLAST, described in Altschul et al., J. Mol. Biol. (1990) 215:403-10.

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In general, variants of the invention have a sequence identity greater than at least about 65%, preferably at least about 75%, more preferably at least about 85%, and can be greater than at least about 90%, 91%, 92%, 93%, 94%, 95%, or 96%, most preferably 97%, 98% or 99%. For the purposes of this invention, a preferred method of calculating percent identity is the Smith-Waterman algorithm, using the following. Global DNA sequence identity must be greater than 65% as determined by the Smith-Waterman homology search algorithm as implemented in MPSRCH program (Oxford Molecular) using an affine gap search with the following search parameters: gap open penalty, 12; and gap extension penalty, 1.

The subject nucleic acids can be cDNAs or genomic DNAs, as well as fragments thereof, particularly fragments that encode a biologically active gene product and/or are useful in the methods disclosed herein (e.g., in diagnosis, as a unique identifier of a differentially expressed gene of interest, etc.). The term "cDNA" as used herein is intended to include all nucleic acids that share the arrangement of sequence

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elements found in native mature mRNA species, where sequence elements are exons and 3' and 5' non-coding regions. Normally mRNA species have contiguous exons, with the intervening introns, when present, being removed by nuclear RNA splicing, to create a continuous open reading frame encoding a polypeptide of the invention.

A genomic sequence of interest comprises the nucleic acid present between the initiation codon and the stop codon, as defined in the listed sequences, including all of the introns that are normally present in a native chromosome. It can further include the 3' and 5' untranslated regions found in the mature mRNA. It can further include specific transcriptional and translational regulatory sequences, such as promoters, enhancers, etc., including about 1 kb, but possibly more, of flanking genomic DNA at either the 5' and 3' end of the transcribed region. The genomic DNA can be isolated as a fragment of 100 kbp or smaller; and substantially free of flanking chromosomal sequence. The genomic DNA flanking the coding region, either 3' and 5', or internal regulatory sequences as sometimes found in introns, contains sequences required for proper tissue, stage-specific, or disease-state specific expression.

The nucleic acid compositions of the subject invention can encode all or a part of the subject polypeptides. Double or single stranded fragments can be obtained from the DNA sequence by chemically synthesizing oligonucleotides in accordance with conventional methods, by restriction enzyme digestion, by PCR amplification, *etc*. Isolated polynucleotides and polynucleotide fragments of the invention comprise at least about 10, about 15, about 20, about 35, about 50, about 100, about 150 to about 200, about 250 to about 300, or about 350 contiguous nt selected from the polynucleotide sequences as shown in SEQ ID NOs:1-3351. The fragments also include those of lengths intermediate to the specifically mentioned lengths, such as 35, 36, 37, 38, 39, etc.; 150, 151, 152, 153, 154, etc. For the most part, fragments will be of at least 15 nt, usually at least 18 nt or 25 nt, and up to at least about 50 contiguous nt in length or more. In a preferred embodiment, the polynucleotide molecules comprise a contiguous sequence of at least 12 nt selected from the group consisting of the polynucleotides shown in SEQ ID NOs:1-3351.

Probes specific to the polynucleotides of the invention can be generated using the polynucleotide sequences disclosed in SEQ ID NOs:1-3351. The probes are preferably at least about a 12, 15, 16, 18, 20, 22, 24, or 25 nt fragment of a corresponding contiguous sequence of SEQ ID NOs:1-3351, and can be less than 2, 1, 0.5, 0.1, or 0.05 kb in length. The probes can be synthesized chemically or can be generated from longer polynucleotides using restriction enzymes. The probes can be

labeled, for example, with a radioactive, biotinylated, or fluorescent tag. Preferably, probes are designed based upon an identifying sequence of a polynucleotide of one of SEQ ID NOs:1-3351. More preferably, probes are designed based on a contiguous sequence of one of the subject polynucleotides that remain unmasked following application of a masking program for masking low complexity (e.g., XBLAST) to the sequence., i.e., one would select an unmasked region, as indicated by the polynucleotides outside the poly-n stretches of the masked sequence produced by the masking program.

The polynucleotides of the subject invention are isolated and obtained in substantial purity, generally as other than an intact chromosome. Usually, the polynucleotides, either as DNA or RNA, will be obtained substantially free of other naturally-occurring nucleic acid sequences, generally being at least about 50%, usually at least about 90% pure and are typically "recombinant", e.g., flanked by one or more nucleotides with which it is not normally associated on a naturally occurring chromosome.

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The polynucleotides of the invention can be provided as a linear molecule or within a circular molecule, and can be provided within autonomously replicating molecules (vectors) or within molecules without replication sequences. Expression of the polynucleotides can be regulated by their own or by other regulatory sequences known in the art. The polynucleotides of the invention can be introduced into suitable host cells using a variety of techniques available in the art, such as transferrin polycation-mediated DNA transfer, transfection with naked or encapsulated nucleic acids, liposome-mediated DNA transfer, intracellular transportation of DNA-coated latex beads, protoplast fusion, viral infection, electroporation, gene gun, calcium phosphate-mediated transfection, and the like.

The subject nucleic acid compositions can be used to, for example, produce polypeptides, as probes for the detection of mRNA of the invention in biological samples (e.g., extracts of human cells) to generate additional copies of the polynucleotides, to generate ribozymes or antisense oligonucleotides, and as single stranded DNA probes or as triple-strand forming oligonucleotides. The probes described herein can be used to, for example, determine the presence or absence of the polynucleotide sequences as shown in SEQ ID NOs:1-3351 or variants thereof in a sample. These and other uses are described in more detail below.

Use of Polynucleotides to Obtain Full-Length cDNA, Gene, and Promoter Region

Full-length cDNA molecules comprising the disclosed polynucleotides are obtained as follows. A polynucleotide having a sequence of one of SEQ ID NOs:1-3351, or a portion thereof comprising at least 12, 15, 18, or 20 nt, is used as a hybridization probe to detect hybridizing members of a cDNA library using probe design methods, cloning methods, and clone selection techniques such as those described in U.S. Patent No. 5,654,173. Libraries of cDNA are made from selected tissues, such as normal or tumor tissue, or from tissues of a mammal treated with, for example, a pharmaceutical agent. Preferably, the tissue is the same as the tissue from which the polynucleotides of the invention were isolated, as both the polynucleotides described herein and the cDNA represent expressed genes. Most preferably, the cDNA library is made from the biological material described herein in the Examples. The choice of cell type for library construction can be made after the identity of the protein encoded by the gene corresponding to the polynucleotide of the invention is known. This will indicate which tissue and cell types are likely to express the related gene, and thus represent a suitable source for the mRNA for generating the cDNA. As described in the Examples, cDNA of the invention was isolated from specific cell or tissue types, and such cells and tissues are preferable for obtaining related nucleic acids.

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Techniques for producing and probing nucleic acid sequence libraries are described, for example, in Sambrook et al., *Molecular Cloning: A Laboratory Manual, 2nd Ed.*, (1989) Cold Spring Harbor Press, Cold Spring Harbor, NY. The cDNA can be prepared by using primers based on sequence from SEQ ID NOs:1-3351. In one embodiment, the cDNA library can be made from only poly-adenylated mRNA. Thus, poly-T primers can be used to prepare cDNA from the mRNA.

Members of the library that are larger than the provided polynucleotides, and preferably that encompass the complete coding sequence of the native message, are obtained. In order to confirm that the entire cDNA has been obtained, RNA protection experiments are performed as follows. Hybridization of a full-length cDNA to an mRNA will protect the RNA from RNase degradation. If the cDNA is not full length, then the portions of the mRNA that are not hybridized will be subject to RNase degradation. This is assayed, as is known in the art, by changes in electrophoretic mobility on polyacrylamide gels, or by detection of released monoribonucleotides. Sambrook et al., *Molecular Cloning: A Laboratory Manual, 2nd Ed.*, (1989) Cold Spring Harbor Press, Cold Spring Harbor, NY. In order to obtain additional sequences

5' to the end of a partial cDNA, 5' RACE (PCR Protocols: A Guide to Methods and Applications, (1990) Academic Press, Inc.) can be performed.

Manner similar to the isolation of full-length cDNAs. Briefly, the provided polynucleotides, or portions thereof, are used as probes to libraries of genomic DNA. Preferably, the library is obtained from the cell type that was used to generate the polynucleotides of the invention, but this is not essential. Most preferably, the genomic DNA is obtained from the biological material described herein in the Examples. Such libraries can be in vectors suitable for carrying large segments of a genome, such as P1 or YAC, as described in detail in Sambrook et al., 9.4-9.30. In addition, genomic sequences can be isolated from human BAC libraries, which are commercially available from Research Genetics, Inc., Huntsville, Alabama, USA, for example. In order to obtain additional 5' or 3' sequences, chromosome walking is performed, as described in Sambrook et al., such that adjacent and overlapping fragments of genomic DNA are isolated. These are mapped and pieced together, as is known in the art, using restriction digestion enzymes and DNA ligase.

Using the polynucleotide sequences of the invention, corresponding full-length genes can be isolated using both classical and PCR methods to construct and probe cDNA libraries. Using either method, Northern blots, preferably, are performed on a number of cell types to determine which cell lines express the gene of interest at the highest level. Classical methods of constructing cDNA libraries are taught in Sambrook et al., *supra*. With these methods, cDNA can be produced from mRNA and inserted into viral or expression vectors. Typically, libraries of mRNA comprising poly(A) tails can be produced with poly(T) primers. Similarly, cDNA libraries can be produced using the instant sequences as primers.

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PCR methods are used to amplify the members of a cDNA library that comprise the desired insert. In this case, the desired insert will contain sequence from the full length cDNA that corresponds to the instant polynucleotides. Such PCR methods include gene trapping and RACE methods as described in Gruber et al., WO 95/04745 and Gruber et al., U.S. Patent No. 5,500,356. Kits are commercially available to perform gene trapping experiments from, for example, Life Technologies, Gaithersburg, Maryland, USA. In preferred embodiments of RACE, a common primer is designed to anneal to an arbitrary adaptor sequence ligated to cDNA ends (Apte and Siebert, *Biotechniques* (1993) 15:890-893; Edwards et al., *Nuc. Acids Res.* (1991) 19:5227-5232). When a single gene-specific RACE primer is paired with the common

primer, preferential amplification of sequences between the single gene specific primer and the common primer occurs. Commercial cDNA pools modified for use in RACE are available.

The promoter region of a gene generally is located 5' to the initiation site for RNA polymerase II. Hundreds of promoter regions contain the "TATA" box, a sequence such as TATTA or TATAA, which is sensitive to mutations. The promoter region can be obtained by performing 5' RACE using a primer from the coding region of the gene. Alternatively, the cDNA can be used as a probe for the genomic sequence, and the region 5' to the coding region is identified by "walking up." If the gene is highly expressed or differentially expressed, the promoter from the gene can be of use in a regulatory construct for a heterologous gene.

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Once the full-length cDNA or gene is obtained, DNA encoding variants can be prepared by site-directed mutagenesis, described in detail in Sambrook et al., 15.3-15.63. The choice of codon or nucleotide to be replaced can be based on disclosure herein on optional changes in amino acids to achieve altered protein structure and/or function.

As an alternative method to obtaining DNA or RNA from a biological material, nucleic acid comprising nucleotides having the sequence of one or more polynucleotides of the invention can be synthesized. Thus, the invention encompasses nucleic acid molecules ranging in length from 15 nt (corresponding to at least 15 contiguous nt of one of SEQ ID NOs:1-3351) up to a maximum length suitable for one or more biological manipulations, including replication and expression, of the nucleic acid molecule. The invention includes but is not limited to (a) nucleic acid having the size of a full gene, and comprising at least one of SEQ ID NOs:1-3351; (b) the nucleic acid of (a) also comprising at least one additional polynucleotide or gene, operably linked to permit expression of a fusion protein; (c) an expression vector comprising (a) or (b); (d) a plasmid comprising (a) or (b); and (e) a recombinant viral particle comprising (a) or (b). Once provided with the polynucleotides disclosed herein, construction or preparation of (a) - (e) are well within the skill in the art.

The sequence of a nucleic acid comprising at least 15 contiguous nt of at least any one of SEQ ID NOs:1-3351, preferably the entire sequence of at least any one of SEQ ID NOs:1-3351, is not limited and can be any sequence of A, T, G, and/or C (for DNA) and A, U, G, and/or C (for RNA) or modified bases thereof, including inosine and pseudouridine. The choice of sequence will depend on the desired function and can be dictated by coding regions desired, the intron-like regions desired, and the

regulatory regions desired. Where the entire sequence of any one of SEQ ID NOs:1-3351 is within the nucleic acid, the nucleic acid obtained is referred to herein as a polynucleotide comprising the sequence of any one of SEQ ID NOs:1-3351.

Expression of Polypeptide Encoded by Full-Length cDNA or Full-Length Gene

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The provided polynucleotides (e.g., a polynucleotide having a sequence of one of SEQ ID NOs:1-3351), the corresponding cDNA, or the full-length gene is used to express a partial or complete gene product. Constructs of polynucleotides having sequences of SEQ ID NOs:1-3351 can be generated synthetically. Alternatively, single-step assembly of a gene and entire plasmid from large numbers of oligodeoxyribonucleotides is described by, e.g., Stemmer et al., Gene (Amsterdam) (1995) 164(1):49-53. In this method, assembly PCR (the synthesis of long DNA sequences from large numbers of oligodeoxyribonucleotides (oligos)) is described. The method is derived from DNA shuffling (Stemmer, Nature (1994) 370:389-391), and does not rely on DNA ligase, but instead relies on DNA polymerase to build increasingly longer DNA fragments during the assembly process.

Appropriate polynucleotide constructs are purified using standard recombinant DNA techniques as described in, for example, Sambrook et al., *Molecular Cloning: A Laboratory Manual, 2nd Ed.*, (1989) Cold Spring Harbor Press, Cold Spring Harbor, NY, and under current regulations described in United States Dept. of HHS, National Institute of Health (NIH) Guidelines for Recombinant DNA Research. The gene product encoded by a polynucleotide of the invention is expressed in any expression system, including, for example, bacterial, yeast, insect, amphibian and mammalian systems. Vectors, host cells and methods for obtaining expression in same are well known in the art. Suitable vectors and host cells are described in U.S. Patent No. 5,654,173.

Polynucleotide molecules comprising a polynucleotide sequence provided herein are generally propagated by placing the molecule in a vector. Viral and non-viral vectors are used, including plasmids. The choice of plasmid will depend on the type of cell in which propagation is desired and the purpose of propagation. Certain vectors are useful for amplifying and making large amounts of the desired DNA sequence. Other vectors are suitable for expression in cells in culture. Still other vectors are suitable for transfer and expression in cells in a whole animal or person. The choice of appropriate vector is well within the skill of the art. Many such vectors are

available commercially. Methods for preparation of vectors comprising a desired sequence are well known in the art.

The polynucleotides set forth in SEQ ID NOs:1-3351 or their corresponding full-length polynucleotides are linked to regulatory sequences as appropriate to obtain the desired expression properties. These can include promoters (attached either at the 5' end of the sense strand or at the 3' end of the antisense strand), enhancers, terminators, operators, repressors, and inducers. The promoters can be regulated or constitutive. In some situations it may be desirable to use conditionally active promoters, such as tissue-specific or developmental stage-specific promoters. These are linked to the desired nucleotide sequence using the techniques described above for linkage to vectors. Any techniques known in the art can be used.

When any appropriate host cells or organisms are used to replicate and/or express the polynucleotides or nucleic acids of the invention, the resulting replicated nucleic acid, RNA, expressed protein or polypeptide, is within the scope of the invention as a product of the host cell or organism. The product is recovered by any appropriate means known in the art.

Once the gene corresponding to a selected polynucleotide is identified, its expression can be regulated in the cell to which the gene is native. For example, an endogenous gene of a cell can be regulated by an exogenous regulatory sequence as disclosed in U.S. Patent No. 5,641,670.

Identification of Functional and Structural Motifs of Novel Genes

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Translations of the nucleotide sequence of the provided polynucleotides, cDNAs or full genes can be aligned with individual known sequences. Similarity with individual sequences can be used to determine the activity of the polypeptides encoded by the polynucleotides of the invention. Also, sequences exhibiting similarity with more than one individual sequence can exhibit activities that are characteristic of either or both individual sequences.

The full length sequences and fragments of the polynucleotide sequences of the nearest neighbors can be used as probes and primers to identify and isolate the full length sequence corresponding to provided polynucleotides. The nearest neighbors can indicate a tissue or cell type to be used to construct a library for the full-length sequences corresponding to the provided polynucleotides.

Typically, a selected polynucleotide is translated in all six frames to determine the best alignment with the individual sequences. The sequences disclosed

herein in the Sequence Listing are in a 5' to 3' orientation and translation in three frames can be sufficient. These amino acid sequences are referred to, generally, as query sequences, which will be aligned with the individual sequences. Databases with individual sequences are described in "Computer Methods for Macromolecular Sequence Analysis" *Methods in Enzymology* (1996) 266, Doolittle, Academic Press, Inc., a division of Harcourt Brace & Co., San Diego, California, USA. Databases include Genbank, EMBL, and DNA Database of Japan (DDBJ).

Query and individual sequences can be aligned using the methods and computer programs described above, and include BLAST, available over the world wide web at http://www.ncbi.nlm.nhi.gov/BLAST. Another alignment algorithm is Fasta, available in the Genetics Computing Group (GCG) package, Madison, Wisconsin, USA, a wholly owned subsidiary of Oxford Molecular Group, Inc. Other techniques for alignment are described in Doolittle, supra. Preferably, an alignment program that permits gaps in the sequence is utilized to align the sequences. The Smith-Waterman is one type of algorithm that permits gaps in sequence alignments. See Meth. Mol. Biol. (1997) 70: 173-187. Also, the GAP program using the Needleman and Wunsch alignment method can be utilized to align sequences. An alternative search strategy uses MPSRCH software, which runs on a MASPAR computer. MPSRCH uses a Smith-Waterman algorithm to score sequences on a massively parallel computer. This approach improves ability to identify sequences that are distantly related matches, and is especially tolerant of small gaps and nucleotide sequence errors. Amino acid sequences encoded by the provided polynucleotides can be used to search both protein and DNA databases.

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High Similarity. In general, in alignment results considered to be of high similarity, the percent of the alignment region length is typically at least about 55% of total length query sequence; more typically, at least about 58%; even more typically; at least about 60% of the total residue length of the query sequence. Usually, percent length of the alignment region can be as much as about 62%; more usually, as much as about 64%; even more usually, as much as about 66%. Further, for high similarity, the region of alignment, typically, exhibits at least about 75% of sequence identity; more typically, at least about 78%; even more typically; at least about 80% sequence identity. Usually, percent sequence identity can be as much as about 82%; more usually, as much as about 84%; even more usually, as much as about 86%.

The p value is used in conjunction with these methods. If high similarity is found, the query sequence is considered to have high similarity with a profile

sequence when the p value is less than or equal to about 10^{-2} ; more usually; less than or equal to about 10^{-3} ; even more usually; less than or equal to about 10^{-4} . More typically, the p value is no more than about 10^{-5} ; more typically; no more than or equal to about 10^{-10} ; even more typically; no more than or equal to about 10^{-15} for the query sequence to be considered high similarity.

Similarity Determined by Sequence Identity Alone. Sequence identity alone can be used to determine similarity of a query sequence to an individual sequence and can indicate the activity of the sequence. Such an alignment, preferably, permits gaps to align sequences. Typically, the query sequence is related to the profile sequence if the sequence identity over the entire query sequence is at least about 15%; more typically, at least about 20%; even more typically, at least about 50%. Sequence identity alone as a measure of similarity is most useful when the query sequence is usually, at least 80 residues in length; more usually, 90 residues; even more usually, at least 95 amino acid residues in length. More typically, similarity can be concluded based on sequence identity alone when the query sequence is preferably 100 residues in length; more preferably, 120 residues in length; even more preferably, 150 amino acid residues in length.

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Alignments with Profile and Multiple Aligned Sequences. Translations of the provided polynucleotides can be aligned with amino acid profiles that define either protein families or common motifs. Also, translations of the provided polynucleotides can be aligned to multiple sequence alignments (MSA) comprising the polypeptide sequences of members of protein families or motifs. Similarity or identity with profile sequences or MSAs can be used to determine the activity of the gene products (e.g., polypeptides) encoded by the provided polynucleotides or corresponding cDNA or genes. For example, sequences that show an identity or similarity with a chemokine profile or MSA can exhibit chemokine activities.

Profiles can be designed manually by (1) creating an MSA, which is an alignment of the amino acid sequence of members that belong to the family and (2) constructing a statistical representation of the alignment. Such methods are described, for example, in Birney et al., *Nucl. Acid Res.* (1996) 24(14): 2730-2739. MSAs of some protein families and motifs are publicly available. MSAs are described also in Sonnhammer et al., *Proteins* (1997) 28: 405-420. A brief description of MSAs is reported in Pascarella et al., *Prot. Eng.* (1996) 9(3):249-251. Techniques for building profiles from MSAs are described in Sonnhammer et al., *supra*; Birney et al., *supra*;

and "Computer Methods for Macromolecular Sequence Analysis," Methods in Enzymology (1996) 266, Doolittle, Academic Press, Inc., San Diego, California, USA.

Similarity between a query sequence and a protein family or motif can be determined by (a) comparing the query sequence against the profile and/or (b) aligning the query sequence with the members of the family or motif. Typically, a program such as Searchwise is used to compare the query sequence to the statistical representation of the multiple alignment, also known as a profile (see Birney et al., *supra*). Other techniques to compare the sequence and profile are described in Sonnhammer et al., *supra* and Doolittle, *supra*.

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Next, methods described by Feng et al., J. Mol. Evol. (1987) 25:351 and Higgins et al., CABIOS (1989) 5:151 can be used align the query sequence with the members of a family or motif, also known as a MSA. Sequence alignments can be generated using any of a variety of software tools. Examples include PileUp, which creates a multiple sequence alignment, and is described in Feng et al., J. Mol. Evol. (1987) 25:351. Another method, GAP, uses the alignment method of Needleman et al., J. Mol. Biol. (1970) 48:443. GAP is best suited for global alignment of sequences. A third method, BestFit, functions by inserting gaps to maximize the number of matches using the local homology algorithm of Smith et al., Adv. Appl. Math. (1981) 2:482. In general, the following factors are used to determine if a similarity between a query sequence and a profile or MSA exists: (1) number of conserved residues found in the query sequence, (2) percentage of conserved residues found in the query sequence, (3) number of frameshifts, and (4) spacing between conserved residues.

Some alignment programs that both translate and align sequences can make any number of frameshifts when translating the nucleotide sequence to produce the best alignment. The fewer frameshifts needed to produce an alignment, the stronger the similarity or identity between the query and profile or MSAs. For example, a weak similarity resulting from no frameshifts can be a better indication of activity or structure of a query sequence, than a strong similarity resulting from two frameshifts. Preferably, three or fewer frameshifts are found in an alignment; more preferably two or fewer frameshifts; even more preferably, one or fewer frameshifts; even more preferably, no frameshifts are found in an alignment of query and profile or MSAs.

Conserved residues are those amino acids found at a particular position in all or some of the family or motif members. Alternatively, a position is considered conserved if only a certain class of amino acids is found in a particular position in all or

some of the family members. For example, the N-terminal position can contain a positively charged amino acid, such as lysine, arginine, or histidine.

Typically, a residue of a polypeptide is conserved when a class of amino acids or a single amino acid is found at a particular position in at least about 40% of all class members; more typically, at least about 50%; even more typically, at least about 60% of the members. Usually, a residue is conserved when a class or single amino acid is found in at least about 70% of the members of a family or motif; more usually, at least about 80%; even more usually, at least about 90%; even more usually, at least about 95%.

A residue is considered conserved when three unrelated amino acids are found at a particular position in the some or all of the members; more usually, two unrelated amino acids. These residues are conserved when the unrelated amino acids are found at particular positions in at least about 40% of all class member; more typically, at least about 50%; even more typically, at least about 60% of the members. Usually, a residue is conserved when a class or single amino acid is found in at least about 70% of the members of a family or motif; more usually, at least about 80%; even more usually, at least about 90%; even more usually, at least about 95%.

A query sequence has similarity to a profile or MSA when the query sequence comprises at least about 25% of the conserved residues of the profile or MSA; more usually, at least about 30%; even more usually; at least about 40%. Typically, the query sequence has a stronger similarity to a profile sequence or MSA when the query sequence comprises at least about 45% of the conserved residues of the profile or MSA; more typically, at least about 50%; even more typically; at least about 55%.

Identification of Secreted and Membrane-Bound Polypeptides

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Both secreted and membrane-bound polypeptides of the present invention are of particular interest. For example, levels of secreted polypeptides can be assayed in body fluids that are convenient, such as blood, plasma, serum, and other body fluids such as urine, prostatic fluid and semen. Membrane-bound polypeptides are useful for constructing vaccine antigens or inducing an immune response. Such antigens would comprise all or part of the extracellular region of the membrane-bound polypeptides. Because both secreted and membrane-bound polypeptides comprise a fragment of contiguous hydrophobic amino acids, hydrophobicity predicting algorithms can be used to identify such polypeptides.

A signal sequence is usually encoded by both secreted and membrane-bound polypeptide genes to direct a polypeptide to the surface of the cell. The signal sequence usually comprises a stretch of hydrophobic residues. Such signal sequences can fold into helical structures. Membrane-bound polypeptides typically comprise at least one transmembrane region that possesses a stretch of hydrophobic amino acids that can transverse the membrane. Some transmembrane regions also exhibit a helical structure. Hydrophobic fragments within a polypeptide can be identified by using computer algorithms. Such algorithms include Hopp & Woods, *Proc. Natl. Acad. Sci. USA* (1981) 78:3824-3828; Kyte & Doolittle, *J. Mol. Biol.* (1982) 157: 105-132; and RAOAR algorithm, Degli Esposti et al., *Eur. J. Biochem.* (1990) 190: 207-219.

Another method of identifying secreted and membrane-bound polypeptides is to translate the polynucleotides of the invention in all six frames and determine if at least 8 contiguous hydrophobic amino acids are present. Those translated polypeptides with at least 8; more typically, 10; even more typically, 12 contiguous hydrophobic amino acids are considered to be either a putative secreted or membrane bound polypeptide. Hydrophobic amino acids include alanine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, threonine, tryptophan, tyrosine, and valine

Identification of the Function of an Expression Product of a Full-Length Gene

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Ribozymes, antisense constructs, and dominant negative mutants can be used to determine function of the expression product of a gene corresponding to a polynucleotide provided herein. The phosphoramidite method of oligonucleotide synthesis can be used to construct antisense molecules and ribozymes. See Beaucage et al., *Tet. Lett.* (1981) 22:1859 and U.S. Patent No. 4,668,777. Automated devices for synthesis are available to create oligonucleotides using this chemistry. Examples of such devices include Biosearch 8600, Models 392 and 394 by Applied Biosystems, a division of Perkin-Elmer Corp., Foster City, California, USA; and Expedite by Perceptive Biosystems, Framingham, Massachusetts, USA. Synthetic RNA, phosphate analog oligonucleotides, and chemically derivatized oligonucleotides can also be produced, and can be covalently attached to other molecules. RNA oligonucleotides can be synthesized, for example, using RNA phosphoramidites. This method can be performed on an automated synthesizer, such as Applied Biosystems, Models 392 and 394, Foster City, California, USA.

Oligonucleotides of up to 200 nt can be synthesized, more typically, 100 nt, more typically 50 nt; even more typically 30 to 40 nt. These synthetic fragments can be annealed and ligated together to construct larger fragments. See, for example, Sambrook et al., *supra*. Trans-cleaving catalytic RNAs (ribozymes) are RNA molecules possessing endoribonuclease activity. Ribozymes are specifically designed for a particular target, and the target message must contain a specific nucleotide sequence. They are engineered to cleave any RNA species site-specifically in the background of cellular RNA. The cleavage event renders the mRNA unstable and prevents protein expression. Importantly, ribozymes can be used to inhibit expression of a gene of unknown function for the purpose of determining its function in an *in vitro* or *in vivo* context, by detecting the phenotypic effect.

Antisense nucleic acids are designed to specifically bind to RNA, resulting in the formation of RNA-DNA or RNA-RNA hybrids, with an arrest of DNA replication, reverse transcription or messenger RNA translation. Antisense polynucleotides based on a selected polynucleotide sequence can interfere with expression of the corresponding gene. Antisense polynucleotides are typically generated within the cell by expression from antisense constructs that contain the antisense strand as the transcribed strand. Antisense polynucleotides based on the disclosed polynucleotides will bind and/or interfere with the translation of mRNA comprising a sequence complementary to the antisense polynucleotide. The expression products of control cells and cells treated with the antisense construct are compared to detect the protein product of the gene corresponding to the polynucleotide upon which the antisense construct is based. The protein is isolated and identified using routine biochemical methods.

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Given the extensive background literature and clinical experience in antisense therapy, one skilled in the art can use selected polynucleotides of the invention as additional potential therapeutics. The choice of polynucleotide can be narrowed by first testing them for binding to "hot spot" regions of the genome of cancerous cells. If a polynucleotide is identified as binding to a "hot spot," testing the polynucleotide as an antisense compound in the corresponding cancer cells is warranted.

Dominant negative mutations also are readily generated for corresponding proteins that are active as homomultimers. A mutant polypeptide will interact with wild-type polypeptides (made from the other allele) and form a non-functional multimer. Thus, a mutation is in a substrate-binding domain, a catalytic

domain, or a cellular localization domain. Preferably, the mutant polypeptide will be overproduced. Point mutations are made that have such an effect. In addition, fusion of different polypeptides of various lengths to the terminus of a protein can yield dominant negative mutants. General strategies are available for making dominant negative mutants (see, e.g., Herskowitz, Nature (1987) 329:219). Such techniques can be used to create loss of function mutations, which are useful for determining protein function.

Polypeptides and Variants Thereof

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The polypeptides of the invention include those encoded by the disclosed polynucleotides, as well as nucleic acids that, by virtue of the degeneracy of the genetic code, are not identical in sequence to the disclosed polynucleotides. Thus, the invention includes within its scope a polypeptide encoded by a polynucleotide having the sequence of any one of SEQ ID NOs:1-3351 or a variant thereof.

In general, the term "polypeptide" as used herein refers to both the full length polypeptide encoded by the recited polynucleotide, the polypeptide encoded by the gene represented by the recited polynucleotide, as well as portions or fragments thereof. "Polypeptides" also includes variants of the naturally occurring proteins, where such variants are homologous or substantially similar to the naturally occurring protein, and can be of an origin of the same or different species as the naturally occurring protein (e.g., human, murine, or some other species that naturally expresses the recited polypeptide, usually a mammalian species). In general, variant polypeptides have a sequence that has at least about 80%, usually at least about 90%, and more usually at least about 98% sequence identity with a differentially expressed polypeptide of the invention, as measured by BLAST using the parameters described above. The variant polypeptides can be naturally or non-naturally glycosylated, i.e., the polypeptide has a glycosylation pattern that differs from the glycosylation pattern found in the corresponding naturally occurring protein.

The invention also encompasses homologs of the disclosed polypeptides (or fragments thereof) where the homologs are isolated from other species, *i.e.*, other animal or plant species, where such homologs, usually mammalian species, *e.g.*, rodents, such as mice, rats; domestic animals, *e.g.*, horse, cow, dog, cat; and humans. By "homolog" is meant a polypeptide having at least about 35%, usually at least about 40% and more usually at least about 60% amino acid sequence identity to a particular differentially expressed protein as identified above, where sequence identity is determined using the BLAST algorithm, with the parameters described above.

In general, the polypeptides of the subject invention are provided in a non-naturally occurring environment, e.g., are separated from their naturally occurring environment. In certain embodiments, the subject protein is present in a composition that is enriched for the protein as compared to a control. As such, purified polypeptide is provided, where by purified is meant that the protein is present in a composition that is substantially free of non-differentially expressed polypeptides, where by substantially free is meant that less than 90%, usually less than 60% and more usually less than 50% of the composition is made up of non-differentially expressed polypeptides.

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Also within the scope of the invention are variants; variants of polypeptides include mutants, fragments, and fusions. Mutants can include amino acid substitutions, additions or deletions. The amino acid substitutions can be conservative amino acid substitutions or substitutions to eliminate non-essential amino acids, such as to alter a glycosylation site, a phosphorylation site or an acetylation site, or to minimize misfolding by substitution or deletion of one or more cysteine residues that are not necessary for function. Conservative amino acid substitutions are those that preserve the general charge, hydrophobicity/ hydrophilicity, and/or steric bulk of the amino acid substituted. Variants can be designed so as to retain biological activity of a particular region of the protein (e.g., a functional domain and/or, where the polypeptide is a member of a protein family, a region associated with a consensus sequence). Selection of amino acid alterations for production of variants can be based upon the accessibility (interior vs. exterior) of the amino acid (see, e.g., Go et al., Int. J. Peptide Protein Res. (1980) 15:211), the thermostability of the variant polypeptide (see, e.g., Querol et al., Prot. Eng. (1996) 9:265), desired glycosylation sites (see, e.g., Olsen and Thomsen, J. Gen. Microbiol. (1991) 137:579), desired disulfide bridges (see, e.g., Clarke et al., Biochemistry (1993) 32:4322; and Wakarchuk et al., Protein Eng. (1994) 7:1379), desired metal binding sites (see, e.g., Toma et al., Biochemistry (1991) 30:97, and Haezerbrouck et al., Protein Eng. (1993) 6:643), and desired substitutions with in proline loops (see, e.g., Masul et al., Appl. Env. Microbiol. (1994) 60:3579). Cysteinedepleted muteins can be produced as disclosed in U.S. Patent No. 4,959,314.

Variants also include fragments of the polypeptides disclosed herein, particularly biologically active fragments and/or fragments corresponding to functional domains. Fragments of interest will typically be at least about 10 aa to at least about 15 aa in length, usually at least about 50 aa in length, and can be as long as 300 aa in length or longer, but will usually not exceed about 1000 aa in length, where the fragment will have a stretch of amino acids that is identical to a polypeptide encoded by a

polynucleotide having a sequence of any SEQ ID NOs:1-3351, or a homolog thereof. The protein variants described herein are encoded by polynucleotides that are within the scope of the invention. The genetic code can be used to select the appropriate codons to construct the corresponding variants.

Computer-Related Embodiments 5

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In general, a library of polynucleotides is a collection of sequence information, which information is provided in either biochemical form (e.g., as a collection of polynucleotide molecules), or in electronic form (e.g., as a collection of polynucleotide sequences stored in a computer-readable form, as in a computer system The sequence information of the and/or as part of a computer program). polynucleotides can be used in a variety of ways, e.g., as a resource for gene discovery, as a representation of sequences expressed in a selected cell type (e.g., cell type markers), and/or as markers of a given disease or disease state. In general, a disease marker is a representation of a gene product that is present in all cells affected by disease either at an increased or decreased level relative to a normal cell (e.g., a cell of the same or similar type that is not substantially affected by disease). For example, a polynucleotide sequence in a library can be a polynucleotide that represents an mRNA, polypeptide, or other gene product encoded by the polynucleotide, that is either overexpressed or underexpressed in a breast ductal cell affected by cancer relative to a normal (i.e., substantially disease-free) breast cell.

The nucleotide sequence information of the library can be embodied in any suitable form, e.g., electronic or biochemical forms. For example, a library of sequence information embodied in electronic form comprises an accessible computer data file (or, in biochemical form, a collection of nucleic acid molecules) that contains the representative nucleotide sequences of genes that are differentially expressed (e.g., overexpressed or underexpressed) as between, for example, i) a cancerous cell and a normal cell; ii) a cancerous cell and a dysplastic cell; iii) a cancerous cell and a cell affected by a disease or condition other than cancer; iv) a metastatic cancerous cell and a normal cell and/or non-metastatic cancerous cell; v) a malignant cancerous cell and a non-malignant cancerous cell (or a normal cell) and/or vi) a dysplastic cell relative to a normal cell. Other combinations and comparisons of cells affected by various diseases or stages of disease will be readily apparent to the ordinarily skilled artisan. Biochemical embodiments of the library include a collection of nucleic acids that have

the sequences of the genes in the library, where the nucleic acids can correspond to the entire gene in the library or to a fragment thereof, as described in greater detail below.

The polynucleotide libraries of the subject invention generally comprise sequence information of a plurality of polynucleotide sequences, where at least one of the polynucleotides has a sequence of any of SEQ ID NOs:1-3351. By plurality is meant at least 2, usually at least 3 and can include up to all of SEQ ID NOs:1-3351. The length and number of polynucleotides in the library will vary with the nature of the library, e.g., if the library is an oligonucleotide array, a cDNA array, a computer database of the sequence information, etc.

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Where the library is an electronic library, the nucleic acid sequence information can be present in a variety of media. "Media" refers to a manufacture, other than an isolated nucleic acid molecule, that contains the sequence information of the present invention. Such a manufacture provides the genome sequence or a subset thereof in a form that can be examined by means not directly applicable to the sequence as it exists in a nucleic acid. For example, the nucleotide sequence of the present invention, e.g., the nucleic acid sequences of any of the polynucleotides of SEQ ID NOs:1-3351, can be recorded on computer readable media, e.g., any medium that can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as a floppy disc, a hard disc storage medium, and a magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. One of skill in the art can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising a recording "Recorded" refers to a process for storing of the present sequence information. information on computer readable medium, using any such methods as known in the art. Any convenient data storage structure can be chosen, based on the means used to access the stored information. A variety of data processor programs and formats can be used for storage, e.g., word processing text file, database format, etc. In addition to the sequence information, electronic versions of the libraries of the invention can be provided in conjunction or connection with other computer-readable information and/or 30 other types of computer-readable files (e.g., searchable files, executable files, etc., including, but not limited to, for example, search program software, etc.).

By providing the nucleotide sequence in computer readable form, the information can be accessed for a variety of purposes. Computer software to access sequence information is publicly available. For example, the BLAST (Altschul et al.,

supra.) and BLAZE (Brutlag et al. Comp. Chem. (1993) 17:203) search algorithms on a Sybase system can be used to identify open reading frames (ORFs) within the genome that contain homology to ORFs from other organisms.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based system are suitable for use in the present invention. The data storage means can comprise any manufacture comprising a recording of the present sequence information as described above, or a memory access means that can access such a manufacture.

"Search means" refers to one or more programs implemented on the computer-based system, to compare a target sequence or target structural motif, or expression levels of a polynucleotide in a sample, with the stored sequence information. Search means can be used to identify fragments or regions of the genome that match a particular target sequence or target motif. A variety of known algorithms are publicly known and commercially available, e.g., MacPattern (EMBL), BLASTN and BLASTX (NCBI). A "target sequence" can be any polynucleotide or amino acid sequence of six or more contiguous nucleotides or two or more amino acids, preferably from about 10 to 100 amino acids or from about 30 to 300 nt. A variety of comparing means can be used to accomplish comparison of sequence information from a sample (e.g., to analyze target sequences, target motifs, or relative expression levels) with the data storage means. A skilled artisan can readily recognize that any one of the publicly available homology search programs can be used as the search means for the computer based systems of the present invention to accomplish comparison of target sequences and motifs. Computer programs to analyze expression levels in a sample and in controls are also known in the art.

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A "target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration that is formed upon the folding of the target motif, or on consensus sequences of regulatory or active sites. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are

not limited to, hairpin structures, promoter sequences and other expression elements such as binding sites for transcription factors.

A variety of structural formats for the input and output means can be used to input and output the information in the computer-based systems of the present invention. One format for an output means ranks the relative expression levels of different polynucleotides. Such presentation provides a skilled artisan with a ranking of relative expression levels to determine a gene expression profile.

As discussed above, the "library" of the invention also encompasses biochemical libraries of the polynucleotides of SEQ ID NOs:1-3351, e.g., collections of nucleic acids representing the provided polynucleotides. The biochemical libraries can take a variety of forms, e.g., a solution of cDNAs, a pattern of probe nucleic acids stably associated with a surface of a solid support (i.e., an array) and the like. Of particular interest are nucleic acid arrays in which one or more of SEQ ID NOs:1-3351 is represented on the array. By array is meant an article of manufacture that has at least a substrate with at least two distinct nucleic acid targets on one of its surfaces, where the number of distinct nucleic acids can be considerably higher, typically being at least 10 nt, usually at least 20 nt and often at least 25 nt. A variety of different array formats have been developed and are known to those of skill in the art. The arrays of the subject invention find use in a variety of applications, including gene expression analysis, drug screening, mutation analysis and the like, as disclosed in the above-listed exemplary patent documents.

In addition to the above nucleic acid libraries, analogous libraries of polypeptides are also provided, where the where the polypeptides of the library will represent at least a portion of the polypeptides encoded by SEQ ID NOs:1-3351.

25 Use of Polynucleotide Probes in Mapping, and in Tissue Profiling

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Polynucleotide probes, generally comprising at least 12 contiguous nt of a polynucleotide as shown in the Sequence Listing, are used for a variety of purposes, such as chromosome mapping of the polynucleotide and detection of transcription levels. Additional disclosure about preferred regions of the disclosed polynucleotide sequences is found in the Examples. A probe that hybridizes specifically to a polynucleotide disclosed herein should provide a detection signal at least 5-, 10-, or 20-fold higher than the background hybridization provided with other unrelated sequences.

<u>Detection of Expression Levels</u>. Nucleotide probes are used to detect expression of a gene corresponding to the provided polynucleotide. In Northern blots,

mRNA is separated electrophoretically and contacted with a probe. A probe is detected as hybridizing to an mRNA species of a particular size. The amount of hybridization is quantitated to determine relative amounts of expression, for example under a particular condition. Probes are used for *in situ* hybridization to cells to detect expression. Probes can also be used *in vivo* for diagnostic detection of hybridizing sequences. Probes are typically labeled with a radioactive isotope. Other types of detectable labels can be used such as chromophores, fluors, and enzymes. Other examples of nucleotide hybridization assays are described in WO92/02526 and U.S. Patent No. 5,124,246.

Alternatively, the Polymerase Chain Reaction (PCR) is another means for detecting small amounts of target nucleic acids (see, e.g., Mullis et al., Meth. Enzymol. (1987) 155:335; U.S. Patent No. 4,683,195; and U.S. Patent No. 4,683,202). Two primer polynucleotides nucleotides that hybridize with the target nucleic acids are used to prime the reaction. The primers can be composed of sequence within or 3' and 5' to the polynucleotides of the Sequence Listing. Alternatively, if the primers are 3' and 5' to these polynucleotides, they need not hybridize to them or the complements. After 15 amplification of the target with a thermostable polymerase, the amplified target nucleic acids can be detected by methods known in the art, e.g., Southern blot. mRNA or cDNA can also be detected by traditional blotting techniques (e.g., Southern blot, Northern blot, etc.) described in Sambrook et al., "Molecular Cloning: A Laboratory Manual" (New York, Cold Spring Harbor Laboratory, 1989) (e.g., without PCR 20 amplification). In general, mRNA or cDNA generated from mRNA using a polymerase enzyme can be purified and separated using gel electrophoresis, and transferred to a solid support, such as nitrocellulose. The solid support is exposed to a labeled probe, washed to remove any unhybridized probe, and duplexes containing the labeled probe are detected. 25

Mapping. Polynucleotides of the present invention can be used to identify a chromosome on which the corresponding gene resides. Such mapping can be useful in identifying the function of the polynucleotide-related gene by its proximity to other genes with known function. Function can also be assigned to the polynucleotide-related gene when particular syndromes or diseases map to the same chromosome. For example, use of polynucleotide probes in identification and quantification of nucleic acid sequence aberrations is described in U.S. Patent No. 5,783,387. An exemplary mapping method is fluorescence in situ hybridization (FISH), which facilitates comparative genomic hybridization to allow total genome assessment of changes in relative copy number of DNA sequences (see, e.g., Valdes et al., Methods in Molecular

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Biology (1997) 68:1). Polynucleotides can also be mapped to particular chromosomes using, for example, radiation hybrids or chromosome-specific hybrid panels. See Leach et al., Advances in Genetics, (1995) 33:63-99; Walter et al., Nature Genetics (1994) 7:22; Walter and Goodfellow, Trends in Genetics (1992) 9:352. Panels for radiation hybrid mapping are available from Research Genetics, Inc., Huntsville, Alabama, USA. The statistical program RHMAP can be used to construct a map based on the data from radiation hybridization with a measure of the relative likelihood of one order versus another. RHMAP is available via the world wide web at http://www.sph.umich.edu/group/statgen/software. In addition, commercial programs are available for identifying regions of chromosomes commonly associated with disease, such as cancer.

Tissue Typing or Profiling. Expression of specific mRNA corresponding to the provided polynucleotides can vary in different cell types and can be tissue-specific. This variation of mRNA levels in different cell types can be exploited with nucleic acid probe assays to determine tissue types. For example, PCR, branched DNA probe assays, or blotting techniques utilizing nucleic acid probes substantially identical or complementary to polynucleotides listed in the Sequence Listing can determine the presence or absence of the corresponding cDNA or mRNA.

Tissue typing can be used to identify the developmental organ or tissue source of a metastatic lesion by identifying the expression of a particular marker of that organ or tissue. If a polynucleotide is expressed only in a specific tissue type, and a metastatic lesion is found to express that polynucleotide, then the developmental source of the lesion has been identified. Expression of a particular polynucleotide can be assayed by detection of either the corresponding mRNA or the protein product.

<u>Use of Polymorphisms</u>. A polynucleotide of the invention can be used in forensics, genetic analysis, mapping, and diagnostic applications where the corresponding region of a gene is polymorphic in the human population. Any means for detecting a polymorphism in a gene can be used, including, but not limited to electrophoresis of protein polymorphic variants, differential sensitivity to restriction enzyme cleavage, and hybridization to allele-specific probes.

30 Antibody Production

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Expression products of a polynucleotide of the invention, as well as the corresponding mRNA, cDNA, or complete gene, can be prepared and used for raising antibodies for experimental, diagnostic, and therapeutic purposes. For polynucleotides to which a corresponding gene has not been assigned, this provides an additional

method of identifying the corresponding gene. The polynucleotide or related cDNA is expressed as described above, and antibodies are prepared. These antibodies are specific to an epitope on the polypeptide encoded by the polynucleotide, and can precipitate or bind to the corresponding native protein in a cell or tissue preparation or in a cell-free extract of an *in vitro* expression system.

Methods for production of monoclonal and polyclonal antibodies that specifically bind a selected antigen are well known in the art. The antibodies specifically bind to epitopes present in the polypeptides encoded by polynucleotides disclosed in the Sequence Listing. Typically, at least 6, 8, 10, or 12 contiguous amino acids are required to form an epitope. Epitopes that involve non-contiguous amino acids may require a longer polypeptide, e.g., at least 15, 25, or 50 amino acids. Antibodies that specifically bind to human polypeptides encoded by the provided polynucleotides should provide a detection signal at least 5-, 10-, or 20-fold higher than a detection signal provided with other proteins when used in Western blots or other immunochemical assays. Preferably, antibodies that specifically polypeptides of the invention do not bind to other proteins in immunochemical assays at detectable levels and can immunoprecipitate the specific polypeptide from solution.

The invention also contemplates naturally occurring antibodies specific for a polypeptide of the invention. For example, serum antibodies to a polypeptide of the invention in a human population can be purified by methods well known in the art, e.g., by passing antiserum over a column to which the corresponding selected polypeptide or fusion protein is bound. The bound antibodies can then be eluted from the column, for example using a buffer with a high salt concentration.

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In addition to the antibodies discussed above, the invention also contemplates genetically engineered antibodies, antibody derivatives (e.g., single chain antibodies, antibody fragments (e.g., Fab, etc.)), according to methods well known in the art.

Other embodiments of the present invention include humanized monoclonal antibodies capable of binding to the polypeptides of the invention. The phrase "humanized antibody" refers to an antibody derived from a non-human antibody - typically a mouse monoclonal antibody. Alternatively, a humanized antibody may be derived from a chimeric antibody that retains or substantially retains the antigen-binding properties of the parental, non-human, antibody but which exhibits diminished immunogenicity as compared to the parental antibody when administered to humans. The phrase "chimeric antibody," as used herein, refers to an antibody containing

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sequence derived from two different antibodies (see, e.g., U.S. Patent No. 4,816,567) which typically originate from different species. Most typically, chimeric antibodies comprise human and murine antibody fragments, generally human constant and mouse variable regions.

Because humanized antibodies are far less immunogenic in humans than the parental mouse monoclonal antibodies, they can be used for the treatment of humans with far less risk of anaphylaxis. Thus, these antibodies may be preferred in therapeutic applications that involve *in vivo* administration to a human such as, *e.g.*, use as radiation sensitizers for the treatment of neoplastic disease or use in methods to reduce the side effects of, *e.g.*, cancer therapy.

Humanized antibodies may be achieved by a variety of methods including, for example: (1) grafting the non-human complementarity determining regions (CDRs) onto a human framework and constant region (a process referred to in the art as "humanizing"), or, alternatively, (2) transplanting the entire non-human variable domains, but "cloaking" them with a human-like surface by replacement of surface residues (a process referred to in the art as "veneering"). In the present invention, humanized antibodies will include both "humanized" and "veneered" antibodies. These methods are disclosed in, e.g., Jones et al., Nature 321:522-525 (1986); Morrison et al., Proc. Natl. Acad. Sci., U.S.A., 81:6851-6855 (1984); Morrison and Oi, Adv. Immunol., 44:65-92 (1988); Verhoeyer et al., Science 239:1534-1536 (1988); Padlan, Molec. Immun. 28:489-498 (1991); Padlan, Molec. Immunol. 31(3):169-217 (1994); and Kettleborough, C.A. et al., Protein Eng. 4(7):773-83 (1991) each of which is incorporated herein by reference.

The phrase "complementarity determining region" refers to amino acid sequences which together define the binding affinity and specificity of the natural Fv region of a native immunoglobulin binding site. See, e.g., Chothia et al., J. Mol. Biol. 196:901-917 (1987); Kabat et al., U.S. Dept. of Health and Human Services NIH Publication No. 91-3242 (1991). The phrase "constant region" refers to the portion of the antibody molecule that confers effector functions. In the present invention, mouse constant regions are substituted by human constant regions. The constant regions of the subject humanized antibodies are derived from human immunoglobulins. The heavy chain constant region can be selected from any of the five isotypes: alpha, delta, epsilon, gamma or mu.

One method of humanizing antibodies comprises aligning the nonhuman heavy and light chain sequences to human heavy and light chain sequences,

selecting and replacing the non-human framework with a human framework based on such alignment, molecular modeling to predict the conformation of the humanized sequence and comparing to the conformation of the parent antibody. This process is followed by repeated back mutation of residues in the CDR region which disturb the structure of the CDRs until the predicted conformation of the humanized sequence model closely approximates the conformation of the non-human CDRs of the parent non-human antibody. Such humanized antibodies may be further derivatized to facilitate uptake and clearance, e.g., via Ashwell receptors. See, e.g., U.S. Patent Nos. 5,530,101 and 5,585,089 which patents are incorporated herein by reference.

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Humanized antibodies can also be produced using transgenic animals that are engineered to contain human immunoglobulin loci. For example, WO 98/24893 discloses transgenic animals having a human Ig locus wherein the animals do not produce functional endogenous immunoglobulins due to the inactivation of endogenous heavy and light chain loci. WO 91/10741 also discloses transgenic non-primate mammalian hosts capable of mounting an immune response to an immunogen, wherein the antibodies have primate constant and/or variable regions, and wherein the endogenous immunoglobulin-encoding loci are substituted or inactivated. WO 96/30498 discloses the use of the Cre/Lox system to modify the immunoglobulin locus in a mammal, such as to replace all or a portion of the constant or variable region to form a modified antibody molecule. WO 94/02602 discloses non-human mammalian hosts having inactivated endogenous Ig loci and functional human Ig loci. U.S. Patent No. 5,939,598 discloses methods of making transgenic mice in which the mice lack endogenous heavy claims, and express an exogenous immunoglobulin locus comprising one or more xenogeneic constant regions.

Using a transgenic animal described above, an immune response can be produced to a selected antigenic molecule, and antibody-producing cells can be removed from the animal and used to produce hybridomas that secrete human monoclonal antibodies. Immunization protocols, adjuvants, and the like are known in the art, and are used in immunization of, for example, a transgenic mouse as described in WO 96/33735. This publication discloses monoclonal antibodies against a variety of antigenic molecules including IL-6, IL-8, TNF, human CD4, L-selectin, gp39, and tetanus toxin. The monoclonal antibodies can be tested for the ability to inhibit or neutralize the biological activity or physiological effect of the corresponding protein. WO 96/33735 discloses that monoclonal antibodies against IL-8, derived from immune cells of transgenic mice immunized with IL-8, blocked IL-8-induced functions of

Human monoclonal antibodies with specificity for the antigen used to neutrophils. immunize transgenic animals are also disclosed in WO 96/34096.

Polynucleotides or Arrays for Diagnostics

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Polynucleotide arrays are created by spotting polynucleotide probes onto a substrate (e.g., glass, nitrocellose, etc.) in a two-dimensional matrix or array having bound probes. The probes can be bound to the substrate by either covalent bonds or by non-specific interactions, such as hydrophobic interactions. Samples of polynucleotides can be detectably labeled (e.g., using radioactive or fluorescent labels) and then hybridized to the probes. Double stranded polynucleotides, comprising the labeled sample polynucleotides bound to probe polynucleotides, can be detected once the unbound portion of the sample is washed away. Techniques for constructing arrays and methods of using these arrays are described in EP 799 897; WO 97/29212; WO 97/27317; EP 785 280; WO 97/02357; U.S. Patent No. 5,593,839; U.S. Patent No. 5,578,832; EP 728 520; U.S. Patent No. 5,599,695; EP 721 016; U.S. Patent No. 5,556,752; WO 95/22058; and U.S. Patent No. 5,631,734. Arrays can be used to, for example, examine differential expression of genes and can be used to determine gene For example, arrays can be used to detect differential expression of a polynucleotide between a test cell and control cell (e.g., cancer cells and normal cells). For example, high expression of a particular message in a cancer cell, which is not 20 observed in a corresponding normal cell, can indicate a cancer specific gene product. Exemplary uses of arrays are further described in, for example, Pappalarado et al., Sem. Radiation Oncol. (1998) 8:217; and Ramsay, Nature Biotechnol. (1998) 16:40.

Differential Expression in Diagnosis

The polynucleotides of the invention can also be used to detect differences in expression levels between two cells, e.g., as a method to identify abnormal or diseased tissue in a human. For polynucleotides corresponding to profiles of protein families, the choice of tissue can be selected according to the putative biological function. In general, the expression of a gene corresponding to a specific polynucleotide is compared between a first tissue that is suspected of being diseased and a second, normal tissue of the human. The tissue suspected of being abnormal or diseased can be derived from a different tissue type of the human, but preferably it is derived from the same tissue type; for example an intestinal polyp or other abnormal growth should be compared with normal intestinal tissue. The normal tissue can be the

same tissue as that of the test sample, or any normal tissue of the patient, especially those that express the polynucleotide-related gene of interest (e.g., brain, thymus, testis, heart, prostate, placenta, spleen, small intestine, skeletal muscle, pancreas, and the mucosal lining of the colon). A difference between the polynucleotide-related gene, mRNA, or protein in the two tissues which are compared, for example in molecular weight, amino acid or nucleotide sequence, or relative abundance, indicates a change in the gene, or a gene which regulates it, in the tissue of the human that was suspected of being diseased. Examples of detection of differential expression and its use in diagnosis of cancer are described in U.S. Patent Nos. 5,688,641 and 5,677,125.

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A genetic predisposition to disease in a human can also be detected by comparing expression levels of an mRNA or protein corresponding to a polynucleotide of the invention in a fetal tissue with levels associated in normal fetal tissue. Fetal tissues that are used for this purpose include, but are not limited to, amniotic fluid, chorionic villi, blood, and the blastomere of an in vitro-fertilized embryo. comparable normal polynucleotide-related gene is obtained from any tissue. The mRNA or protein is obtained from a normal tissue of a human in which the polynucleotiderelated gene is expressed. Differences such as alterations in the nucleotide sequence or size of the same product of the fetal polynucleotide-related gene or mRNA, or alterations in the molecular weight, amino acid sequence, or relative abundance of fetal protein, can indicate a germline mutation in the polynucleotide-related gene of the fetus, which indicates a genetic predisposition to disease. In general, diagnostic, prognostic, and other methods of the invention based on differential expression involve detection of a level or amount of a gene product, particularly a differentially expressed gene product, in a test sample obtained from a patient suspected of having or being susceptible to a disease (e.g., breast cancer, lung cancer, colon cancer and/or metastatic forms thereof), and comparing the detected levels to those levels found in normal cells (e.g., cells substantially unaffected by cancer) and/or other control cells (e.g., to differentiate a cancerous cell from a cell affected by dysplasia). Furthermore, the severity of the disease can be assessed by comparing the detected levels of a differentially expressed gene product with those levels detected in samples representing the levels of differentially gene product associated with varying degrees of severity of disease. It should be noted that use of the term "diagnostic" herein is not necessarily meant to exclude "prognostic" or "prognosis," but rather is used as a matter of convenience.

The term "differentially expressed gene" is generally intended to encompass a polynucleotide that can, for example, include an open reading frame

encoding a gene product (e.g., a polypeptide), and/or introns of such genes and adjacent 5' and 3' non-coding nucleotide sequences involved in the regulation of expression, up to about 20 kb beyond the coding region, but possibly further in either direction. The gene can be introduced into an appropriate vector for extrachromosomal maintenance or for integration into a host genome. In general, a difference in expression level associated with a decrease in expression level of at least about 25%, usually at least about 50% to 75%, more usually at least about 90% or more is indicative of a differentially expressed gene of interest, i.e., a gene that is underexpressed or down-regulated in the test sample relative to a control sample. Furthermore, a difference in expression level associated with an increase in expression of at least about 25%, usually at least about 50% to 75%, more usually at least about 90% and can be at least about 1½-fold, usually at least about 2-fold to about 10-fold, and can be about 100-fold to about 1,000-fold increase relative to a control sample is indicative of a differentially expressed gene of interest, i.e., an overexpressed or up-regulated gene.

"Differentially expressed polynucleotide" as used herein means a nucleic acid molecule (RNA or DNA) comprising a sequence that represents a differentially expressed gene, e.g., the differentially expressed polynucleotide comprises a sequence (e.g., an open reading frame encoding a gene product) that uniquely identifies a differentially expressed gene so that detection of the differentially expressed polynucleotide in a sample is correlated with the presence of a differentially expressed gene in a sample. "Differentially expressed polynucleotides" is also meant to encompass fragments of the disclosed polynucleotides, e.g., fragments retaining biological activity, as well as nucleic acids homologous, substantially similar, or substantially identical (e.g., having about 90% sequence identity) to the disclosed polynucleotides.

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"Diagnosis" as used herein generally includes determination of a subject's susceptibility to a disease or disorder, determination as to whether a subject is presently affected by a disease or disorder, as well as to the prognosis of a subject affected by a disease or disorder (e:g., identification of pre-metastatic or metastatic cancerous states, stages of cancer, or responsiveness of cancer to therapy). The present invention particularly encompasses diagnosis of subjects in the context of breast cancer (e.g., carcinoma in situ (e.g., ductal carcinoma in situ), estrogen receptor (ER)-positive breast cancer, ER-negative breast cancer, or other forms and/or stages of breast cancer), lung cancer (e.g., small cell carcinoma, non-small cell carcinoma, mesothelioma, and

other forms and/or stages of lung cancer), and colon cancer (e.g., adenomatous polyp, colorectal carcinoma, and other forms and/or stages of colon cancer).

"Sample" or "biological sample" as used throughout here are generally meant to refer to samples of biological fluids or tissues, particularly samples obtained from tissues, especially from cells of the type associated with the disease for which the diagnostic application is designed (e.g., ductal adenocarcinoma), and the like. "Samples" is also meant to encompass derivatives and fractions of such samples (e.g., cell lysates). Where the sample is solid tissue, the cells of the tissue can be dissociated or tissue sections can be analyzed.

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Methods of the subject invention useful in diagnosis or prognosis typically involve comparison of the abundance of a selected differentially expressed gene product in a sample of interest with that of a control to determine any relative differences in the expression of the gene product, where the difference can be measured qualitatively and/or quantitatively. Quantitation can be accomplished, for example, by comparing the level of expression product detected in the sample with the amounts of product present in a standard curve. A comparison can be made visually; by using a technique such as densitometry, with or without computerized assistance; by preparing a representative library of cDNA clones of mRNA isolated from a test sample, sequencing the clones in the library to determine that number of cDNA clones corresponding to the same gene product, and analyzing the number of clones corresponding to that same gene product relative to the number of clones of the same gene product in a control sample; or by using an array to detect relative levels of hybridization to a selected sequence or set of sequences, and comparing the hybridization pattern to that of a control. The differences in expression are then correlated with the presence or absence of an abnormal expression pattern. A variety of different methods for determining the nucleic acid abundance in a sample are known to those of skill in the art (see, e.g., WO 97/27317). In general, diagnostic assays of the invention involve detection of a gene product of a the polynucleotide sequence (e.g., mRNA or polypeptide) that corresponds to a sequence of SEQ ID NOs:1-3351. The patient from whom the sample is obtained can be apparently healthy, susceptible to 30 disease (e.g., as determined by family history or exposure to certain environmental factors), or can already be identified as having a condition in which altered expression of a gene product of the invention is implicated.

Diagnosis can be determined based on detected gene product expression levels of a gene product encoded by at least one, preferably at least two or more, at least 35

3 or more, or at least 4 or more of the polynucleotides having a sequence set forth in SEQ ID NOs:1-3351, and can involve detection of expression of genes corresponding to all of SEQ ID NOs:1-3351 and/or additional sequences that can serve as additional diagnostic markers and/or reference sequences. Where the diagnostic method is designed to detect the presence or susceptibility of a patient to cancer, the assay preferably involves detection of a gene product encoded by a gene corresponding to a polynucleotide that is differentially expressed in cancer. Examples of such differentially expressed polynucleotides are described in the Examples below. Given the provided polynucleotides and information regarding their relative expression levels provided herein, assays using such polynucleotides and detection of their expression levels in diagnosis and prognosis will be readily apparent to the ordinarily skilled artisan.

Any of a variety of detectable labels can be used in connection with the various embodiments of the diagnostic methods of the invention. Suitable detectable labels include fluorochromes, (e.g., fluorescein isothiocyanate (FITC), rhodamine, Texas Red, phycoerythrin, allophycocyanin, 6-carboxyfluorescein (6-FAM), 2',7'-dimethoxy-4',5'-dichloro-6-carboxyfluorescein, 6-carboxy-X-rhodamine (ROX), 6-carboxy-2',4',7',4,7-hexachlorofluorescein (HEX), 5-carboxyfluorescein (5-FAM) or N,N,N',N'-tetramethyl-6-carboxyrhodamine (TAMRA)), radioactive labels, (e.g., ³²P, ³⁵S, ³H, etc.), and the like. The detectable label can involve a two stage systems (e.g., biotin-avidin, hapten-anti-hapten antibody, etc.)

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Reagents specific for the polynucleotides and polypeptides of the invention, such as antibodies and nucleotide probes, can be supplied in a kit for detecting the presence of an expression product in a biological sample. The kit can also contain buffers or labeling components, as well as instructions for using the reagents to detect and quantify expression products in the biological sample. Exemplary embodiments of the diagnostic methods of the invention are described below in more detail.

Polypeptide detection in diagnosis. In one embodiment, the test sample is assayed for the level of a differentially expressed polypeptide. Diagnosis can be accomplished using any of a number of methods to determine the absence or presence or altered amounts of the differentially expressed polypeptide in the test sample. For example, detection can utilize staining of cells or histological sections with labeled antibodies, performed in accordance with conventional methods. Cells can be permeabilized to stain cytoplasmic molecules. In general, antibodies that specifically bind a differentially expressed polypeptide of the invention are added to a sample, and

incubated for a period of time sufficient to allow binding to the epitope, usually at least about 10 minutes. The antibody can be detectably labeled for direct detection (e.g., using radioisotopes, enzymes, fluorescers, chemiluminescers, and the like), or can be used in conjunction with a second stage antibody or reagent to detect binding (e.g., biotin with horseradish peroxidase-conjugated avidin, a secondary antibody conjugated to a fluorescent compound, e.g., fluorescein, rhodamine, Texas red, etc.). The absence or presence of antibody binding can be determined by various methods, including flow cytometry of dissociated cells, microscopy, radiography, scintillation counting, etc. Any suitable alternative methods can of qualitative or quantitative detection of levels or amounts of differentially expressed polypeptide can be used, for example ELISA, western blot, immunoprecipitation, radioimmunoassay, etc.

mRNA detection. The diagnostic methods of the invention can also or alternatively involve detection of mRNA encoded by a gene corresponding to a differentially expressed polynucleotides of the invention. Any suitable qualitative or quantitative methods known in the art for detecting specific mRNAs can be used. mRNA can be detected by, for example, in situ hybridization in tissue sections, by reverse transcriptase-PCR, or in Northern blots containing poly A+ mRNA. One of skill in the art can readily use these methods to determine differences in the size or amount of mRNA transcripts between two samples. mRNA expression levels in a sample can also be determined by generation of a library of expressed sequence tags (ESTs) from the sample, where the EST library is representative of sequences present in the sample (Adams, et al., (1991) Science 252:1651). Enumeration of the relative representation of ESTs within the library can be used to approximate the relative representation of the gene transcript within the starting sample. The results of EST analysis of a test sample can then be compared to EST analysis of a reference sample to determine the relative expression levels of a selected polynucleotide, particularly a polynucleotide corresponding to one or more of the differentially expressed genes described herein. Alternatively, gene expression in a test sample can be performed using serial analysis of gene expression (SAGE) methodology (e.g., Velculescu et al., Science (1995) 270:484) or differential display (DD) methodology (see, e.g., U.S. Patent NOs. 5,776,683 and 5,807,680).

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Alternatively, gene expression can be analyzed using hybridization analysis. Oligonucleotides or cDNA can be used to selectively identify or capture DNA or RNA of specific sequence composition, and the amount of RNA or cDNA hybridized to a known capture sequence determined qualitatively or quantitatively, to provide

information about the relative representation of a particular message within the pool of cellular messages in a sample. Hybridization analysis can be designed to allow for concurrent screening of the relative expression of hundreds to thousands of genes by using, for example, array-based technologies having high density formats, including filters, microscope slides, or microchips, or solution-based technologies that use spectroscopic analysis (e.g., mass spectrometry). One exemplary use of arrays in the diagnostic methods of the invention is described below in more detail.

Use of a single gene in diagnostic applications. The diagnostic methods of the invention can focus on the expression of a single differentially expressed gene. For example, the diagnostic method can involve detecting a differentially expressed gene, or a polymorphism of such a gene (e.g., a polymorphism in an coding region or control region), that is associated with disease. Disease-associated polymorphisms can include deletion or truncation of the gene, mutations that alter expression level and/or affect activity of the encoded protein, etc.

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A number of methods are available for analyzing nucleic acids for the presence of a specific sequence, e.g., a disease associated polymorphism. Where large amounts of DNA are available, genomic DNA is used directly. Alternatively, the region of interest is cloned into a suitable vector and grown in sufficient quantity for analysis. Cells that express a differentially expressed gene can be used as a source of mRNA, which can be assayed directly or reverse transcribed into cDNA for analysis. The nucleic acid can be amplified by conventional techniques, such as the polymerase chain reaction (PCR), to provide sufficient amounts for analysis, and a detectable label can be included in the amplification reaction (e.g., using a detectably labeled primer or detectably labeled oligonucleotides) to facilitate detection. Alternatively, various methods are also known in the art that utilize oligonucleotide ligation as a means of detecting polymorphisms, see e.g., Riley et al., Nucl. Acids Res. (1990) 18:2887; and Delahunty et al., Am. J. Hum. Genet. (1996) 58:1239.

The amplified or cloned sample nucleic acid can be analyzed by one of a number of methods known in the art. The nucleic acid can be sequenced by dideoxy or other methods, and the sequence of bases compared to a selected sequence, e.g., to a wild-type sequence. Hybridization with the polymorphic or variant sequence can also be used to determine its presence in a sample (e.g., by Southern blot, dot blot, etc.). The hybridization pattern of a polymorphic or variant sequence and a control sequence to an array of oligonucleotide probes immobilized on a solid support, as described in U.S. Patent No. 5,445,934, or in WO 95/35505, can also be used as a means of identifying

polymorphic or variant sequences associated with disease. Single strand conformational polymorphism (SSCP) analysis, denaturing gradient gel electrophoresis (DGGE), and heteroduplex analysis in gel matrices are used to detect conformational changes created by DNA sequence variation as alterations in electrophoretic mobility. Alternatively, where a polymorphism creates or destroys a recognition site for a restriction endonuclease, the sample is digested with that endonuclease, and the products size fractionated to determine whether the fragment was digested. Fractionation is performed by gel or capillary electrophoresis, particularly acrylamide or agarose gels.

Screening for mutations in a gene can be based on the functional or antigenic characteristics of the protein. Protein truncation assays are useful in detecting deletions that can affect the biological activity of the protein. Various immunoassays designed to detect polymorphisms in proteins can be used in screening. Where many diverse genetic mutations lead to a particular disease phenotype, functional protein assays have proven to be effective screening tools. The activity of the encoded protein can be determined by comparison with the wild-type protein.

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Pattern matching in diagnosis using arrays. In another embodiment, the diagnostic and/or prognostic methods of the invention involve detection of expression of a selected set of genes in a test sample to produce a test expression pattern (TEP). The TEP is compared to a reference expression pattern (REP), which is generated by detection of expression of the selected set of genes in a reference sample (e.g., a positive or negative control sample). The selected set of genes includes at least one of the genes of the invention, which genes correspond to the polynucleotide sequences of SEQ ID NOs:1-3351. Of particular interest is a selected set of genes that includes genes differentially expressed in the disease for which the test sample is to be screened.

"Reference sequences" or "reference polynucleotides" as used herein in the context of differential gene expression analysis and diagnosis/prognosis refers to a selected set of polynucleotides, which selected set includes at least one or more of the differentially expressed polynucleotides described herein. A plurality of reference sequences, preferably comprising positive and negative control sequences, can be included as reference sequences. Additional suitable reference sequences are found in Genbank, Unigene, and other nucleotide sequence databases (including, e.g., expressed sequence tag (EST), partial, and full-length sequences).

"Reference array" means an array having reference sequences for use in hybridization with a sample, where the reference sequences include all, at least one of,

or any subset of the differentially expressed polynucleotides described herein. Usually such an array will include at least 3 different reference sequences, and can include any one or all of the provided differentially expressed sequences. Arrays of interest can further comprise sequences, including polymorphisms, of other genetic sequences, particularly other sequences of interest for screening for a disease or disorder (e.g., cancer, dysplasia, or other related or unrelated diseases, disorders, or conditions). The oligonucleotide sequence on the array will usually be at least about 12 nt in length, and can be of about the length of the provided sequences, or can extend into the flanking regions to generate fragments of 100 nt to 200 nt in length or more. Reference arrays can be produced according to any suitable methods known in the art. For example, methods of producing large arrays of oligonucleotides are described in U.S. Patent NOs. 5,134,854 and 5,445,934 using light-directed synthesis techniques. Using a computer controlled system, a heterogeneous array of monomers is converted, through simultaneous coupling at a number of reaction sites, into a heterogeneous array of polymers. Alternatively, microarrays are generated by deposition of pre-synthesized oligonucleotides onto a solid substrate, for example as described in PCT published 15 application no. WO 95/35505.

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A "reference expression pattern" or "REP" as used herein refers to the relative levels of expression of a selected set of genes, particularly of differentially expressed genes, that is associated with a selected cell type, e.g., a normal cell, a cancerous cell, a cell exposed to an environmental stimulus, and the like. A "test expression pattern" or "TEP" refers to relative levels of expression of a selected set of genes, particularly of differentially expressed genes, in a test sample (e.g., a cell of unknown or suspected disease state, from which mRNA is isolated).

REPs can be generated in a variety of ways according to methods well known in the art. For example, REPs can be generated by hybridizing a control sample to an array having a selected set of polynucleotides (particularly a selected set of differentially expressed polynucleotides), acquiring the hybridization data from the array, and storing the data in a format that allows for ready comparison of the REP with a TEP. Alternatively, all expressed sequences in a control sample can be isolated and sequenced, e.g., by isolating mRNA from a control sample, converting the mRNA into cDNA, and sequencing the cDNA. The resulting sequence information roughly or precisely reflects the identity and relative number of expressed sequences in the sample. The sequence information can then be stored in a format (e.g., a computer-readable format) that allows for ready comparison of the REP with a TEP. The REP can be

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normalized prior to or after data storage, and/or can be processed to selectively remove sequences of expressed genes that are of less interest or that might complicate analysis (e.g., some or all of the sequences associated with housekeeping genes can be eliminated from REP data).

TEPs can be generated in a manner similar to REPs, e.g., by hybridizing a test sample to an array having a selected set of polynucleotides, particularly a selected set of differentially expressed polynucleotides, acquiring the hybridization data from the array, and storing the data in a format that allows for ready comparison of the TEP with a REP. The REP and TEP to be used in a comparison can be generated simultaneously, or the TEP can be compared to previously generated and stored REPs.

In one embodiment of the invention, comparison of a TEP with a REP involves hybridizing a test sample with a reference array, where the reference array has one or more reference sequences for use in hybridization with a sample. The reference sequences include all, at least one of, or any subset of the differentially expressed polynucleotides described herein. Hybridization data for the test sample is acquired, the data normalized, and the produced TEP compared with a REP generated using an array having the same or similar selected set of differentially expressed polynucleotides. Probes that correspond to sequences differentially expressed between the two samples will show decreased or increased hybridization efficiency for one of the samples relative to the other.

Methods for collection of data from hybridization of samples with a reference arrays are well known in the art. For example, the polynucleotides of the reference and test samples can be generated using a detectable fluorescent label, and hybridization of the polynucleotides in the samples detected by scanning the microarrays for the presence of the detectable label using, for example, a microscope and light source for directing light at a substrate. A photon counter detects fluorescence from the substrate, while an x-y translation stage varies the location of the substrate. A confocal detection device that can be used in the subject methods is described in U.S. Patent No. 5,631,734. A scanning laser microscope is described in Shalon et al., Genome Res. (1996) 6:639. A scan, using the appropriate excitation line, is performed for each fluorophore used. The digital images generated from the scan are then combined for subsequent analysis. For any particular array element, the ratio of the fluorescent signal from one sample (e.g., a test sample) is compared to the fluorescent signal from another sample (e.g., a reference sample), and the relative signal intensity determined.

Methods for analyzing the data collected from hybridization to arrays are well known in the art. For example, where detection of hybridization involves a fluorescent label, data analysis can include the steps of determining fluorescent intensity as a function of substrate position from the data collected, removing outliers, *i.e.*, data deviating from a predetermined statistical distribution, and calculating the relative binding affinity of the targets from the remaining data. The resulting data can be displayed as an image with the intensity in each region varying according to the binding affinity between targets and probes.

In general, the test sample is classified as having a gene expression profile corresponding to that associated with a disease or non-disease state by comparing the TEP generated from the test sample to one or more REPs generated from reference samples (e.g., from samples associated with cancer or specific stages of cancer, dysplasia, samples affected by a disease other than cancer, normal samples, etc.). The criteria for a match or a substantial match between a TEP and a REP include expression of the same or substantially the same set of reference genes, as well as expression of these reference genes at substantially the same levels (e.g., no significant difference between the samples for a signal associated with a selected reference sequence after normalization of the samples, or at least no greater than about 25% to about 40% difference in signal strength for a given reference sequence. In general, a pattern match between a TEP and a REP includes a match in expression, preferably a match in qualitative or quantitative expression level, of at least one of, all or any subset of the differentially expressed genes of the invention.

Pattern matching can be performed manually, or can be performed using a computer program. Methods for preparation of substrate matrices (e.g., arrays), design of oligonucleotides for use with such matrices, labeling of probes, hybridization conditions, scanning of hybridized matrices, and analysis of patterns generated, including comparison analysis, are described in, for example, U.S. Patent No. 5,800,992.

Diagnosis, Prognosis and Management of Cancer

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The polynucleotides of the invention and their gene products are of particular interest as genetic or biochemical markers (e.g., in blood or tissues) that will detect the earliest changes along the carcinogenesis pathway and/or to monitor the efficacy of various therapies and preventive interventions. For example, the level of expression of certain polynucleotides can be indicative of a poorer prognosis, and

therefore warrant more aggressive chemo- or radio-therapy for a patient or vice versa. The correlation of novel surrogate tumor specific features with response to treatment and outcome in patients can define prognostic indicators that allow the design of tailored therapy based on the molecular profile of the tumor. These therapies include antibody targeting and gene therapy. Determining expression of certain polynucleotides and comparison of a patients profile with known expression in normal tissue and variants of the disease allows a determination of the best possible treatment for a patient, both in terms of specificity of treatment and in terms of comfort level of the patient. Surrogate tumor markers, such as polynucleotide expression, can also be used to better classify, and thus diagnose and treat, different forms and disease states of cancer. Two classifications widely used in oncology that can benefit from identification of the expression levels of the polynucleotides of the invention are staging of the cancerous disorder, and grading the nature of the cancerous tissue.

The polynucleotides of the invention can be useful to monitor patients having or susceptible to cancer to detect potentially malignant events at a molecular level before they are detectable at a gross morphological level. Furthermore, a polynucleotide of the invention identified as important for one type of cancer can also have implications for development or risk of development of other types of cancer, e.g., where a polynucleotide is differentially expressed across various cancer types. Thus, for example, expression of a polynucleotide that has clinical implications for metastatic colon cancer can also have clinical implications for stomach cancer or endometrial cancer.

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Staging. Staging is a process used by physicians to describe how advanced the cancerous state is in a patient. Generally, if a cancer is only detectable in the area of the primary lesion without having spread to any lymph nodes it is called Stage I. If it has spread only to the closest lymph nodes, it is called Stage II. In Stage III, the cancer has generally spread to the lymph nodes in near proximity to the site of the primary lesion. Cancers that have spread to a distant part of the body, such as the liver, bone, brain or other site, are Stage IV, the most advanced stage.

The polynucleotides of the invention can facilitate fine-tuning of the staging process by identifying markers for the aggresivity of a cancer, e.g., the metastatic potential, as well as the presence in different areas of the body. Thus, a Stage II cancer with a polynucleotide signifying a high metastatic potential cancer can be used to change a borderline Stage II tumor to a Stage III tumor, justifying more aggressive

therapy. Conversely, the presence of a polynucleotide signifying a lower metastatic potential allows more conservative staging of a tumor.

Grading of cancers. Grade is a term used to describe how closely a tumor resembles normal tissue of its same type. The microscopic appearance of a tumor is used to identify tumor grade based on parameters such as cell morphology, cellular organization, and other markers of differentiation. As a general rule, the grade of a tumor corresponds to its rate of growth or aggressiveness, with undifferentiated or high-grade tumors being more aggressive than well differentiated or low-grade tumors. The following guidelines are generally used for grading tumors: 1) GX Grade cannot be assessed; 2) G1 Well differentiated; G2 Moderately well differentiated; 3) G3 Poorly differentiated; 4) G4 Undifferentiated. The polynucleotides of the invention can be especially valuable in determining the grade of the tumor, as they not only can aid in determining the differentiation status of the cells of a tumor, they can also identify factors other than differentiation that are valuable in determining the aggressivity of a tumor, such as metastatic potential.

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Detection of lung cancer. The polynucleotides of the invention can be used to detect lung cancer in a subject. Although there are more than a dozen different kinds of lung cancer, the two main types of lung cancer are small cell and nonsmall cell, which encompass about 90% of all lung cancer cases. Small cell carcinoma (also called oat cell carcinoma) usually starts in one of the larger bronchial tubes, grows fairly rapidly, and is likely to be large by the time of diagnosis. Nonsmall cell lung cancer (NSCLC) is made up of three general subtypes of lung cancer. Epidermoid carcinoma (also called squamous cell carcinoma) usually starts in one of the larger bronchial tubes and grows relatively slowly. The size of these tumors can range from very small to quite large. Adenocarcinoma starts growing near the outside surface of the lung and can vary in both size and growth rate. Some slowly growing adenocarcinomas are described as alveolar cell cancer. Large cell carcinoma starts near the surface of the lung, grows rapidly, and the growth is usually fairly large when diagnosed. Other less common forms of lung cancer are carcinoid, cylindroma, mucoepidermoid, and malignant mesothelioma.

The polynucleotides of the invention, e.g., polynucleotides differentially expressed in normal cells versus cancerous lung cells (e.g., tumor cells of high or low metastatic potential) or between types of cancerous lung cells (e.g., high metastatic versus low metastatic), can be used to distinguish types of lung cancer as well as identifying traits specific to a certain patient's cancer and selecting an appropriate

For example, if the patient's biopsy expresses a polynucleotide that is associated with a low metastatic potential, it may justify leaving a larger portion of the patient's lung in surgery to remove the lesion. Alternatively, a smaller lesion with expression of a polynucleotide that is associated with high metastatic potential may justify a more radical removal of lung tissue and/or the surrounding lymph nodes, even if no metastasis can be identified through pathological examination.

The majority of breast cancers are Detection of breast cancer. adenocarcinomas subtypes, which can be summarized as follows: 1) ductal carcinoma in situ (DCIS), including comedocarcinoma; 2) infiltrating (or invasive) ductal carcinoma (IDC); 3) lobular carcinoma in situ (LCIS); 4) infiltrating (or invasive) lobular carcinoma (ILC); 5) inflammatory breast cancer; 6) medullary carcinoma; 7) mucinous carcinoma; 8) Paget's disease of the nipple; 9) Phyllodes tumor; and 10) tubular carcinoma.

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The expression of polynucleotides of the invention can be used in the diagnosis and management of breast cancer, as well as to distinguish between types of breast cancer. Detection of breast cancer can be determined using expression levels of any of the appropriate polynucleotides of the invention, either alone or in combination. Determination of the aggressive nature and/or the metastatic potential of a breast cancer can also be determined by comparing levels of one or more polynucleotides of the invention and comparing levels of another sequence known to vary in cancerous tissue, e.g., ER expression. In addition, development of breast cancer can be detected by examining the ratio of expression of a differentially expressed polynucleotide to the levels of steroid hormones (e.g., testosterone or estrogen) or to other hormones (e.g., growth hormone, insulin). Thus expression of specific marker polynucleotides can be used to discriminate between normal and cancerous breast tissue, to discriminate 25 between breast cancers with different cells of origin, to discriminate between breast cancers with different potential metastatic rates, etc.

The polynucleotides of the invention Detection of colon cancer. exhibiting the appropriate expression pattern can be used to detect colon cancer in a subject. Colorectal cancer is one of the most common neoplasms in humans and perhaps the most frequent form of hereditary neoplasia. Prevention and early detection are key factors in controlling and curing colorectal cancer. Colorectal cancer begins as polyps, which are small, benign growths of cells that form on the inner lining of the colon. Over a period of several years, some of these polyps accumulate additional mutations and become cancerous. Multiple familial colorectal cancer disorders have

been identified, which are summarized as follows: 1) Familial adenomatous polyposis (FAP); 2) Gardner's syndrome; 3) Hereditary nonpolyposis colon cancer (HNPCC); and 4) Familial colorectal cancer in Ashkenazi Jews. The expression of appropriate polynucleotides of the invention can be used in the diagnosis, prognosis and management of colorectal cancer. Detection of colon cancer can be determined using expression levels of any of these sequences alone or in combination with the levels of expression. Determination of the aggressive nature and/or the metastatic potential of a colon cancer can be determined by comparing levels of one or more polynucleotides of the invention and comparing total levels of another sequence known to vary in cancerous tissue, e.g., expression of p53, DCC ras, lor FAP (see, e.g., Fearon ER, et al., Cell (1990) 61(5):759; Hamilton SR et al., Cancer (1993) 72:957; Bodmer W, et al., Nat Genet. (1994) 4(3):217; Fearon ER, Ann N Y Acad Sci. (1995) 768:101). For example, development of colon cancer can be detected by examining the ratio of any of the polynucleotides of the invention to the levels of oncogenes (e.g., ras) or tumor Thus expression of specific marker suppressor genes (e.g., FAP or p53). polynucleotides can be used to discriminate between normal and cancerous colon tissue, to discriminate between colon cancers with different cells of origin, to discriminate between colon cancers with different potential metastatic rates, etc.

Use of Polynucleotides to Screen for Peptide Analogs and Antagonists

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Polypeptides encoded by the instant polynucleotides and corresponding full length genes can be used to screen peptide libraries to identify binding partners, such as receptors, from among the encoded polypeptides. Peptide libraries can be synthesized according to methods known in the art (see, e.g., U.S. Patent No. 5,010,175, and WO 91/17823). Agonists or antagonists of the polypeptides if the invention can be screened using any available method known in the art, such as signal transduction, antibody binding, receptor binding, mitogenic assays, chemotaxis assays, etc. The assay conditions ideally should resemble the conditions under which the native activity is exhibited in vivo, that is, under physiologic pH, temperature, and ionic strength. Suitable agonists or antagonists will exhibit strong inhibition or enhancement of the native activity at concentrations that do not cause toxic side effects in the subject. Agonists or antagonists that compete for binding to the native polypeptide can require concentrations equal to or greater than the native concentration, while inhibitors capable of binding irreversibly to the polypeptide can be added in concentrations on the order of the native concentration.

Such screening and experimentation can lead to identification of a novel polypeptide binding partner, such as a receptor, encoded by a gene or a cDNA corresponding to a polynucleotide of the invention, and at least one peptide agonist or antagonist of the novel binding partner. Such agonists and antagonists can be used to modulate, enhance, or inhibit receptor function in cells to which the receptor is native, or in cells that possess the receptor as a result of genetic engineering. Further, if the novel receptor shares biologically important characteristics with a known receptor, information about agonist/antagonist binding can facilitate development of improved agonists/antagonists of the known receptor.

10 Pharmaceutical Compositions and Therapeutic Uses

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can invention of the Pharmaceutical compositions polypeptides, antibodies, or polynucleotides (including antisense nucleotides and ribozymes) of the claimed invention in a therapeutically effective amount. The term "therapeutically effective amount" as used herein refers to an amount of a therapeutic agent to treat, ameliorate, or prevent a desired disease or condition, or to exhibit a detectable therapeutic or preventative effect. The effect can be detected by, for example, chemical markers or antigen levels. Therapeutic effects also include reduction in physical symptoms, such as decreased body temperature. The precise effective amount for a subject will depend upon the subject's size and health, the nature and extent of the condition, and the therapeutics or combination of therapeutics selected for administration. Thus, it is not useful to specify an exact effective amount in advance. However, the effective amount for a given situation is determined by routine experimentation and is within the judgment of the clinician. For purposes of the present invention, an effective dose will generally be from about 0.01 mg/ kg to 50 mg/kg or 0.05 mg/kg to about 10 mg/kg of the DNA constructs in the individual to which it is administered.

A pharmaceutical composition can also contain a pharmaceutically acceptable carrier. The term "pharmaceutically acceptable carrier" refers to a carrier for administration of a therapeutic agent, such as antibodies or a polypeptide, genes, and other therapeutic agents. The term refers to any pharmaceutical carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition, and which can be administered without undue toxicity. Suitable carriers can be large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers,

and inactive virus particles. Such carriers are well known to those of ordinary skill in the art. Pharmaceutically acceptable carriers in therapeutic compositions can include liquids such as water, saline, glycerol and ethanol. Auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, can also be present in such vehicles. Typically, the therapeutic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection can also be prepared. Liposomes are of a pharmaceutically acceptable carrier. included within the definition Pharmaceutically acceptable salts can also be present in the pharmaceutical composition, e.g., mineral acid salts such as hydrochlorides, hydrobromides, phosphates, sulfates, and the like; and the salts of organic acids such as acetates, A thorough discussion of propionates, malonates, benzoates, and the like. pharmaceutically acceptable excipients is available in Remington's Pharmaceutical Sciences (Mack Pub. Co., New Jersey, 1991).

Delivery Methods. Once formulated, the compositions of the invention can be (1) administered directly to the subject (e.g., as polynucleotide or polypeptides); or (2) delivered ex vivo, to cells derived from the subject (e.g., as in ex vivo gene therapy). Direct delivery of the compositions will generally be accomplished by parenteral injection, e.g., subcutaneously, intraperitoneally, intravenously or intramuscularly, intratumoral or to the interstitial space of a tissue. Other modes of administration include oral and pulmonary administration, suppositories, and transdermal applications, needles, and gene guns or hyposprays. Dosage treatment can be a single dose schedule or a multiple dose schedule.

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Methods for the ex vivo delivery and reimplantation of transformed cells into a subject are known in the art and described in e.g., International Publication No. WO 93/14778. Examples of cells useful in ex vivo applications include, for example, stem cells, particularly hematopoetic, lymph cells, macrophages, dendritic cells, or tumor cells. Generally, delivery of nucleic acids for both ex vivo and in vitro applications can be accomplished by, for example, dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei, all well known in the art.

Once a gene corresponding to a polynucleotide of the invention has been found to correlate with a proliferative disorder, such as neoplasia, dysplasia, and hyperplasia, the disorder can be amenable to treatment by administration of a

therapeutic agent based on the provided polynucleotide, corresponding polypeptide or other corresponding molecule (e.g., antisense, ribozyme, etc.).

The dose and the means of administration of the inventive pharmaceutical compositions are determined based on the specific qualities of the therapeutic composition, the condition, age, and weight of the patient, the progression For example, administration of of the disease, and other relevant factors. polynucleotide therapeutic compositions agents of the invention includes local or systemic administration, including injection, oral administration, particle gun or catheterized administration, and topical administration. Preferably, the therapeutic polynucleotide composition contains an expression construct comprising a promoter operably linked to a polynucleotide of at least 12, 22, 25, 30, or 35 contiguous nt of the polynucleotide disclosed herein. Various methods can be used to administer the therapeutic composition directly to a specific site in the body. For example, a small metastatic lesion is located and the therapeutic composition injected several times in several different locations within the body of tumor. Alternatively, arteries which serve a tumor are identified, and the therapeutic composition injected into such an artery, in order to deliver the composition directly into the tumor. A tumor that has a necrotic center is aspirated and the composition injected directly into the now empty center of the tumor. The antisense composition is directly administered to the surface of the tumor, for example, by topical application of the composition. X-ray imaging is used to assist in certain of the above delivery methods.

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Receptor-mediated targeted delivery of therapeutic compositions containing an antisense polynucleotide, subgenomic polynucleotides, or antibodies to specific tissues can also be used. Receptor-mediated DNA delivery techniques are described in, for example, Findeis et al., *Trends Biotechnol.* (1993) 11:202; Chiou et al., *Gene Therapeutics: Methods And Applications Of Direct Gene Transfer* (J.A. Wolff, ed.) (1994); Wu et al., *J. Biol. Chem.* (1988) 263:621; Wu et al., *J. Biol. Chem.* (1994) 269:542; Zenke et al., *Proc. Natl. Acad. Sci.* (USA) (1990) 87:3655; Wu et al., *J. Biol. Chem.* (1991) 266:338. Therapeutic compositions containing a polynucleotide are administration in a gene therapy protocol. Concentration ranges of about 500 ng to about 50 mg, about 1 mg to about 2 mg, about 5 mg to about 500 mg, and about 20 mg to about 100 mg of DNA can also be used during a gene therapy protocol. Factors such as method of action (e.g., for enhancing or inhibiting levels of the encoded gene product) and efficacy of transformation and expression are considerations which will

affect the dosage required for ultimate efficacy of the antisense subgenomic polynucleotides. Where greater expression is desired over a larger area of tissue, larger amounts of antisense subgenomic polynucleotides or the same amounts readministered in a successive protocol of administrations, or several administrations to different adjacent or close tissue portions of, for example, a tumor site, may be required to effect a positive therapeutic outcome. In all cases, routine experimentation in clinical trials will determine specific ranges for optimal therapeutic effect. For polynucleotide-related genes encoding polypeptides or proteins with anti-inflammatory activity, suitable use, doses, and administration are described in U.S. Patent No. 5,654,173.

The therapeutic polynucleotides and polypeptides of the present invention can be delivered using gene delivery vehicles. The gene delivery vehicle can be of viral or non-viral origin (see generally, Jolly, Cancer Gene Therapy (1994) 1:51; Kimura, Human Gene Therapy (1994) 5:845; Connelly, Human Gene Therapy (1995) 1:185; and Kaplitt, Nature Genetics (1994) 6:148). Expression of such coding sequences can be induced using endogenous mammalian or heterologous promoters. Expression of the coding sequence can be either constitutive or regulated.

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Viral-based vectors for delivery of a desired polynucleotide and expression in a desired cell are well known in the art. Exemplary viral-based vehicles include, but are not limited to, recombinant retroviruses (see, e.g., WO 90/07936; WO 94/03622; WO 93/25698; WO 93/25234; U.S. Patent No. 5, 219,740; WO 93/11230; WO 93/10218; U.S. Patent No. 4,777,127; GB Patent No. 2,200,651; EP 0 345 242; and WO 91/02805), alphavirus-based vectors (e.g., Sindbis virus vectors, Semliki forest virus (ATCC VR-67; ATCC VR-1247), Ross River virus (ATCC VR-373; ATCC VR-1246) and Venezuelan equine encephalitis virus (ATCC VR-923; ATCC VR-1250; ATCC VR 1249; ATCC VR-532), and adeno-associated virus (AAV) vectors (see, e.g., WO 94/12649, WO 93/03769; WO 93/19191; WO 94/28938; WO 95/11984 and WO 95/00655). Administration of DNA linked to killed adenovirus as described in Curiel, Hum. Gene Ther. (1992) 3:147 can also be employed.

Non-viral delivery vehicles and methods can also be employed, including, but not limited to, polycationic condensed DNA linked or unlinked to killed adenovirus alone (see, e.g., Curiel, Hum. Gene Ther. (1992) 3:147); ligand-linked DNA(see, e.g., Wu, J. Biol. Chem. 264:16985 (1989)); eukaryotic cell delivery vehicles cells (see, e.g., U.S. Patent No. 5,814,482; WO 95/07994; WO 96/17072; WO 95/30763; and WO 97/42338) and nucleic charge neutralization or fusion with cell membranes. Naked DNA can also be employed. Exemplary naked DNA introduction 35

methods are described in WO 90/11092 and U.S. Patent No. 5,580,859. Liposomes that can act as gene delivery vehicles are described in U.S. Patent No. 5,422,120; WO 95/13796; WO 94/23697; WO 91/14445; and EP 0524968. Additional approaches are described in Philip, *Mol. Cell Biol.* 14:2411 (1994), and in Woffendin, *Proc. Natl. Acad. Sci.* (1994) 91:1581.

Further non-viral delivery suitable for use includes mechanical delivery systems such as the approach described in Woffendin et al., *Proc. Natl. Acad. Sci. USA* 91(24):11581 (1994). Moreover, the coding sequence and the product of expression of such can be delivered through deposition of photopolymerized hydrogel materials or use of ionizing radiation (see, *e.g.*, U.S. Patent No. 5,206,152 and WO 92/11033). Other conventional methods for gene delivery that can be used for delivery of the coding sequence include, for example, use of hand-held gene transfer particle gun (see, *e.g.*, U.S. Patent No. 5,149,655); use of ionizing radiation for activating transferred gene (see, *e.g.*, U.S. Patent No. 5,206,152 and WO 92/11033).

The present invention will now be illustrated by reference to the following examples which set forth particularly advantageous embodiments. However, it should be noted that these embodiments are illustrative and are not to be construed as restricting the invention in any way.

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EXAMPLES

EXAMPLE 1

SOURCE OF BIOLOGICAL MATERIALS AND OVERVIEW OF NOVEL POLYNUCLEOTIDES

EXPRESSED BY THE BIOLOGICAL MATERIALS

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Cell lines and human normal and tumor tissue were used to construct cDNA libraries from mRNA isolated from the cells and tissues. Most sequences were about 275-300 nucleotides in length. The cells lines include Km12L4-A cell line, a high metastatic colon cancer cell line (Morika, W. A. K. et al., Cancer Research (1988) 48:6863). The KM12L4-A cell line is derived from the KM12C cell line. The KM12C cell line, which is poorly metastatic (low metastatic) was established in culture from a Dukes' stage B2 surgical specimen (Morikawa et al. Cancer Res. (1988) 48:6863). The KML4-A is a highly metastatic subline derived from KM12C (Yeatman et al. Nucl. Acids. Res. (1995) 23:4007; Bao-Ling et al. Proc. Annu. Meet. Am. Assoc. Cancer. Res. (1995) 21:3269). The KM12C and KM12C-derived cell lines (e.g., KM12L4, KM12L4-A, etc.) are well-recognized in the art as model cell lines for the study of colon cancer (see, e.g., Moriakawa et al., supra; Radinsky et al. Clin. Cancer Res. (1995) 1:19; Yeatman et al., (1995) supra; Yeatman et al., Clin. Exp. Metastasis (1996) 14:246). These and other cell lines and tissue are described in Table 6.

The sequences of the isolated polynucleotides were first masked to eliminate low complexity sequences using the XBLAST masking program (Claverie "Effective Large-Scale Sequence Similarity Searches," In: Computer Methods for Macromolecular Sequence Analysis, Doolittle, ed., Meth. Enzymol. 266:212-227 Academic Press, NY, NY (1996); see particularly Claverie, in "Automated DNA Sequencing and Analysis Techniques" Adams et al., eds., Chap. 36, p. 267 Academic Press, San Diego, 1994 and Claverie et al. Comput. Chem. (1993) 17:191). Generally, masking does not influence the final search results, except to eliminate sequences of relative little interest due to their low complexity, and to eliminate multiple "hits" based on similarity to repetitive regions common to multiple sequences, e.g., Alu repeats. The sequences that exhibited greater than 70% overlap, 99% identity, and a p value of less than 1 x 10⁻⁴⁰ were discarded. Sequences from this search also were discarded if the inclusive parameters were met, but the sequence was ribosomal or vector-derived.

The resulting sequences from the previous search were classified into three groups (1, 2 and 3 below) and searched in a BLASTX vs. NRP (non-redundant proteins) database search: (1) unknown (no hits in the Genbank search), (2) weak similarity (greater than 45% identity and p value of less than 1 x 10^{-5}), and (3) high similarity (greater than 60% overlap, greater than 80% identity, and p value less than 1 x 10^{-5}). Sequences having greater than 70% overlap, greater than 99% identity, and p value of less than 1 x 10^{-40} were discarded.

The remaining sequences were classified as unknown (no hits), weak similarity, and high similarity (parameters as above). Two searches were performed on these sequences. First, a BLAST vs. EST database search was performed and sequences with greater than 99% overlap, greater than 99% similarity and a p value of less than 1 x 10⁻⁴⁰ were discarded. Sequences with a p value of less than 1 x 10⁻⁴⁵ when compared to a database sequence of human origin were also excluded. Second, a BLASTN vs. Patent GeneSeq database was performed and sequences having greater than 99% identity, p value less than 1 x 10⁻⁴⁰, and greater than 99% overlap were discarded.

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The remaining sequences were subjected to screening using other rules and redundancies in the dataset. Sequences with a p value of less than 1 x 10⁻¹¹¹ in relation to a database sequence of human origin were specifically excluded. The final result provided the 3351 sequences listed in the accompanying Sequence Listing. Each identified polynucleotide represents sequence from at least a partial mRNA transcript. Polynucleotides that were determined to be novel were assigned a sequence identification number.

The novel polynucleotides were assigned sequence identification numbers SEQ ID NOs:1-3351. The first 1847 DNA sequences corresponding to the novel polynucleotides are provided in the Sequence Listing in Table 1. DNA sequences corresponding to the novel polynucleotides of SEQ ID NOs:1848-3351 are provided in the Sequence Listing in Table 2. The DNA sequences of Table 2, while numbered SEQ ID 1-1504, correspond to SEQ ID NOs:1848-3351 in the Sequence Listing, e.g., Table 2 SEQ ID 1 is SEQ ID NO:1848, Table 2 SEQ ID 2 is SEQ ID NO:1849, etc. Each DNA sequence in Table 4 is uniquely identified by a number that is 1847 less than its SEQ ID NO in the Sequence Listing. Tables 1 and 2 provide: 1) the SEQ ID NO assigned to each sequence for use in the present specification or a corresponding number; 2) the sequence name used as an internal identifier of the sequence; 3) the name assigned to the clone from which the

sequence was isolated; and 4) the number of the cluster to which the sequence is assigned (Cluster ID; where the cluster ID is 0, the sequence was not assigned to any cluster).

Because the provided polynucleotides represent partial mRNA transcripts, two or more polynucleotides of the invention may represent different regions of the same mRNA transcript and the same gene. Thus, if two or more SEQ ID NOs: are identified as belonging to the same clone, then either sequence can be used to obtain the full-length mRNA or gene.

EXAMPLE 2

RESULTS OF PUBLIC DATABASE SEARCH TO IDENTIFY FUNCTION OF GENE PRODUCTS

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SEQ ID NOs:1-3351 were translated in all three reading frames to determine the best alignment with the individual sequences. These amino acid sequences and nucleotide sequences are referred to, generally, as query sequences, which are aligned with the individual sequences. Query and individual sequences were aligned using the BLAST programs, available over the world wide web at http://www.ncbi.nlm.nih.gov/BLAST/. Again the sequences were masked to various extents to prevent searching of repetitive sequences or poly-A sequences, using the XBLAST program for masking low complexity as described above in Example 1.

Tables 3 and 4 (inserted before the claims) show the results of the alignments. Table 3 contains alignment information for SEQ ID NOs:1-1847 and Table 4 contains alignment information for SEQ ID NOs:1848-3351. The DNA sequences of Table 4, while numbered SEQ ID 1-1504, correspond to SEQ ID NOs:1848-3351. Each DNA sequence in Table 4 is uniquely identified by a number that is 1847 less than its SEQ ID NO. Tables 3 and 4 refer to each sequence by its SEQ ID NO or a corresponding number, the accession numbers and descriptions of nearest neighbors from the Genbank and Non-Redundant Protein searches, and the p values of the search results.

For each of SEQ ID NOs:1-1847, the best alignment to a protein or DNA sequence is included in Table 3, and the best alignment for each of SEQ ID NOs:1848-3351 is included in Table 4. The activity of the polypeptide encoded by SEQ ID NOs:1-3351 is the same or similar to the nearest neighbor reported in Table 3 or 4. The accession number of the nearest neighbor is reported, providing a reference to the activities exhibited by the nearest neighbor. The search program and database used for the alignment also are indicated as well as a calculation of the p value.

Full length sequences or fragments of the polynucleotide sequences of the nearest neighbors can be used as probes and primers to identify and isolate the full length sequence of SEQ ID NOs:1-3351. The nearest neighbors can indicate a tissue or cell type to be used to construct a library for the full-length sequences of SEQ ID NOs:1-3351.

EXAMPLE 3 Members of Protein Families

The sequences (SEQ ID NOs:1-3351) were used to conduct a profile search as described in the specification above. Several of the polynucleotides of the invention were found to encode polypeptides having characteristics of a polypeptide belonging to a known protein families (and thus represent new members of these protein families) and/or comprising a known functional domain (Table 5). "Start" and "stop" in Table 3 indicate the position within the individual sequences that align with the query sequence having the indicated SEQ ID NO. The direction indicates the orientation of the query sequence with respect to the individual sequence, where forward (for) indicates that the alignment is in the same direction (left to right) as the sequence provided in the Sequence Listing and reverse (rev) indicates that the alignment is with a sequence complementary to the sequence provided in the Sequence

Some polynucleotides exhibited multiple profile hits because, for example, the particular sequence contains overlapping profile regions, and/or the sequence contains two different functional domains. These profile hits are described in more detail below.

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Ank Repeats (ANK). SEQ ID NOs:187, 1268, 1804, 1819, 1830, 1839, 2652, 3015 and 3267 represent polynucleotides encoding an Ank repeat-containing protein. The ankyrin motif is a 33 amino acid sequence named for the protein ankyrin which has 24 tandem 33-amino-acid motifs. Ank repeats were originally identified in the cell-cycle-control protein cdc10 (Breeden et al., Nature (1987) 329:651). Proteins containing ankyrin repeats include ankyrin, myotropin, I-kappaB proteins, cell cycle protein cdc10, the Notch receptor (Matsuno et al., Development (1997) 124(21):4265); G9a (or BAT8) of the class III region of the major histocompatibility complex (Biochem J. 290:811-818, 1993), FABP, GABP, 53BP2, Lin12, glp-1, SW14, and SW16. The functions of the ankyrin repeats are compatible with a role in protein-

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protein interactions (Bork, Proteins (1993) 17(4):363; Lambert and Bennet, Eur. J. Biochem. (1993) 211:1; Kerr et al., Current Op. Cell Biol. (1992) 4:496; Bennet et al., J. Biol. Chem. (1980) 255:6424).

ATPases Associated with Various Cellular Activities (ATPases). Sequences within SEQ ID NOs:431, 639, 2135, 2684, 2859, 3197 and 3266 correspond to a sequence that encodes a novel member of the "ATPases Associated with diverse cellular Activities" (AAA) protein family. The AAA protein family is composed of a large number of ATPases that share a conserved region of about 220 amino acids that contains an ATP-binding site (Froehlich et al., J. Cell Biol. (1991) 114:443; Erdmann et al., Cell (1991) 64:499; Peters et al., EMBO J. (1990) 9:1757; Kunau et al., Biochimie (1995)**BioEssays** al., Confalonieri et 75:209-224; (1993)http://yeamob.pci.chemie.uni-tuebingen.de/AAA/Description.html). The proteins that belong to this family either contain one or two AAA domains. In general, the AAA domains in these proteins act as ATP-dependent protein clamps (Confalonieri et al. (1995) BioEssays 17:639). In addition to the ATP-binding 'A' and 'B' motifs, which are located in the N-terminal half of this domain, there is a highly conserved region located in the central part of the domain which was used in the development of the signature pattern. The consensus pattern is: [LIVMT]-x-[LIVMT]-[LIVMF]-x-[GATMC]-[ST]-[NS]-x(4)-[LIVM]-D-x-A-[LIFA]-x-R.

Bromodomain (bromodomain). SEQ ID NO:1814 represents a polynucleotide encoding a polypeptide having a bromodomain region (Haynes et al., 1992, Nucleic Acids Res. 20:2693-2603, Tamkun et al., 1992, Cell 68:561-572, and Tamkun, 1995, Curr. Opin. Genet. Dev. 5:473-477), which is a conserved region of about 70 amino acids. The bromodomain is thought to be involved in protein-protein interactions and may be important for the assembly or activity of multicomponent complexes involved in transcriptional activation. The consensus pattern, which spans a major part of the bromodomain, is: [STANVF]-x(2)-F-x(4)-[DNS]-x(5,7)-[DENQTF]-Y-[HFY]-x(2)- [LIVMFY]-x(3)-[LIVM]-x(4)-[LIVM]-x(6,8)-Y-x(12,13)-[LIVM]-x(2)-N-[SACF]-x(2)-[FY].

Basic Region Plus Leucine Zipper Transcription Factors (BZIP). SEQ ID NOs:410, 552, 768, 822, 836, 1288, 1365, 1454, 1540, 1549, 1556, 1557, 1563, 1622, 1630, 1704, 1808, 2363, 2424, 3147, 3152, 3158 and 3208 represent polynucleotides encoding a novel member of the family of basic region plus leucine zipper transcription factors. The bZIP superfamily (Hurst, *Protein Prof.* (1995) 2:105; and Ellenberger, *Curr. Opin. Struct. Biol.* (1994) 4:12) of eukaryotic DNA-binding

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transcription factors encompasses proteins that contain a basic region mediating sequence-specific DNA-binding followed by a leucine zipper required for dimerization. The consensus pattern for this protein family is: [KR]-x(1,3)-[RKSAQ]-N-x(2)-[SAQ](2)-x-[RKTAENQ]-x-R-x-[RK].

EF Hand (EFhand). SEQ ID NOs:820, 1755 and 3285 correspond to polynucleotides encoding a novel protein in the family of EF-hand proteins. Many calcium-binding proteins belong to the same evolutionary family and share a type of calcium-binding domain known as the EF-hand (Kawasaki et al., *Protein. Prof.* (1995) 2:305-490). This type of domain consists of a twelve residue loop flanked on both sides by a twelve residue alpha-helical domain. In an EF-hand loop the calcium ion is coordinated in a pentagonal bipyramidal configuration. The six residues involved in the binding are in positions 1, 3, 5, 7, 9 and 12; these residues are denoted by X, Y, Z, -Y, -X and -Z. The invariant Glu or Asp at position 12 provides two oxygens for liganding Ca (bidentate ligand). The consensus pattern includes the complete EF-hand loop as well as the first residue which follows the loop and which seem to always be hydrophobic:

D-x-[DNS]-{ILVFYW}-[DENSTG]-[DNQGHRK]-{GP}-[LIVMC]-[DENQSTAGC]-x(2)-[DE]-[LIVMFYW].

Ets Domain (Ets Nterm). SEQ ID NO:1811 represents a polynucleotide encoding a polypeptide with N-terminal homology in ETS domain. Proteins of this family contain a conserved domain, the "ETS-domain," that is involved in DNA binding. The domain appears to recognize purine-rich sequences; it is about 85 to 90 amino acids in length, and is rich in aromatic and positively charged residues (Wasylyk, et al., Eur. J. Biochem. (1993) 211:718). The ets gene family encodes a novel class of DNA-binding proteins, each of which binds a specific DNA sequence and comprises an ets domain that specifically interacts with sequences containing the common core trinucleotide sequence GGA. In addition to an ets domain, native ets proteins comprise other sequences which can modulate the biological specificity of the protein. Ets genes and proteins are involved in a variety of essential biological processes including cell growth, differentiation and development, and three members are implicated in oncogenic process.

G-Protein Alpha Subunit (G-alpha). SEQ ID NO:1846 represents a polynucleotide encoding a novel polypeptide of the G-protein alpha subunit family. Guanine nucleotide binding proteins (G-proteins) are a family of membrane-associated proteins that couple extracellularly-activated integral-membrane receptors to intracellular effectors, such as ion channels and enzymes that vary the concentration of

second messenger molecules. G-proteins are composed of 3 subunits (alpha, beta and gamma) which, in the resting state, associate as a trimer at the inner face of the plasma membrane. The alpha subunit binds GTP and exhibits GTPase activity. G-protein alpha subunits are 350-400 amino acids in length and have molecular weights in the range 40-45 kDa. Seventeen distinct types of alpha subunit have been identified in mammals, and fall into 4 main groups on the basis of both sequence similarity and function: alpha-s, alpha-q, alpha-i and alpha-12 (Simon et al., Science (1993) 252:802). They are often N-terminally acylated, usually with myristate and/or palmitoylate, and these fatty acid modifications can be important for membrane association and high- affinity interactions with other proteins.

10 Helicases conserved C-terminal domain (helicase C). NOs:1496, 2826 and 2871 represent polynucleotides encoding novel members of the DEAD/H helicase family. A number of eukaryotic and prokaryotic proteins have been characterized (Schmid S.R., et al., Mol. Microbiol. (1992) 6:283; Linder P., et al., Nature (1989) 337:121; Wassarman D.A., et al., Nature (1991) 349:463) on the basis of their structural similarity. All are involved in ATP-dependent, nucleic-acid unwinding. 15 All DEAD box family members of the above proteins share a number of conserved sequence motifs, some of which are specific to the DEAD family while others are shared by other ATP-binding proteins or by proteins belonging to the helicases 'superfamily' (Hodgman T.C., Nature (1988) 333:22 and Nature (1988) 333:578 (Errata). One of these motifs, called the "D-E-A-D-box", represents a special version of 20 the B motif of ATP-binding proteins. Some other proteins belong to a subfamily which have His instead of the second Asp and are thus said to be "D-E-A-H-box" proteins (Wassarman D.A., et al., Nature (1991) 349:463; Harosh I., et al., Nucleic Acids Res. (1991) 19:6331; Koonin E.V. et al., J. Gen. Virol. (1992) 73:989. The following signature patterns are used to identify members of both subfamilies: 1) [LIVMF](2)-D-E-A-D-[RKEN]-x-[LIVMFYGSTN]; and 2) [GSAH]-x-[LIVMF](3)-D-E-[ALIV]-H-[NECR].

Homeobox domain (homeobox). SEQ ID NOs:1676, 1820 and 1821 represent polynucleotides encoding proteins having a homeobox domain. The homeobox is a protein domain of 60 amino acids (Gehring In: Guidebook to the Homeobox Genes, Duboule D., Ed., pp. 1-10, Oxford University Press, Oxford, (1994); Buerglin In: Guidebook to the Homeobox Genes, pp25-72, Oxford University Press, Oxford, (1994); Gehring, Trends Biochem. Sci. (1992) 17:277-280; Gehring et al., Annu. Rev. Genet. (1986) 20:147-173; Schofield, Trends Neurosci. (1987) 10:3-6) first

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identified in a number of Drosophila homeotic and segmentation proteins. It is extremely well conserved in many other animals, including vertebrates. This domain binds DNA through a helix-turn-helix type of structure. Several proteins that contain a homeobox domain play an important role in development. Most of these proteins are sequence-specific DNA-binding transcription factors. The homeobox domain is also very similar to a region of the yeast mating type proteins. These are sequence-specific DNA-binding proteins that act as master switches in yeast differentiation by controlling gene expression in a cell type-specific fashion.

A schematic representation of the homeobox domain is shown below.

The helix-turn-helix region is shown by the symbols 'H' (for helix), and 't' (for turn).

The pattern detects homeobox sequences 24 residues long and spans positions 34 to 57 of the homeobox domain. The consensus pattern is as follows: [LIVMFYG]-[ASLVR]-x(2)-[LIVMSTACN]-x-[LIVM]-x(4)-[LIV]-[RKNQESTAIY]-[LIVFSTNKH]-W-[FYVC]-x-[NDQTAH]-x(5)-[RKNAIMW].

MAP kinase kinase (mkk). SEQ ID NOs:29, 31, 196, 3175, 3190 and 3281 represent novel members of the MAP kinase kinase family. MAP kinases (MAPK) are involved in signal transduction, and are important in cell cycle and cell 20 growth controls. The MAP kinase kinases (MAPKK) are dual-specificity protein kinases which phosphorylate and activate MAP kinases. MAPKK homologues have Moreover, the been found in yeast, invertebrates, amphibians, and mammals. MAPKK/MAPK phosphorylation switch constitutes a basic module activated in distinct pathways in yeast and in vertebrates. MAPKKs are essential transducers through which signals must pass before reaching the nucleus. For review, see, e.g., Biologique Biol Cell (1993) 79:193-207; Nishida et al., Trends Biochem Sci (1993) 18:128-31; Ruderman, Curr Opin Cell Biol (1993) 5:207-13; Dhanasekaran et al., Oncogene (1998) 17:1447-55; Kiefer et al., Biochem Soc Trans (1997) 25:491-8; and Hill, Cell Signal 30 (1996) 8:533-44.

Protein Kinase (protkinase). SEQ ID NOs:1157, 1478, 1496, 2286, 2969 and 3190 represent polynucleotides encoding protein kinases. Protein kinases catalyze phosphorylation of proteins in a variety of pathways, and are implicated in cancer. Eukaryotic protein kinases (Hanks S.K., et al., FASEB J. (1995) 9:576; Hunter T., Meth. Enzymol. (1991) 200:38; Hanks S.K., et al., Meth. Enzymol. (1991) 200:38; Hanks S.K.,

Curr. Opin. Struct. Biol. (1991) 1:369; Hanks S.K. et al., Science (1988) 241:42) are enzymes that belong to a very extensive family of proteins which share a conserved catalytic core common to both serine/threonine and tyrosine protein kinases. There are a number of conserved regions in the catalytic domain of protein kinases. The first region, which is located in the N-terminal extremity of the catalytic domain, is a glycine-rich stretch of residues in the vicinity of a lysine residue, which has been shown to be involved in ATP binding. The second region, which is located in the central part of the catalytic domain, contains a conserved aspartic acid residue which is important for the catalytic activity of the enzyme (Knighton D.R. et al., Science (1991) 253:407).
The protein kinase profile includes two signature patterns for this second region: one specific for serine/threonine kinases and the other for tyrosine kinases. A third profile is based on the alignment in (Hanks S.K. et al., FASEB J. (1995) 9:576) and covers the entire catalytic domain.

The consensus patterns are as follows: 1) [LIV]-G-{P}-G-{P}-[FYWMGSTNH]-[SGA]-{PW}-[LIVCAT]-{PD}-x-[GSTACLIVMFY]-x(5,18)-[LIVMFYWCSTAR]-[AIVP]-[LIVMFAGCKR]-K, where K binds ATP; 2) [LIVMFYC]-x-[HY]-x-D-[LIVMFY]-K-x(2)-N-[LIVMFYCT](3), where D is an active site residue; and 3) [LIVMFYC]-x-[HY]-x-D-[LIVMFY]-[RSTAC]-x(2)-N-[LIVMFYC], where D is an active site residue.

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If a protein analyzed includes two of the above protein kinase signatures, the probability of it being a protein kinase is close to 100%.

Ras family proteins (ras). SEQ ID NOs:1688 and 3258 represent polynucleotides encoding novel members of the ras family of small GTP/GDP-binding proteins (Valencia et al., 1991, Biochemistry 30:4637-4648). Ras family members generally require a specific guanine nucleotide exchange factor (GEF) and a specific GTPase activating protein (GAP) as stimulators of overall GTPase activity. Among ras-related proteins, the highest degree of sequence conservation is found in four regions that are directly involved in guanine nucleotide binding. The first two constitute most of the phosphate and Mg2+ binding site (PM site) and are located in the first half of the G-domain. The other two regions are involved in guanosine binding and are located in the C-terminal half of the molecule. Motifs and conserved structural features of the ras-related proteins are described in Valencia et al., 1991, Biochemistry 30:4637-4648. A major consensus pattern of ras proteins is: D-T-A-G-Q-E-K-[LF]-G-G-L-R-[DE]-G-Y-Y.

Thioredoxin family active site (Thioredox). SEQ ID NO:1677 represents a polynucleotide encoding a protein having a thioredoxin family active site. Thioredoxins (Holmgren A., Annu. Rev. Biochem. (1985) 54:237; Gleason F.K. et al., FEMS Microbiol. Rev. (1988) 54:271; Holmgren, A. J. Biol. Chem. (1989) 264:13963; Eklund H. et al., Proteins (1991) 11:13) are small proteins of approximately one hundred amino- acid residues which participate in various redox reactions via the reversible oxidation of an active center disulfide bond. They exist in either a reduced form or an oxidized form where the two cysteine residues are linked in an intramolecular disulfide bond. Thioredoxin is present in prokaryotes and eukaryotes and the sequence around the redox-active disulfide bond is well conserved. All PDI contains two or three (ERp72) copies of the thioredoxin domain. The consensus pattern is:

[LIVMF]-[LIVMSTA]-x-[LIVMFYC]-[FYWSTHE]-x(2)-[FYWGTN]-C-[GATPLVE]-[PHYWSTA]-C-x(6)-[LIVMFYWT] (where the two C's form the redoxactive bond).

Trypsin (trypsin). SEQ ID NO:1410 corresponds to a novel serine protease of the trypsin family. The catalytic activity of the serine proteases from the trypsin family is provided by a charge relay system involving an aspartic acid residue hydrogen-bonded to a histidine, which itself is hydrogen-bonded to a serine. The sequences in the vicinity of the active site serine and histidine residues are well conserved in this family of proteases (Brenner S., *Nature* (1988) 334:528). The consensus patterns for this trypsin protein family are: 1) [LIVM]-[ST]-A-[STAG]-H-C, where H is the active site residue; and 2) [DNSTAGC]-[GSTAPIMVQH]-x(2)-G-[DE]-S-G-[GS]-[SAPHV]- [LIVMFYWH]-[LIVMFYSTANQH], where S is the active site residue. All sequences known to belong to this family are detected by the above consensus sequences, except for 18 different proteases which have lost the first conserved glycine. If a protein includes both the serine and the histidine active site signatures, the probability of it being a trypsin family serine protease is 100%.

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WD Domain, G-Beta Repeats (WD domain). SEQ ID NOs:1336, 1380, 1711, 1762, 1909, 2218, 3047, 3108 and 3292 represent novel members of the WD domain/G-beta repeat family. Beta-transducin (G-beta) is one of the three subunits (alpha, beta, and gamma) of the guanine nucleotide-binding proteins (G proteins) which act as intermediaries in the transduction of signals generated by transmembrane receptors (Gilman, Annu. Rev. Biochem. (1987) 56:615). The alpha subunit binds to and hydrolyzes GTP; the functions of the beta and gamma subunits are less clear but they seem to be required for the replacement of GDP by GTP as well as for membrane

anchoring and receptor recognition. In higher eukaryotes, G-beta exists as a small multigene family of highly conserved proteins of about 340 amino acid residues. Structurally, G-beta consists of eight tandem repeats of about 40 residues, each containing a central Trp-Asp motif (this type of repeat is sometimes called a WD-40 repeat). The consensus pattern for the WD domain/G-Beta repeat family is: [LIVMSTAC]-[LIVMFYWSTAGC]-[LIMSTAG]-[LIVMSTAGC]-x(2)-[DN]-x(2)-[LIVMWSTAC]-x-[LIVMFSTAG]-W-[DEN]-[LIVMFSTAGCN].

wnt Family of Developmental Signaling Proteins (Wnt dev sign). SEQ ID NO:1538 corresponds to a novel member of the wnt family of developmental signaling proteins. Wnt-1 (previously known as int-1), the seminal member of this family, (Nusse R., Trends Genet. (1988) 4:291) is thought to play a role in intercellular communication and seems to be a signalling molecule important in the development of the central nervous system (CNS). All wnt family proteins share the following features characteristics of secretory proteins: a signal peptide, several potential N-glycosylation sites and 22 conserved cysteines that are probably involved in disulfide bonds. The Wnt proteins seem to adhere to the plasma membrane of the secreting cells and are therefore likely to signal over only few cell diameters. The consensus pattern, which is based upon a highly conserved region including three cysteines, is as follows: C-K-C-H-G-[LIVMT]-S-G-x-C.

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Protein Tyrosine Phosphatase (Y phosphatase). represents a polynucleotide encoding a protein tyrosine kinase. Tyrosine specific protein phosphatases (EC 3.1.3.48) (PTPase) (Fischer et al., Science (1991) 253:401; Charbonneau et al., Annu. Rev. Cell Biol. (1992) 8:463; Trowbridge, J. Biol. Chem. (1991) 266:23517; Tonks et al., Trends Biochem. Sci. (1989) 14:497; and Hunter, Cell (1989) 58:1013) catalyze the removal of a phosphate group attached to a tyrosine residue. These enzymes are very important in the control of cell growth, proliferation, differentiation and transformation. Multiple forms of PTPase have been characterized and can be classified into two categories: soluble PTPases and transmembrane receptor proteins that contain PTPase domain(s). Structurally, all known receptor PTPases are made up of a variable length extracellular domain, followed by a transmembrane region and a C-terminal catalytic cytoplasmic domain. PTPase domains consist of about 300 amino acids. The search of two conserved cysteines has been shown to be absolutely required for activity. Furthermore, a number of conserved residues in its immediate vicinity have also been shown to be important. The consensus pattern for PTPases is: [LIVMF]-H-C-x(2)-G-x(3)-[STC]-[STAGP]-x-[LIVMFY]; C is the active site residue. 35

Zinc Finger, C2H2 Type (Zincfing C2H2). SEQ ID NOs:308, 807, 1324, 1503, 1527, 3081, 3193 and 3306 correspond to polynucleotides encoding novel members of the of the C2H2 type zinc finger protein family. Zinc finger domains (Klug et al., Trends Biochem. Sci. (1987) 12:464; Evans et al., Cell (1988) 52:1; Payre et al., FEBS Lett. (1988) 234:245; Miller et al., EMBO J. (1985) 4:1609; and Berg, Proc. Natl. Acad. Sci. USA (1988) 85:99) are nucleic acid-binding protein structures. In addition to the conserved zinc ligand residues, it has been shown that a number of other positions are also important for the structural integrity of the C2H2 zinc fingers. (Rosenfeld et al., J. Biomol. Struct. Dyn. (1993) 11:557) The best conserved position is found four residues after the second cysteine; it is generally an aromatic or aliphatic residue. The consensus pattern for C2H2 zinc fingers is: C-x(2,4)-C-x(3)-[LIVMFYWC]-x(8)-H-x(3,5)-H. The two C's and two H's are zinc ligands.

Src homology 2. SEQ ID NOs:186, 2591, 3307 and 3339 represent polynucleotides encoding novel members of the family of Src homology 2 (SH2) proteins. The Src homology 2 (SH2) domain is a protein domain of about 100 amino acid residues first identified as a conserved sequence region between the oncoproteins Src and Fps (Sadowski I. et al., *Mol. Cell. Biol.* 6:4396-4408 (1986)). Similar sequences are found in many other intracellular signal-transducing proteins (Russel R.B. et al., *FEBS Lett.* 304:15-20 (1992)). SH2 domains function as regulatory modules of intracellular signalling cascades by interacting with high affinity to phosphotyrosine-containing target peptides in a sequence-specific and phosphorylation-dependent manner (Marangere L.E.M., Pawson T., *J. Cell Sci. Suppl.* 18:97-104 (1994); Pawson T., Schlessinger J., *Curr. Biol.* 3:434-442 (1993); Mayer B.J., Baltimore D., *Trends Cell. Biol.* 3:8-13 (1993); Pawson T., *Nature* 373:573-580 (1995)).

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The SH2 domain has a conserved 3D structure consisting of two alpha helices and six to seven beta-strands. The core of the domain is formed by a continuous beta-meander composed of two connected beta-sheets (Kuriyan J., Cowburn D., Curr. Opin. Struct. Biol. 3:828-837(1993)). The profile to detect SH2 domains is based on a structural alignment consisting of 8 gap-free blocks and 7 linker regions totaling 92 match positions.

Src homology 3. SEQ ID NO:234, 1832, and 1835 represent polynucleotides encoding novel members of the family of Src homology 3 (SH3) proteins. The Src homology 3 (SH3) domain is a small protein domain of about 60 amino acid residues first identified as a conserved sequence in the non-catalytic part of several cytoplasmic protein tyrosine kinases (e.g., Src, Abl, Lck) (Mayer B.J. et al.,

Nature 332:272-275 (1988)). Since then, it has been found in a great variety of other intracellular or membrane-associated proteins (Musacchio A. et al., FEBS Lett. 307:55-61 (1992); Pawson T., Schlessinger J., Curr. Biol. 3:434-442 (1993); Mayer B.J., Baltimore D., Trends Cell Biol. 3:8-13 (1993); Pawson T., Nature 373:573-580 (1995)).

The SH3 domain has a characteristic fold which consists of five or six beta strands arranged as two tightly packed anti-parallel beta sheets. The linker regions may contain short helices (Kuriyan J., Cowburn D., Curr. Opin. Struct. Biol. 3:828-837 (1993)).

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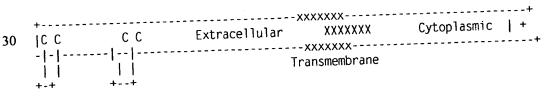
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The function of the SH3 domain may be to mediate assembly of specific protein complexes via binding to proline-rich peptides (Morton C.J., Campbell I.D., Curr. Biol. 4:615-617 (1994)).

In general SH3 domains are found as single copies in a given protein, but there are a significant number of proteins with two SH3 domains and a few with 3 or 4 copies.

SEQ ID NOs:746 and 1192 represent Fibronectin type III. polynucleotides encoding novel members of the family of fibronectin type III proteins. A number of receptors for lymphokines, hematopoeitic growth factors and growth hormone-related molecules have been found to share a common binding domain. (Bazan J.F., Biochem. Biophys. Res. Commun. 164:788-795 (1989); Bazan J.F., Proc. Natl. Acad. Sci. U.S.A. 87:6934-6938 (1990); Cosman D. et al., Trends Biochem. Sci. 15:265-270 (1990); d'Andrea A.D., Fasman G.D., Lodish H.F., Cell 58:1023-1024 20 (1989); d'Andrea A.D., Fasman G.D., Lodish H.F., Curr. Opin. Cell Biol. 2:648-651 (1990)).

The conserved region constitutes all or part of the extracellular ligandbinding region and is about 200 amino acid residues long. In the N-terminal of this domain there are two pairs of cysteines known, in the growth hormone receptor, to be involved in disulfide bonds.



Two patterns detect this family of receptors. The first one is derived from the first N-terminal disulfide loop, the second is a tryptophan-rich pattern located at the C-terminal extremity of the extracellular region.

A consensus for this protein family is: C-[LVFYR]-x(7,8)-[STIVDN]-C-x-W (The two C's are linked by a disulfide bond]. A second consensus for this protein family is: [STGL]-x-W-[SG]-x-W-S.

LIM domain containing proteins. SEQ ID NOs:1269, 1309, 1360, and 1386 represent polynucleotides encoding novel members of the family of LIM domain containing proteins. A number of proteins contain a conserved cysteine-rich domain of about 60 amino-acid residues. (Freyd G. et al., *Nature 344*:876-879 (1990); Baltz R. et al., *Plant Cell 4*:1465-1466 (1992); Sanchez-Garcia I., Rabbitts T.H., *Trends Genet.* 10:315-320 (1994)).

In the LIM domain, there are seven conserved cysteine residues and a histidine. The arrangement followed by these conserved residues is C-x(2)-C- x(16,23)-H-x(2)-[CH]-x(2)-C-x(2)-C-x(16,21)-C-x(2,3)-[CHD]. The LIM domain binds two zinc ions (Michelsen J.W. et al., *Proc. Natl. Acad. Sci. U.S.A. 90*:4404-4408 (1993)). LIM does not bind DNA, rather it seems to act as interface for protein-protein interaction.

The consensus for this protein family is: C-x(2)-C-x(15,21)-[FYWH]-H-x(2)-[CH]-x(2)-C-x(2)-C-x(3)- [LIVMF]. The 5 C's and the H bind zinc.

C2 domain (protein kinase C like). SEQ ID NOs:1325 and 2282 represent polynucleotides encoding novel members of the family of C2 domain containing proteins. Some isozymes of protein kinase C (PKC) contain a domain, known as C2, of about 116 amino-acid residues, which is located between the two copies of the C1 domain (that bind phorbol esters and diacylglycerol) and the protein kinase catalytic domain. (Azzi A. et al., *Eur. J. Biochem.* 208:547-557 (1992); Stabel S., Semin. Cancer Biol. 5:277-284 (1994)).

The C2 domain is involved in calcium-dependent phospholipid binding (Davletov B.A., Suedhof T.C., *J. Biol. Chem.* 268:26386-26390 (1993)). Since domains related to the C2 domain are also found in proteins that do not bind calcium, other putative functions for the C2 domain include binding to inositol-1,3,5-tetraphosphate. (Fukuda M., et al., *J. Biol. Chem.* 269:29206-29211 (1994).)

The consensus pattern for the C2 domain is located in a conserved part of that domain, the connecting loop between beta strands 2 and 3. The profile for the C2 domain covers the total domain. The consensus for this protein family is:: [ACG]-x(2)-L-x(2,3)-D-x(1,2)-[NGSTLIF]-[GTMR]-x-[STAP]-D- [PA]-[FY]

Serine proteases, trypsin family, active sites. SEQ ID NO:1410 represents a polynucleotide encoding a novel member of the family of serine protease, trypsin proteins. The catalytic activity of the serine proteases from the trypsin family is

provided by a charge relay system involving an aspartic acid residue hydrogen-bonded to a histidine, which itself is hydrogen-bonded to a serine. The sequences in the vicinity of the active site serine and histidine residues are well conserved in this family of proteases (Brenner S., *Nature 334*:528-530 (1988)).

A consensus for this protein family is: [LIVM]-[ST]-A-[STAG]-H-C [H is the active site residue]. A second consensus for this protein family is: [DNSTAGC]-[GSTAPIMVQH]-x(2)-G-[DE]-S-G-[GS]-[SAPHV]- [LIVMFYWH]- [LIVMFYSTANQH] [S is the active site residue].

RNA Recognition Motif Domain (RRM, RBD, or RNP). SEQ ID NOs: 1464 and 1514 represent polynucleotides encoding novel members of the family of RNA recognition motif domain proteins (Bandziulis R.J. et al., Genes Dev. 3:431-437 (1989); Dreyfuss G. et al., Trends Biochem. Sci. 13:86-91 (1988)).

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Inside the putative RNA-binding domain there are two regions which are highly conserved. The first one is a hydrophobic segment of six residues (which is called the RNP-2 motif); the second one is an octapeptide motif (which is called RNP-1 or RNP-CS). The position of both motifs in the domain is shown in the following schematic representation:

As a consensus pattern for this type of domain the RNP-1 motif was used. The consensus for this protein family is: [RK]-G-{EDRKHPCG}-[AGSCI]-[FY]-[LIVA]-x-[FYLM]

Phosphatidylinositol-specific phospholipase C, Y Domain. SEQ ID NO: 1707 represents a polynucleotide encoding a novel member of the phosphatidylinositol-specific phospholipase C, Y domain family of proteins. Phosphatidylinositol-specific phospholipase C (EC3.1.4.11), a eukaryotic intracellular enzyme, plays an important role in signal transduction processes (Meldrum E. et al., *Biochim. Biophys. Acta 1092*:49-71 (1991)). It catalyzes the hydrolysis of 1-phosphatidyl-D-myo-inositol-3,4,5- triphosphate into the second messenger molecules diacylglycerol and inositol-1,4,5-triphosphate. This catalytic process is tightly regulated by reversible phosphorylation and binding of regulatory proteins (Rhee S.G., Choi K.D., *Adv. Second Messenger Phosphoprotein Res. 26*:35-61 (1992); Rhee S.G., Choi K.D., *J. Biol. Chem. 267*:12393-12396 (1992); Sternweis P.C., Smrcka A.V., Trends Biochem. *Sci. 17*:502-506 (1992)).

All eukaryotic PI-PLCs contain two regions of homology, referred to as "X-box" and "Y-box". The order of these two regions is the same (NH2-X-Y-COOH), but the spacing is variable. In most isoforms, the distance between these two regions is only 50-100 residues but in the gamma isoforms one PH domain, two SH2 domains, and one SH3 domain are inserted between the two PLC-specific domains. The two conserved regions have been shown to be important for the catalytic activity. At the C-terminal of the Y-box, there is a C2 domain possibly involved in Ca-dependent membrane attachment.

Serine Carboxypeptidases. SEQ ID NO:1744 represents a polynucleotide encoding a novel member of the serine carboxypeptidases family of proteins. Carboxypeptidases may be either metallo carboxypeptidases or serine carboxypeptidases (EC 3.4.16.5 and EC 3.4.16.6). The catalytic activity of the serine carboxypeptidases, like that of the trypsin family serine proteases, is provided by a charge relay system involving an aspartic acid residue hydrogen-bonded to a histidine, which is itself hydrogen-bonded to a serine (Liao D.I., Remington S.J., *J. Biol. Chem.* 265:6528-6531 (1990)).

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The sequences surrounding the active site serine and histidine residues are highly conserved in all these serine carboxypeptidases. A consensus for this protein family is: [LIVM]-x-[GTA]-E-S-Y-[AG]-[GS] [S is the active site residue]. A second consensus for this protein family is: [LIVF]-x(2)-[LIVSTA]-x-[IVPST]-x-[GSDNQL]-[SAGV]-[SG]-H-x- [IVAQ]-P-x(3)-[PSA] [H is the active site residue].

dsrm Double-Stranded RNA Binding Motif. SEQ ID NO:1818 represents a polynucleotide encoding a novel member of the dsrm double-stranded RNA binding motif proteins. In eukaryotic cells, a multitude of RNA-binding proteins play key roles in the posttranscriptional regulation of gene expression. Characterization of these proteins has led to the identification of several RNA-binding motifs. Several human and other vertebrate genetic disorders are caused by aberrant expression of RNA-binding proteins. (C. G. Burd & G. Dreyfuss, *Science* 265: 615-621 (1994)).

Proteins containing double stranded RNA binding motifs bind to specific RNA targets. Double stranded RNA binding motifs are exemplified by interferon-induced protein kinase in humans, which is part of the cellular response to dsRNA.

SEQ ID NOs:2577, 3183 and 3195 encode members of the 4 transmembrane integral membrane protein family. This family consists of type III proteins, which are integral membrane proteins that contain a N-terminal membrane-anchoring domain that is not cleaved during biosynthesis, and which functions as a translocation

signal and a membrane anchor. The proteins also have three additional transmembrane regions. The consensus pattern is: G-x(3)-[LIVMF]-x(2)-[GSA]-[LIVMF] (2)-G-C-x-[GA]-[STA]-x(20-[eG]-x(20-[CwN]-[LIVM](2).

SEQ ID NO:2944 encodes a polypeptide having a calpain large subunit, domain III. Calpains are a family of intracellular proteases that play a variety of biological roles. Calpain 3, also known as p94, is predominantly expressed in skeletal muscle and plays a role in limb-girdle muscular dystrophy type 2A. (Sorimachi, H. et al., Biochem. J. 328:721-732, 1997).

SEQ ID NOs:1911 and 1980 encode polypeptides having a C3HC4 type zinc finger domain (RING finger), which is a cysteine-rich domain of 40 to 60 residues that binds two atoms of zinc, and is believed to be involved in mediating protein-protein interactions. Mammalian proteins of this family include V(D)J recombination activating protein, which activates the rearrangement of immunoglobulin and T-cell receptor genes; breast cancer type 1 susceptibility protein (BRCA1); bmi-1 proto-oncogene; cbl proto-oncogene; and mel-18 protein, which is expressed in a variety of tumor cells and is a transcriptional repressor that recognizes and binds a specific DNA sequence. The consensus pattern is: C-x-H-x-[LIVMFY]-C-x(2)-C-[LIVMYA].

SEQ ID NO:3274 encodes a eukaryotic transcription factor with a fork head domain, of about 100 amino acid residues. Proteins of this group are transcription factors, including mammalian transcription factors HNF-3-alpha, -beta, and -gamma; interleukin-enhancer binding factor; and HTLF, which binds to a region of human T-cell leukemia virus long terminal repeat. The consensus pattern is [KR]-P-[PTQ]-[FYLVQH]-S-[FY]x(2)-[LIVM]-X(3,4)-[AC]-[LIM].

SEQ ID NO:3345 encodes a polypeptide having a PDZ domain. Several dozen signaling proteins belong to this group of proteins that have 80-100 residue repeats known as PDZ domains. Several of the proteins interact with the C-terminal tetrapeptide motifs X-Ser/Thr/X-Val-COO- of ion channels and/or receptors. (Ponting, C. P., Protein Sci. 6;464-468, 1997.)

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SEQ ID NO:3351 encodes a polypeptide in the family of phorbol esters/glycerol binding proteins. Phorbol esters (PE) are analogues of diacylglycerol (DAG) and potent tumor promoters. DAG activates a family of serine-threonine protein kinases, known as protein kinase C. The N-terminal region of protein kinase C binds PE and DAG, and contains one or two copies of a cysteine-rich domain of about 50 amino acid residues. Other proteins having this domain include diacylglycerol kinase; the vav oncogene; and N-chimaerin, a brain-specific protein. The DAG/PE binding

domain binds two zinc ions through the six cysteines and two histidines that are conserved in the domain. The consensus pattern is: H-x-[LIVMFYW]-x(8, 11)-C-x(2)-C-x-(3)-[LIVMFC]-x(5, 10)-C-x(2)-C-x(4)-[HD]-x(2)-C-x(5, 9)-C.

SEQ ID NO:2216 encodes a polypeptide having a WW/rsp5/WWP domain. The protein is named for the presence of conserved aromatic positions, generally tryptophan, as well as a conserved proline. Proteins having the domain include dystrophin, vertebrate YAP protein, and IQGAP, a human GTPase activating protein which acts on ras. The consensus pattern is: W-x(9,11)-[VFY]-[FYW]-x(6,7)-[GSTNE]-[GSTQCR]-[FYW]-x(2)-P.

SEQ ID NO:2428 encodes a member of the dual specificity phosphatase family, having a catalytic domain, and SEQ IDS NOs:2281 and 2310 encode members of the protein tyrosine phosphatase family. These families are related and classified as tyrosine specific protein phosphatases. The enzymes catalyze the removal of a phosphate group from a tyrosine residue, and are important in the control of cell growth, proliferation, differentiation, and transformation. The consensus pattern is [LIVMF]-H-C-x(2)-G-x-(3)-[STC]-[STAGP]-x-[LIVMFY].

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Table 1

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3		RTA00002712F.a.06.1.P.Seq	F	M00023282.A:C02	CH04MAL
4	29372	RTA00002694F.b.02.1.P.Seq	F	M00043419D:A10	CH20COHLV
5	455003	RTA00002684F.d.03.2.P.Seq	F	M00040118D:G10	CH09LNL
7	380625	RTA00002691F.b.05.3.P.Seq	F	M00043306D:B07	CH17COHLV
	450959	RTA00002680F.b.04.1.P.Seq	F	M00039775A:A09	CH09LNL
9	397851 20652	RTA00002710F.k.01.1.P.Seq	F	M00022440B:E01	CH03MAH
	97830	RTA00002663F.k.18.1.P.Seq		M00022767B:G11	СН03МАН
10		RTA00002670F.j.23.1.P.Seq	F	M00033442A:D06	CH09LNL
11	373071 162369	RTA00002713F.e.01.1.P.Seq	F	M00027292D:F10	CH04MAL
12		RTA00002685F.f.15.2.P.Seq		M00039508A:C12	CHIZEDT
13	401247	RTA00002669F.i.15.3.P.Seq		M00033231D:B09	CH08LNH
14	430738	RTA00002711F.c.14.1.P.Seq		M00022860C:G04	CH03MAH
15		RTA00002681F.p.01.2.P.Seq		M00039909C:G05	CH09LNL
16	375772	RTA00002669F.j.01.3.P.Seq		M00033243B:A05	CH08FNH
17	430689	RTA00002677F.d.07.2.P.Seq		M00039345C:C12	CH09LNL
18	376546	RTA00002667F.f.17.1.P.Seq		M00032790B:A07	CH08LNH
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	376814	RTA000026745.h.02.1.P.Seq		M00039139C:G12	CH0°LNL
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24	379114	RTA00002681F.n.24.2.P.Sec	F	M00039903C:F03	CH0oLNL
26	380668	RTA00002670F.p.11.1.P.Sec	F	M00033581C:H10	CH09LNL
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31	430896	RTA00002669F.b.20.3.P.Sec		M00033185C:D01	CH08LNH
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35		RTA00002673F.k.16.2.P.Sec		M00039097D:D06	CH09LNL
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50	375730	RTA00002678F.h.15.1.P.Seq	F	M00032811B:D02	CH08LNH
51	428959	RTA00002677F.c.03.2.P.Seq	F	M00039341C:H11	CH09LNL
52	376851	RTA00002677F.d.U.3.P.Seq	F	M00038272A:G01	CH09LNL
53	373808	RTA00002671F.d.14.2.P.Seq	F	M00039258B:E06	CH09LNL
54	376168	RTA00002675F.n.17.1.P.Seq	F	M00027135A:B11	CH04MAL
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89	373837	RTA00002672F.p.22.1.P.Sc		M00039476B:A02	CH09LNL
90	376435	RTA00002678F.h.17.2.P.Sc		M00038638D:H03	CH09LNL
91		RTA00002672F.b.20.1.P.S		M00039328D:D07	CH09LNL
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97	14197	RTA000027101 1113 11.05 RTA00002684F.c.04.2.P.Seq	F	M00040115B:H12	CH09LNL
98	380666	RTA000026841.6.0 vizzr.564	F	M00039404B:A05	CH09LNL
99	377352	RTA00002677F.::13:2.1:35eq RTA00002682F.a.03.1.P.Seq	F	M00039914D:G12	CH09LNL
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101	428269	RTA000026671F.1.13.3.P.Seq	F	M00038327A:C11	CH09LNL
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104	377504		F	M00022183B:C02	CH03MAH
105	33508	RTA00002710F.g.17.1.P.Seq		M00007157C:F11	CH02COH
106	129179	RTA00002662F.d.19.2.P.Seq		M00039328D:D07	CH09LNL
107	377086	RTA00002676F.p.07.2.P.Seq		M00039233A:A03	CH09LNL
108	375872	RTA00002675F.h.15.1.P.Seq		M00039303C:F11	CH09LNL
109	375652	RTA00002676F.i.07.3.P.Seq	F	M00039144C:E06	CH09LNL
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111	378983	RTA00002682F.a.07.1.P.Seq		M00040302C:A04	CH09LNL
112	.377343	RTA00002684F.g.04.1.P.Seq	F	M00039869B:F06	CH09LNL
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120	177367	RTA00002663F.m.22.1.P.Sec	g F	M00040305C:H06	CH09LNL
121	377788	RTA00002684F.g.24.1.P.Sec	F F	M00039230D:G12	CH09LNL
122	375058	RTA00002675F.h.02.1.P.Sec	F	M00039230D:012	CH09LNL
123	380412	RTA00002680F.k.15.2.P.Sec	F	M00039818B:B04	CH03MAH
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-		RTA00002676F.d.07.2.P.Se	q F	M00039281D:B04	
132		RTA00002709F.b.05.1.P.Se	q F	M00005358B:B06	CH02COH
133		RTA00002668F.i.23.1.P.Se	q F	M00033007C:E01	CH08LNH
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179	32279	RTA00002709F.d.23.1.P.Se	q F	M00039782A:H10	CH09LNL
180	376379	RTA00002680F.c.15.1.P.Se	q F	M00039782A:H10	CH09LNL
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193	186655	RTA0000271211121111115eq	F	M00039766D:H01	CH14EDT
194	404682	RTA00002709F.c.05.2.P.Seq	F	M00005457C:A03	CH02COH
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200	430738	RTA00002712F.g.22.1.P.Seq		M00026882D:G09	CH04MAL
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212	378891	RTA00002672F.i.18.1.P.Seq		M00039533D:F04	CH12EDT
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218		RTA00002682F.e.10.1.P.Sec	<u> </u>	M00004152A:C12	CH01COH
219		RTA00002708F.f.17.1.P.Sec	<u>' </u>	M00042895A:D10	CH15CON
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225	41126	RTA00002713F.I.12.1.P.Se		M00027625A:H01	CH04MAL
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230	376746	RTA00002674F.f.12.2.P.Se	q F	M00039177B:D03	CH09LNL
23		RTA00002674F.n.21.2.P.Se	eq F	M00039177B:B03	CH20COHLV
233		RTA00002694F.c.10.1.P.Se	eq F	M00040105C:F11	CH09LNL
233		RTA00002683F.p.17.2.P.Sc	q F	M00039105C:B08	CH09LNL
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251	378764	RTA00002681F.j.04.1.P.Seq		M00033276B:G08	CH08LNH
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260	375389	RTA00002674F.a.13.2.P.Seq		M00022127C:H03	СН03МАН
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287	429547	RTA00002668F.c.07.1.P.Seq	F	M00032937B:009	CH09LNL
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290	380325	RTA00002670F.p.22.2.P.Seq	F	M00039896C:H01	CH09LNL
291	378326	RTA00002681F.m.11.2.P.Seq	F	M00039390C:H01	CH09LNL
292	375618	RTA00002675F.d.13.1.P.Seq	F	M00006977C:G04	CH02COH
293	20999	RTA00002709F.j.16.1.P.Seq	F	M00022793D:B01	СНОЗМАН
294	29102	RTA00002710F.p.18.1.P.Seq	F	M00032743D.B01 M00039778C:A04	CH09LNL
295	379334	RTA00002680F.b.22.1.P.Seq		M00006886D:H02	CH02COH
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298	373325	RTA00002672F.c.14.2.P.Seq	F	M00038662B:A12	CH09LNL
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310	375458	RTA00002678F.1.06.2.P.Seq	F	M00039611D:D11	CH09LNL
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334	25238	RTA00002710F.n.08.1.P.Seq		M00040085D:A10	CH09LNL
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340	379690	RTA00002681F.d.12.2.P.Sec	۱۱ <u>-</u>	M00039839C:G15 M00039079A:A05	CH09LNL
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351		RTA00002713F.e.07.1.P.S	***	M00040010.4:F10	CH09LNL
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354		RTA00002671F.g.01.1.P.S		M00039340A:D05	CH09LNL
355	25(00)	RTA00002677F.b.16.2.P.S		M00033358A:H12	CH09LNL
350		RTA00002670F.d.05.2.P.S	,04	M00039006D:B01	CH09LNL
35		RTA00002672F.g.24.2.P.S	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	M00028210B:D02	CH08LNH
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36		RTA00002676F.a.21.2.P.	Seq F	M00039465A:A08	CH09LNL
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378	379598	RTA00002710F.j.23.1.P.Seq	F	M00022434D:D06	CH03MAH
379	45300	RTA00002710F.J.25.1.1.5eq	F	M00005384A:C11	CH02COH
380	23030	RTA00002709F.b.10.1.P.Seq	F	M00039720D:D02	CH09LNL
381	379928	RTA00002679F.o.06.1.P.Seq	F	M00032829B:E06	CH08LNH
382	430191	RTA00002667F.k.01.1.P.Seq	F	M00039228A:B05	CH09LNL
383	374684	RTA00002675F.g.02.1.P.Seq		M00039299B:G12	CH09LNL
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386	380673	RTA00002673F.j.13.1.P.Seq		M00039702.A:B12	CH09LNL
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389	378673	RTA00002680F.p.21.2.P.Sed	F	M000333300D:H12	CH09LNL
390	372909	RTA00002670F.a.12.2,P.Sec	F	M00033300D:1112	CH09LNL
391	373300	RTA00002674F.c.21.1.P.Sec	F	M00039120B:A00	CH09LNL
392	379318	RTA00002683F.h.16.2.P.Sec	F F	M00039890A:H05	CH09LNL
393	378319	RTA00002681F.k.07.2.P.Sec	1 F	M00039890A:1102 M00039230A:A10	CH09LNL
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394	374328	RTA00002673F.c.24.2.P.Se	9 F	M00039061B:F08	CH09LNL
395	374328	RTA00002673F.d.01.2.P.Se	q F	M00039061B:F08	CH08LNH
396	428401	RTA00002667F.b.07.1.P.Se	9 <u> </u>	M00032725C:F06	CH14EDT
397	136202	RTA00002687F.p.05.2.P.Se	q <u>F</u>	M00040349D:B09	CH09LNL
398		RTA00002673F.c.15.1.P.Se	9	M00039059C:G08	CHOICOH
399	374394	RTA00002708F.c.17.1.P.Se	q <u>F</u>	M00003816D:E11	CH09LNL
400		RTA00002681F.h.11.1.P.Se	q F	M00039876D:H09	CH04MAL
401		RTA00002712F.p.17.2.P.Se	q F	M00027178B:G09	СНОСОН
402		RTA00002709F.d.14.1.P.Sc	q F	M00005623D:G12	CH09LNL
403		RTA00002670F.k.07.2.P.Se	q F	M00033446D:B02	CH02COH
404		RTA00002709F.f.18.1.P.Se	q F	M00006657C:G05	CH02COH
40:		RTA00002709F.m.09.2.P.S	eq F	M00007194A:B09	
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40		RTA00002714F.c.10.1.P.S	eq F	M00027836D:F12	CH04MAL
40		RTA000027141:c:10	ea F	M00032737B:E09	CH08LNH
40		RTA00002669F.1.14.2.P.S	eo F	M00033276B:G08	CH08LNH
41		RTA00002682F.h.08.1.P.S	eg F	M00039983D:A06	CH09LNL
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41	5 215605	RTA00002664F.i.20.1.P.S		M00039241A:E11	CH09LNL
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427	186190	RTA00002714F.a.04.1.P.Seq		M00027319D:B11	CH04MAL
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429	7007	RTA00002709F.d.08.1.P.Seq	F	M00039641C:D07	CH12EDT
430	400084	RTA00002685F.o.19.2.P.Seq	F	M00039301B:F06	CH09LNL
431	375648	RTA00002676F.h.18.2.P.Seq	F	M00037301B:100 M00022492C:A02	CH03MAH
432	166493	RTA00002663F.h.08.1.P.Seq	F	M00032492C:A02 M00039984B:G12	CH09LNL
433	379632	RTA00002682F.h.14.1.P.Seq	F	M00039984B:G12 M00039297C:H08	CH09LNL
434	373234	RTA00002676F.g.15.2.P.Seq	F		CH12EDT
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435	186623	RTA00002712F.f.15.1.P.Seq	F	M00026843B:D10	CH04MAL
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437		RTA00002692F.a.01.1.P.Seq	F	M00042584B:C10	CH14EDT
438	451857	RTA00002687F.c.03.2.P.Seq	F	M00039770.A:G11	CH03MAH
439	404620	RTA00002663F.k.23.1.P.Seq	F	M00022797B:G08	CH02COH
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441	42729	RTA0000274F.b.07.1.P.Sec	F	M00039123A:B10	
442	373380	RTA00002673F.c.07.1.P.Sec	F	M00039058C:H02	CH09LNL
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445	16749	RTA00002709F.6.14.2.1.3.P.Sec	F	M00039795D:E10	CH09LNL
446	375592	RTA00002676F.g.06.2.P.Se		M00039295B:D03	CH09LNL
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450	378270	RTA00002680F.h.08.2.P.Se	91	M00033034C:F02	CH08LNH
451	236321	RTA00002668F.k.14.1.P.Se		M00039827B:F07	CH09LNL
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453	373252	RTA00002670F.k.16.2.P.Se	7	M00033446C:G08	CH09LNL
454	384601	RTA00002670F.k.06.2.P.Se	771	M00039746C:G09	CHITEDT
455	403772	RTA00002687F.a.03.2.P.Se	- 4	M00040081C:E01	CH09LNL
456	379566	RTA00002683F.k.04.1.P.Sc	***	M00040349D:B09	CHI-EDT
457		RTA00002687F.p.05.1.P.S	-91	M00027248A:C02	CH04MAL
458		RTA00002713F.c.13.1.P.S	*7	M00039024B:B10	CH09LNL
459		RTA00002672F.j.11.1.P.Se	• • • • • • • • • • • • • • • • • • • •	M00039746C:A08	CH14EDT
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46		RTA00002671F.c.20.1.P.S	eq F	MO0033831B-C11	CH03MAH
		RTA00002711F.b.22.1.P.S	Seq F	M00022834B:G11	CH18CON
46		RTA00002692F.d.05.2.P.S	seq r	M00043003C:D08	CH08LNH
46	121370	RTA00002669F.m.04.2.P.	Seq F	M00033288B:D12	CH04MAL
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46		RTA00002775	Seq F	M00039663C:G09	CH09LNL
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476	129323	RTA00002710F.a.23.1.P.Seq	F	M00007976A:C10	CH03MAH
477	12960	RTA00002710F.a.251111364	F	M00027641C:A03	CH04MAL
478	186730	RTA00002713F.m.24.1.P.Seq	F	M00027596C:E06	CH04MAL
479	59077	RTA00002713F.ht.24.11.15eq	F	M00023316C:G08	CH04MAL
480	185884	RTA00002712F.b.00.11F.Seq RTA00002708F.g.08.1.P.Seq	F	M00004197B:H10	CH01COH
481	19471	RTA00002708F.g.08.1.1 .Seq	F	M00008063B:A06	CHO3MAH
482	45206	RTA00002710F.c.00.11F.Seq RTA00002687F.g.06.2.P.Seq	F	M00040208A:C03	CH14EDT
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486	400052	RTA00002692F.c.14.2.P.Seq		M00042988A:F06	CH18CON
487	452194	RTA00002692F-C-14-22F-Seq		M00007992C:F06	CH03MAH
488	24034	RTA00002710F.8.08.11.P.Seq		M00042905D:D02	CH15CON
489	447544	RTA00002686F.c.23.1.P.Seq		M00040141D:F05	CHISEDT
490	401872	RTA00002686F.C.23.11F.Seq RTA00002674F.g.19.2.P.Seq		M00039139A:C09	CH09LNL
491	376553	RTA00002694F.a.07.1.P.Seq		M00042595A:A11	CH20COHLV
492	455051	RTA00002708F.j.03.1.P.Seq		M00004393B:E07	CH01COH
493	16760	RTA00002708F.j.03.11.P.Seq		M00039015A:D07	CH09LNL
494	374174	RTA00002672F.k.21.2.P.Seq		M00039030B:E02	CH09LNL
495	374283	RTA00002672F.R.21.217.3eq		M00039909C:G05	CH09LNL
496	375772	RTA00002678F.i.03.2.P.Seq		M00039477D:A10	CH09LNL
497	376417	RTA00002666F.o.02.1.P.Seq		M00032678C:D06	CH08LNH
498	428971	RTA00002681F.j.15.1.P.Seq		M00039887C:E07	CH09LNL
499	394098	RTA00002670F.n.03.1.P.Seq		M00033561C:A02	CH09LNL
500	379761.	RTA00002674F.i.08.1.P.Seq	·	M00039144C:E06	CH09LNL
501	374266	RTA00002670F.1.07.1.P.Seq		M00033457D:A05	CH09LNL
502	372946	RTA00002664F.e.08.1.P.Sec		M00027085C:E11	CH04MAL
503	228909	RTA00002665F.e.05.1.P.Sec		M00028354D:A03	CH08LNH
504		RTA00002683F.e.03.1.F.3cc	<u> </u>	M00039816C:D05	CH09LNL
505	I	R1A00002680F.K.19.2.F.366	<u> </u>	M00038259C:H09	CH09LNL
506		RTA00002671F.c.24.2.P.Sec	<u></u>	M00028617C:A12	CH08LNH
507		RTA00002665F.g.15.1.P.Sec	F	M00033437C:C03	CH09LNL
508		RTA00002670F.j.13.1.P.Sec	<u>' </u>	M00039637C:A10	CH09LNL
509		RTA00002678F.p.11.2.P.Sec	<u> </u>	M00022739A:B03	СНОЗМАН
510		RTA00002710F.p.05.1.P.Sec	<u> </u>	M00021972D:C11	CH03MAH
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515		RTA00002667F.m.03.1.P.Se		M00021964C:E10	СНОЗМАН
516		RTA00002710F.e.15.1.P.Se		M00040309A:E11	CH09LNL
517	377565	RTA00002684F.h.19.1.P.Se	41	1	

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SEQ		CEONINGE	ORIENTATION	CLONE ID	LIBRARY
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521	373607	RTA00002674F.d.15.2.P.Seq	F	M00039196B:H06	CH09LNL
522	378781	RTA00002674F.o.14.1.P.Seq		M00032550D:C02	CH08LNH
523	429361	RTA00002666F.d.11.1.P.Seq	F	M00008045A:H02	CH03MAH
524	126754	RTA00002663F.a.16.1.P.Seq	F	M00031417C:G09	CH08LNH
525	428047	RTA00002665F.k.10.1.P.Seq	F	M00031417C:G07 M00005625A:C02	CH02COH
526	18863	RTA00002709F.d.15.1.P.Seq	F	M00003625A:C02 M00033561C:A02	CH09LNL
527	379761	RTA00002670F.n.03.2.P.Seq	F		CH08LNH
528	46407	RTA00002665F.c.10.1.P.Seq	F	M00028196D:A03	CH02COH
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529	427466	RTA00002665F.b.11.1.P.Seq	F	M00028184D:G10	CH12EDT
530		RTA00002685F.c.03.2.P.Seq	F	M00039374B:B07	CH09LNL
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549		RTA00002672F.b.03.2.P.Se	q F -	M00033570C:C10	CH09LNL
550		RTA00002670F.o.06.2.P.Se	eq F	M00032808B:G10	CH08LNH
551		RTA00002667F.h.14.1.P.Se	eq F	M00032808B:G10	CH09LNL
552		RTA00002682F.n.01.1.P.Se	eq F		CH09LNL
	277532	RTA00002672F.d.10.2.P.Se	eq F	M00038991A:D01	CH09LNL
553		RTA00002677F.m.05.2.P.S	eq r	M00039417B:F01	CH09LNL
554		RTA00002681F.f.07.1.P.Se	eq F	M00039866B:A08	CH09LNL
555		RTA00002674F.m.12.1.P.S	leq F	M00039170C:F05	CH09LNL
556		RTA00002673F.d.24.2.P.S	eq F	M00039066D:G08	CH09LNL
55		RTA00002673F.e.01.2.P.S	eq F	M00039066D:G08	
558		RTA00002679F.i.03.1.P.S	eq F	M00039686C:E06	CH09LNL
559		RTA00002680F.e.15.1.P.S	eq F	M00039792A.B04	CH09LNL
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567	379207	RTA00002670F.b.07.2.P.Seq	F	M00033306D.G06	CH08LNH
568	427893	RTA00002665F.k.19.1.P.Seq	F	M00031419D:C04 M00040305A:D11	CH09LNL
569	377530	RTA00002684F.g.19.2.P.Seq	F		CH08LNH
570	429707	RTA00002668F.c.11.1.P.Seq	F	M00032918C:B10	CH08LNH
571	427610	RTA00002665F.i.04.1.P.Seq	F	M00028770A:D04	CH02COH
572	100699	RTA00002662F.b.22.2.P.Seq	F	M00006680B:D02	CH09LNL
	378974	RTA00002682F.m.21.1.P.Seq	F	M00040017.A:C06	CH09LNL
573	373607	RTA00002674F.d.15.1.P.Seq	F	M00039127D:E10	CH08LNH
574	262951	RTA00002665F.d.04.3.P.Seq	F	M00028215D:F03	CH04MAL
575		RTA00002713F.e.11.1.P.Seq	F	M00027301B:B08	CH04MAL
576	30748	RTA00002714F.c.11.1.P.Seq	F	M00027837C:D09	CH04MAL CH09LNL
577	161116	RTA00002682F.p.20.1.P.Seq	F	M00040029A:G04	
578	379211	RTA00002669F.i.24.1.P.Seq	F	M00033243B:A05	CH08LNH
579	430689	RTA00002673F.1.22.2.P.Seq	F	M00039104D:C09	CH09LNL
580	374122	RTA00002677F.h.06.2.P.Seq	F	M00039398A:B10	CH09LNL
581	376521	RTA00002670F.b.12.2.P.Seq	F	M00033308B:G05	CH09LNL
582	372834	RTA000026761.5.1	F	M00040022C:D06	CH09LNL
583	379014	RTA00002677F.b.18.2.P.Sec	F	M00039340B:G08	CH09LNL
584	376344	RTA00002676F.f.01.2.P.Seq	F	M00039288C:B11	CH09LNL
585	376485	RTA00002709F.e.18.1.P.Sec	F	M00005820C:E04	CH02COH
586	21661	RTA00002709F.E.18.1.P.Sec		M00039211A:C12	CH09LNL
587	376539	RTA00002673F.b.13.11.13et	1	M00033223B:H07	CH08LNH
588	431645	RTA0000289Fin:19:3:1:50 RTA00002714F.c.20.1.P.Sec	1	M00028120D:F12	CH04MAL
589	163293	RTA00002713F.c.20.1.P.Set	1	M00027263A:F10	CH04MAL
590	178614	RTA00002/13F.C.20.1.1.5c.	<u> </u>	M00033432B:H10	CH09LNL
591	373274	RTA00002670F.i.22.2.P.Sec	<u> </u>	M00039677A:B08	CH09LNL
592	379820	RTA00002679F.f.15.1.P.Sec	<u> </u>	M00022233C:A12	СН03МАН
593	160536	RTA00002663F.f.10.1.P.Se	1	M00038328D:A03	CH09LNL
594	373313	RTA00002671F.m.02.1.P.Se	71	M00027022D:G11	CH04MAL
595	26429	RTA00002712F.k.23.1.P.Se	71	M00022979.A:D05	CH03MAH
596	17983	RTA00002711F.f.10.1.P.Se	7	M00039888B:D03	CH09LNL
597	375388	RTA00002681F.j.22.2.P.Se	71	M00027094A:B03	CH04MAL
598		RTA00002712F.m.21.1.P.S	- 71	M00005384A:C11	CH02COH
599	23030	RTA00002709F.b.10.2.P.Se	~	M00033457D:A05	CH09LNL
600		RTA00002670F.1.07.2.P.Se	7	M00039792A:B04	CH09LNL
601		RTA00002680F.e.15.2.P.Sc	eq F	M00039080C:H06	CH09LNL
602		RTA00002673F.i.08.1.P.Se		M00039938C:A08	CH09LNL
603		RTA00002682F.e.09.1.P.S	eq F	M00039257D:C03	CH09LNL
604		RTA00002675F.n.15.1.P.S	eq F	M00039685A:A08	CH09LNL
605		RTA00002679F.h.20.1.P.S	eq F	M00039978A:G03	CH09LNL
606	2 = 2 () 2	RTA00002682F.g.08.1.P.S	eq F	M00039815C:F09	CH09LNL
607		RTA00002680F.k.11.1.P.S	eq F	N(00039813C.F09	CH03MAF
608		RTA00002711F.g.06.1.P.S	eq F	M00023024D:F12	
		RTA00002664F.j.08.1.P.S	eq F	M00027733A:A02	
609		RTA00002687F.h.13.1.P.S	ieq F	M00040291D:C05	
610	1 21290	RTA00002712F.g.01.1.P.S	ieq F	M00026859D:D01	1

SEQ		aro vi vir	ORIENTATION	CLONE ID	LIBRARY
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614	69863	RTA00002712F.i.18.1.P.Seq	F	M00039298B:B06	CH09LNL
615	375285	RTA00002676F.g.18.2.P.Seq		M00033437C:C03	CH09LNL
616	373000	RTA00002670F.j.13.2.P.Seq	F	M00039869B:F06	CH09LNL
617	378679	RTA00002681F.f.16.1.P.Seq	F	M000378075:196	CH04MAL
618	45407	RTA00002712F.k.11.1.P.Seq	F	M0002767674:266	CH04MAL
619	16838	RTA00002712F.e.23.1.P.Seq	F	M00027236A:E04	CH04MAL
620	186425	RTA00002713F.c.04.1.P.Seq	F	M00027230A:204	CH09LNL
621	376485	RTA00002676F.e.24.2.P.Seq	F	M00039238C:B11 M00027108C:B03	CH04MAL
622	41108	RTA00002712F.n.12.1.P.Seq	F		CH08LNH
623	430876	RTA00002669F.c.02.1.P.Seq	F	M00033186C:D11	CH04MAL
624	185716	RTA00002713F.1.07.1.P.Seq	F	M00027537C:B01	CH04MAL
625	85338	RTA00002712F.b.18.1.P.Seq	F	M00023333D:C12	CH04MAL
	185597	RTA00002713F.m.23.1.P.Seq	F	M00027596A:A10	CH04MAL
626	139348	RTA00002713F.k.23.1.P.Seq	F	M00027526D:F03	
627	454665	RTA00002693F.d.15.2.P.Seq	F	M00043164C:E12	CH19COP
628		RTA00002713F.1.01.1.P.Seq	F	M00027528C:B10	CH04MAL
629	186387	RTA00002713F.k.24.1.P.Seq	F	M00027528C:B10	CH04MAL
630	186387	RTA00002708F.h.20.1.P.Sec	F	M00004308C:C06	CH01COH
631	21093	RTA00002710F.c.23.1.P.Sec	F	M00021671D:F12	СНОЗМАН
632	20827	RTA00002712F.f.24.1.P.Seq	F	M00026859D:D01	CH04MAL
633	21290	RTA00002712F.d.22.1.P.Sec	F	M00021908D:G12	СНОЗМАН
634	17646	RTA000027101.d.2211.	<u> </u>	M00039736D:G08	CHISEDT
635	402817	RTA00002713F.n.09.1.P.Sec		M00027615A:F10	CH04MAL
636	42854	RTA00002713F.ii.07111.5cc	1	M00033186C:D11	CH08LNH
637	430876	RTA00002679F.a.21.2.P.Sec	11	M00039655C:E08	CH09LNL
638		RTA00002674F.m.03.2.P.Se	1	M00039168C:A04	CH09LNL
639	375848	RTA00002708F.i.06.1.P.Sec	7	M00004340C:C07	CH01COH
640	36165	RTA00002708F.1.06.1.F.560		M00043492.4:E01	CH20COHLV
641	456506	RTA00002694F.d.05.1.P.Se	<u> </u>	M0003901-A:H10	CH09LNL
642	374450	RTA00002672F.i.05.2.P.Se	7	M00040100D:B06	CH09LNL
643		RTA00002683F.o.21.2.P.Se	7	M00038328D:A03	CH09LNL
644	373313	RTA00002671F.m.02.2.P.Se	7	M00039898A:A08	CH09LNL
645	377861	RTA00002681F.m.20.1.P.Se	7	M00033204B:A07	CH08LNH
646	431196	RTA00002669F.f.07.2.P.Se	7	M00040032A:B03	CH09LNL
647	372795	RTA00002683F.a.06.1.P.Se	71	M00001439C:H06	CH01COH
648		RT.A00002661F.b.03.1.P.Se	q F	M00039158B:G12	CH09LNL
649	374410	RTA00002674F.k.11.1.P.Sc	eq F	M00039118D:A06	CH09LNL
650		RTA00002674F.a.01.2.P.Se	eq F	M00033713D::100	CH08LNH
65		RTA00002669F.e.23.2.P.Se	:q F	M00033202D:G00	CH09LNL
65		RTA00002672F.e.19.1.P.Se	eq F		CH08LNH
65		RTA00002666F.d.01.1.P.S	eq F	M00032545B:H09	CH08LNH
65		RTA00002666F.d.03.1.P.S	eq F	M00032545 D:G05	СНОЗМАН
65		RTA00002710F.e.11.1.P.S	eq F	M00021955A:H02	CH03MAH
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	/ 1 4430	RTA00002681F.h.07.2.P.S	ea F	M00039875D:A10	1 しけひりしいし

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661	21028	RTA00002709F.1.09.1.P.Seq	F	M00039011D:C10	CH09LNL
662	374063	RTA00002672F.h.15.2.P.Seq	F	M00040107B:H07	CH09LNL
663	380686	RTA00002684F.a.03.2.P.Seq	F	M00040181B:H09	CHISEDT
664	402950	RTA00002686F.g.11.1.P.Seq	F	M00031485D:G02	CH08LNH
665	428064	RTA00002665F.1.04.1.P.Seq	F	M00004046C:A08	CH01COH
666	23310	RTA00002708F.e.10.1.P.Seq		M00039339C:F03	CH09LNL
667	376233	RTA00002677F.b.15.2.P.Seq	F	M00039168C:A04	CH09LNL
668	375848	RTA00002674F.m.03.1.P.Seq	F	M000391000::10 M00028772C:B09	CH08LNH
669	242251	RTA00002665F.i.08.1.P.Seq	F	M00038999D:C11	CH09LNL
670	374064	RTA00002672F.f.15.2.P.Seq	F	M00033999B:D06	CH03MAH
671	146260	RTA00002663F.d.17.1.P.Seq	F	M00022099B.D00	CH09LNL
	375575	RTA00002677F.e.22.2.P.Seq	F	M00039385B:E09	CH08LNH
672		RTA00002665F.c.15.3.P.Seq	F	M00028201B:H12	CH02COH
673	355518	RTA00002662F.b.08.2.P.Seq	F	M00005539D:G01	CH04MAL
674	184223	RTA00002664F.e.07.2.P.Seq	F	M00027078A:B02	CH04NAE
675	213306	RTA00002668F.b.04.1.P.Sec	F	M00032907A:G04	CH09LNL
676	429566	RTA00002682F.c.09.1.P.Sec	F	M00039927A:F04	CH09LNH
677	378656	RTA00002668F.e.23.1.P.Sec	F	M00032940A:C02	
678	427760	RTA00002683F.a.06.2.P.Sec	F F	M00040032A:B03	CH09LNL
679	372795	RTA00002666F.f.12.1.P.Sec	F	M00032577A:C04	CH08LNH
680	429340	RTA00002668F.e.17.1.P.Sec	a F	M00032939B:E07	CH08LNH
681	429822	RTA00002680F.d.22.2.P.Se	<u> </u>	M00039783B:A06	CH09LNL
682	375224	RTA00002681F.h.07.1.P.Se	7	M00039875D:A10	CH09LNL
683	378347	RTA00002681F.H.07.13.56		M00039987C:G08	CH09LNL
684	380109	RTA00002682F.i.17.1.P.Se	7	M00040097A:C12	CH09LNL
685	379001	RTA00002683F.o.02.1.P.Se	9	M00039304D:B09	CH09LNL
686		RTA00002676F.i.12.3.P.Se	7	M00038661A:A07	CH09LNL
687	377889	RTA00002672F.c.08.2.P.Se	<u> </u>	M00032793A:F06	CH08LNH
688	429883	RTA00002667F.g.05.1.P.Se	71	M00040014B:D01	CH09LNL
689	377067	RTA00002682F.1.24.1.P.Se	<u> </u>	M00039898D:C06	CH09LNL
690	378001	RTA00002681F.m.22.2.P.S	<u> </u>	M00022433A:E02	CH03MAH
691		RTA00002710F.j.21.1.P.Se		M00039793D:C05	CH09LNL
692		RTA00002680F.f.03.1.P.Sc	- 7	M00039898.A:A08	CH09LNL
693		RTA00002681F.m.20.2.P.S	eq F	M00032766C:A04	CH08LNH
694	100610	RTA00002667F.e.09.1.P.S	eq F	M00032763C:G12	CH03MAH
69:		RTA00002710F.i.10.1.P.S	eq F	M00022302C:CD09	CH04MAL
696		RTA00002713F.e.23.1.P.S	eq F	M00027314C:509	CH08LNH
69		RTA00002668F.o.20.2.P.S	Seq F	M00033140B:A04	
		RTA00002670F.h.23.2.P.S	seq r	N10004500D-202	
69		RTA00002709F.f.07.1.P.S	ieq F	M00006599D:B02	
69		RTA00002670F.i.03.2.P.S	seq F	M00033424D:H12	CH09LNL
70		RTA00002671F.d.20.1.P.S	Seq F	M00038272D:F11	CH09LNL
70		RTA00002684F.h.06.2.P.S	Seq F	M00040307B:F01	
70		RTA00002684F.g.04.2.P.S	Seq F	M00040302C:A04	
70			Seq F	M00039286A:C06	
70			Seq F	M00027080A:B01	CH04MAL
70	5 185848	KTA0000_7121.iii.qqq			

					
SEQ		SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
ID	CLUSTER	RTA00002676F.e.18.2.P.Seq	F	M00039287C:A06	CH09LNL
706	374311	RTA00002667F.b.10.1.P.Seq	F	M00032726C:C01	CH08LNH
707	278923	RTA00002667F.0.10.11.1.5eq	F	M00039847.A:F06	CH09LNL
708	378667	RTA00002681F.b.11.2.P.Seq	F	M00039084D:D07	CH09LNL
709	380454	RTA00002673F.j.16.1.P.Seq	F	M00033425A:C10	CH09LNL
710	381576	RTA00002670F.i.04.2.P.Seq	F	M00039260C:G03	CH09LNL
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713	10583	RTA00002711F.h.11.1.P.Seq	F	M00039987C:E12	CH09LNL
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720		RTA00002680F.f.03.2.P.Seq	F	M00004105D:D05	CH01COH
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727		RTA00002663F.j.07.1.P.Sec	q F	M00022640C:C12	CH14EDT
728		RT.A00002687F.d.01.2.P.Se	q	M00039945C:F09	CH12EDT
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754	374763	RTA00002673F.p.21.1.P.Seq	F	M00039118B:C05	CHISEDT
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761	374264	RTA00002671F.b.20.2.P.Seq	F	M00033595A:C11	CH09LNL
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763	375231	RTA00002709F.j.17.1.P.Seq	F	M00006977D:A03	CH09LNL
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765	379403	RTA00002637.d.24.2.P.Seq	F	M00039381D:C02	
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775	376761	RTA00002677F.g.03.2.P.Sec	<u> </u>	M00040115B:A04	CH09LNL
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777	44025	RTA00002684F.c.01.2.P.Sec	<u> </u>	M00039909D:C02	CH09LNL
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783		RTA00002677F.b.14.2.P.Se	~1	M00039407B:G02	CH09FYF
784		RTA00002677F.j.11.2.P.Se		M00039384C:E02	CH09LNL
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786		RTA00002662F.b.01.2.P.Se	eq F	M00039068C:E06	CH09LNL
787		RTA00002673F.e.12.2.P.Sc	eq F	M00032731B:C10	
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		RTA00002683F.c.20.2.P.S	eq F	M00040042B:A10	
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79			Seq F	M00039124C:F0.	
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79		00003670E - 04 3 P	Seq F	M00039636C:D1	CHOSCIA
79	9 377108	KI AUGUSTON PLE MEN			

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800	375657	RTA00002681F.H.13.11F.Seq RTA00002673F.d.08.2.P.Seq	F	M00039063B:D08	CH09LNL
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809	21686	RTA00002712F.g.05.1.P.Seq		M00042623D:D07	CH18CON
810	452038	RTA00002692F.a.09.2.P.Seq		M00023042D:D02	CH03MAH
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812	152487	RTA00002663F.e.12.1.P.Seq		M00039797C:G05	CH09LNL
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818	375443	RTA00002676F.g.19.2.P.Sec	F	M00039298B:B05 M00039082B:A05	CH09LNL
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829		RTA00002687F.f.07.1.P.Se	q F	M00040203A:H06	CH19COP
830		RTA00002693F.b.12.2.P.Se	:q <u>F</u>	M00043093C:G11	CH09LNL
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832		RTA00002694F.d.16.1.P.Se	F	M00043518B:D06	CH09LNL
		RTA00002672F.i.17.2.P.Se	:q F	M00039015D:H04	CH09LNL
833		RTA00002683F.m.08.2.P.S	eq F	M00040090B:G09	CH09LNL
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83		RTA00002686F.p.07.1.P.S	eq F	M00040286C:C02	CHIZEDT
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84		RTA00002670F.i.16.1.P.S	eq F	M00033427D:F01	CH09LNL
84		RTA00002677F.o.18.2.P.S	eq F	M00039425C:G01	CH09LNL
84		RTA00002677F.c.01.1.P.S	· 1	M00032731C:C07	CH08LNH
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856	47231	RTA00002714F.b.15.1.P.Seq	F	M0003958-C:C01	CH12EDT
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870	404277	RTA00002687F.d.18.1.P.Sec	F	M00039948A:E03	CH14EDT
871	403557	RTA00002687F.d.10.1.P.Sec	F	M00039319B:H12	CH09LNL
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873		RTA00002674F.f.21.1.P.Sec	F F	M00039133D:G02	CH09LNL
874		RTA00002672F.c.02.2.P.Sec	9 <u>F</u>	M00038639D.107	CHOCCOH
875		RTA00002709F.a.24.1.P.Sec	q F	M00003351C:G03	CHISEDT
876		RTA00002686F.b.17.1.P.Se	9 F	M00039760B:B03	CH04MAL
877		RTA00002713F.b.04.1.P.Se	9 F	M00027212D:E03	CH01COH
878		RTA00002661F.e.11.1.P.Se	q <u> </u>	M00003770A:E05	CH09LNL
879		RTA00002670F.c.05.2.P.Se	q F	M00033345D:A09	CH09LNL
		RTA00002670F.c.08.2.P.Se	q <u> </u>	M00033346C:A05	CH12EDT
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882		RTA00002688F.d.21.2.P.Se	eq F	M00040394.A:D04	CH04MAL
883		RTA00002664F.c.18.2.P.Se	eq F	M00026918B:D01	CH04.VIAE CH15CON
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88		RTA00002664F.d.21.2.P.S	eq F	M00027035D:C06	
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88	100500	RTA00002666F.c.24.1.P.S	eq F	M00032545B:H09	CH08LNH
88		RTA00002714F.b.20.1.P.S	eq F	M00027818C:C07	CH04MAL
89		RTA000027141:0:2011116	ieg F	M00040377C:G07	CH14EDT
89		RTA00002685F.1.10.1.P.S	ea F	M00039590D:D02	
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ID	CLUSTER	RTA00002676F.d.21.2.P.Seq	F	M00039284D:B12	CH09LNL
894	374639	RTA00002673F.j.14.2.P.Seq	F	M00039084C:H04	CH09LNL
895	380674	RTA00002673F.j.14.1.P.Seq	F	M00039084C:H04	CH09LNL
896	380674	RTA00002664F.d.20.2.P.Seq	F	M00027030C:H06	CH04MAL
897	188972	RTA00002664F.d.20.2.F.Seq	F	M00040131D:G08	CHISEDT
898	402835	RTA00002686F.c.01.1.P.Seq	F	M00039947C:G03	CH14EDT
899	403774	RTA00002687F.d.08.2.P.Seq	F	M00039096.A:A05	CH09LNL
900	374606	RTA00002673F.j.23.2.P.Seq	F	M00022925C:A08	CH03MAH
901	192535	RTA00002663F.m.14.1.P.Seq	F	M00039820B:B06	CH09LNL
902	377926	RTA00002680F.1.16.2.P.Seq	F	M00026926A:E10	CH04MAL
903	186055	RTA00002712F.i.11.1.P.Seq	F	M00040129D:E10	CH09LNL
904	380498	RTA00002684F.f.11.2.P.Seq	F	M00039561A:B07	CH12EDT
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92:		RTA00002687F.h.24.2.P.Se	a F	M00040296D:E09	CH14EDT
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93	3 404642	RTA00002687F.f.02.2.P.S	ea F	M00039816C:D05	CH09LNL
93	4 380413	RTA00002680F.k.19.1.P.S		M00043148C:A09	CH19COP
93	5 287963	RTA00002693F.c.20.2.P.S		M00021852D:A05	СНОЗМАН
93		RTA00002710F.d.09.1.P.S		M00043446C:E12	CH20COHLV
93		RTA00002694F.b.18.1.P.S	eq F	M00042596C:D07	CH20COHLV
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948	401124	RTA00002685F.o.11.2.P.Seq	F	M00039629D:B04	CH12EDT
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952	169464	RTA00002663F.i.19.1.P.Seq	F	M00022602.A:E09	СНОЗМАН
953	451654	RTA00002692F.f.02.2.P.Seq	F	M00043044D:A09	CH18CON
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957	448177	RTA00002690F.e.12.1.P.Seq	F	M00042839B:B11	CH16COP
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966	240318	RTA00002687F.d.04.1.P.Seq	F	M00039947.A:D06	CH14EDT
967	451620	RTA00002691F.d.20.3.P.Seq	F	M00043379D:H02	CH17COHLV
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973	452015	RTA00002692F.c.07.2.P.Seq	F	M00042981B:D11	CH18CON
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976	449040	RTA00002690F.e.14.2.P.Seq	F	M00042841D:H07	CH16COP
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978	400910	RTA00002685F.b.07.1.P.Seq	F	M00039367B:H02	CHIZEDT
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981	452781	RTA00002692F.b.16.2.P.Seq	F	M00042966B:F07	CH18CON
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983	401644	RTA00002687F.a.19.2.P.Seq	F	M00039761D:E10	CH14EDT
984	404402	RTA00002685F.n.24.2.P.Seq	F	M00039624A:H09	CHIZEDT
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990	449794	RTA00002691F.c.22.2.P.Seq	F	M00043361B:A01	CH17COHLV
991	400921	RTA00002685F.b.18.1.P.Seq	F	M00039371B:H06	CH12EDT
992	373874	RTA00002672F.c.22.2.P.Seq	F	M00038663D:H10	CH09LNL
993	401050	RTA00002685F.e.09.2.P.Seq	F	M00039499C:A04	CH12EDT
994	453237	RTA00002693F.c.02.2.P.Seq	F	M00043108A:F06	CH19COP
995	449294	RTA00002690F.c.13.3.P.Seq	F	M00042770C:C04	CH16COP
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997	378014	RTA00002680F.g.17.2.P.Seq	F	M00039799A:D10	CH09LNL
998	404726	RTA00002688F.a.18.2.P.Seq	F	M00040371C:H05	CH14EDT
999	451347	RTA00002691F.b.11.3.P.Seq	F	M00043311C:E03	CH17COHLV
1000	401154	RTA00002685F.e.06.2.P.Seq	F	M00039497C:C06	CH12EDT
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1003	25387	RTA00002711F.f.19.1.P.Seq	F	M00023001C:C08	CH03MAH
1004	377085	RTA00002678F.n.14.1.P.Seq	F	M00039619B:D02	. CH09LNL
1005	403530	RTA00002688F.a.09.2.P.Seq	F	M00040368.A:F01	CH14EDT
1006	372930	RTA00002670F.j.12.2.P.Seq	F	M00033437C:A07	CH09LNL
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1009	449337	RTA00002690F.c.18.3.P.Seq	F	M00042774C:C05	CH16COP
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1017	377632	RTA00002683F.1.18.2.P.Seq	F	M0004008 D: F08	CH09LNL
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1029	373875	RTA00002674F.c.05.1.P.Seq	F	M00039124C:H02	CH09LNL
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1031	33971	RTA00002713F.h.13.1.P.Seq	F	M00027392B:H02	CH04MAL
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1047	402339	RTA00002686F.o.16.1.P.Seq		M00040282.A:A03	CHISEDT
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1053	403242	RTA00002686F.f.16.1.P.Seq		M00040174C:E10	CHISEDT
1054	402182	RTA00002690F.c.12.3.P.Seq		M00042770B:B12	CH16COP
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1109	456233	RTA00002694F.e.08.1.P.Seq		M000436363:C06	CH20COHLV
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1113		RTA00002687F.j.03.2.P.Seq		M00040313D:E04	CH14EDT
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1139	449832	RTA00002691F.e.13.1.P.Seq	F	M00040093B:C02	CH09LNL
1140	379004	RTA00002683F.n.09.2.P.Seq	F	M00043430B:C02	CH20COHLV
1141	455211	RTA00002694F.b.07.1.P.Seq	F	M00040093D:D03	CH09LNL
1142	379021	RTA00002683F.n.13.2.P.Seq		M00039785D:G05	CH09LNL
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117		RTA00002685F.o.10.2.P.S		M00040342B:D12	CH14EDT
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11		RTA00002687F.n.09.1.P.S	eq F	M0003976 B: A04	
	75 395617	RTA00002687F.b.15.1.P.S	eq F	MI0003970 B404	

					
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1179	18139		F	M00039746C:H06	CH14EDT
1180	403898	RTA00002687F.a.05.1.P.Seq	F	M00043078D:D04	CH19COP
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1182	404172	RTA00002687F.d.17.1.P.Seq	F	M00039374C:H12	CH12EDT
1183	400973	RTA00002685F.c.06.2.P.Seq		M00043405A:DII	CH17COHLV
1184	450198	RTA00002691F.e.23.2.P.Seq	F	M00043406B:G12	CH17COHLV
1185	451502	RTA00002691F.f.03.2.P.Seq		M00043220B:C04	CH19COP
1186	454414	RTA00002693F.f.18.2.P.Seq		M00043081D:F05	CH19COP
1187	453752	RTA00002693F.b.02.2.P.Seq		M00040207B:D08	CH14EDT
1188	403700	RTA00002687F.g.03.1.P.Seq		M00040294D:D12	CHI4EDT
1189	403371	RTA00002687F.h.19.1.P.Seq		M00040203B:A05	CH14EDT
1190	14583	RTA00002687F.f.08.1.P.Seq		M00039958C:B09	CH14EDT
1191	404161	RTA00002687F.e.20.1.P.Seq		M00039766A:G07	CH14EDT
1192	403274	RTA00002687F.b.10.1.P.Seq		M00038615A:H12	CH09LNL
1193	373465	RTA00002671F.o.09.1.P.Seq		M00040265D:C08	CHISEDT
1194	402582	RTA00002686F.m.08.1.P.Sec	``	M00040261C:F01	CHISEDT
1195	402241	RTA00002686F.1.16.1.P.Seq		M00033581D:D08	CH09LNL
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1205	235855	RTA00002667F.o.06.1.P.Se		M00040183A:F07	CHISEDT
1206	402789	RTA00002686F.g.16.1.P.Se	7	M00022467C:B12	CH03MAH
1207	19826	RTA00002710F.k.05.1.P.Se		M00039984D:G12	CH09LNL
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121	4 400147	RTA00002685F.g.10.1.P.Se	q F	M00039517B:G12	CH12EDT
121	5 400864	RTA00002685F.g.17.1.P.Se	eq F	M00043328D:H02	CH17COHLV
121	6 451600	RTA00002691F.b.19.3.P.Se	eq F	M00043328D:1102	CH12EDT
121	7 400147	RTA00002685F.g.10.2.P.Se	F F	M00039378D:H07	CHIZEDT
121	8 401655	RTA00002685F.c.22.2.P.Sc	eq F	M00034378D:C10	CH16COP
121		RTA00002690F.a.10.3.P.Sc	eq F	M00042431D.C10	CH14EDT
122		RTA00002688F.a.01.2.P.Sc	eq F	M00043044B:A12	CH18CON
122		RTA00002692F.e.24.1.P.Sc	eq F	M00039515D:C11	CH12EDT
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1226	450773	RTA00002685F.1.24.2.P.Seq	F	M00039595C:E05	CH12EDT
1227	376236	RTA00002688F.c.21.1.P.Seq	F	M00040385C:D02	CH14EDT
1228	422357	RTA00002687F.p.10.2.P.Seq	F	M00040351B:F02	CH14EDT
1229	404532	RTA00002687F.j.23.1.P.Seq	F	M00040317D:F02	CH14EDT
1230	403693	RTA00002687F.j.23.2.P.Seq	F	M00040317D:F02	CH14EDT
1231	403693	RTA00002685F.o.02.2.P.Seq	F	M00039624B:F12	CH12EDT
1232	401515	RTA00002687F.p.10.1.P.Seq	F	M00040351B:F02	CHITEDT
1233	404532	RTA00002692F.d.01.2.P.Seq	F	M00043002A:E05	CH18CON
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1244	456764	RTA00002694F.c.14.1 P.Seq		M00040262B:B06	CHISEDT
1245	401827	RTA00002686F.1.19.1.P.Seq		M00040202.A:F05	CH14EDT
1246	404520	RTA00002687F.f.05.1.P.Seq		M00043366A:A02	CH17COHLV
1241	7 449798	RTA00002691F.d.02.3.P.Sec	11	M00043350D:B11	CH17COHLV
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124	9 377471	RTA00002691F.c.02.3.P.Sec	1	M00039752B:G08	CHISEDT
125	0 400404	RTA00002686F.a.17.1.P.Sec	1	M00043389C:E03	CH17COHLV
125		RTA00002691F.e.08.2.P.Sec	1	M00039958.A:A08	CH14EDT
125	2 404024	RTA00002687F.e.18.1.P.Sec		M00042566C.C05	CH15CON
125	3 446404	RTA00002689F.b.14.1.P.Se	11	M00039411C:E07	CH09LNL
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125		RTA00002678F.e.10.2.P.Se	<u> </u>	M00043066B:H11	CH18CON
125	6 453011	RTA00002692F.f.10.2.P.Se		M00042352D:C01	CH17COHLV
125		RTA00002691F.a.03.3.P.Se	<u> </u>	M0004026 A: E06	CHISEDT
125		RTA00002686F.m.11.1.P.Sc	1	M00043409B:B03	CH17COHLV
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12	64 403397	RTA00002687F.h.02.1.P.S		M00039755A:B08	CHISEDT
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1272	401381	RTA00002685F.o.08.1.P.Seq	F	M00039626D:F04	CH12EDT
1273	428491	RTA00002666F.c.05.1.P.Seq	F	M00032535D:H01	CH08LNH
1274	54656	RTA00002661F.i.22.2.P.Seq	F	M00004372B:F07	CH01COH
1275	379183	RTA00002679F.i.17.1.P.Seq	F	M00039688C.G06	CH09LNL
1276	25594	RTA00002711F.f.07.1.P.Seq	F	M00022968B:E02	CHOSMAH
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1278	16789	RTA00002709F.b.09.2.P.Seq	F	M00005382B:F08	CH02COH
1279	23292	RTA00002708F.c.02.1.P.Seq	F	M00003750D:E06	CH01COH
1280	373982	RTA00002673F.b.24.2.P.Seq	F	M00039058A:A04	CH09LNL
1281	373982	RTA00002673F.c.01.2.P.Seq	F	M00039058A:A04	CH09LNL
1282	449911	RTA00002691F.e.02.2.P.Seq	F	M00043384B:B02	CH17COHLV
1283	450633	RTA00002691F.f.02.2.P.Seq	F	M00043405C:G12	CH17COHLV
1284	23939	RTA00002713F.j.14.1.P.Seq	F	M00027486A:F06	CH04MAL
1285	450633	RTA00002691F.f.02.1.P.Seq	F	M00043405C:G12	CH17COHLV
1286	379122	RTA00002672F.n.14.1.P.Seq		M00039039B:F09	CH09LNL
1287	449429	RTA00002690F.a.16.3.P.Seq	F	M0004243TA:D04	CH16COP
1288	430578	RTA00002668F.g.18.1.P.Seq		M00032984C:G05	CH08LNH
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1290	425824	RTA00002687F.b.17.2.P.Seq		M0003976TC:E12	CHI-EDT
1291	401266	RTA00002685F.i.11.2.P.Seq		M00039535D:D10	CHIZEDT
1292	377949	RTA00002674F.p.04.1.P.Seq	F	M00039200A:C10	CH09LNL
1293	12926	RTA00002710F.e.21.1.P.Seq		M00022005C.C06	CH03MAH
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1300	400968	RTA00002685F.g.24.2.P.Seq		M00039521D:H03	CH12EDT
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1320	26017	RTA00002670F.o.06.1.P.Seq	F	M00033570C:C10	CH09LNL
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1328		RTA00002710F.a.21.1.P.Seq	F	M00007972B:H12	CH03MAH
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1360		RTA00002669F.g.24.2.P.Se	q F	M0003321SA:C04	CH08LNH
136		RTA00002682F.m.14.1.P.Se	q F	M00040015C:F08	CH09LNL
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136		RTA00002686F.g.15.1.P.Se		M00040182D:D06	CHISEDT
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1367	379011	RTA00002681F.n.23.1.P.Seq	F.	M00039903C:D01	CH09LNL
1368	404048	RTA00002687F.g.01.1.P.Seq	F	M00040206A:A07	CH14EDT
1369	404048	RTA00002687F.g.01.2.P.Seq	F	M00040206A:A07	CH14EDT
1370	452398	RTA00002692F.f.17.2.P.Seq	F	M00043125C:A11	CH18CON
1371	403686	RTA00002687F.d.03.1.P.Seq	F	M00039946B:F08	CH14EDT
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1373	404048	RTA00002687F.f.24.2.P.Seq	F	M00040206A:A07	CH14EDT
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1375	450627	RTA00002691F.f.01.2.P.Seq	F	M00043405C:G02	CH17COHLV
1376	375589	RTA00002680F.f.06.2.P.Seq	F	M00039794A:E04	CH09LNL
1377	379011	RTA00002681F.n.23.2.P.Seq	F	M00039903C:D01	CH09LNL
1378	16789	RTA00002709F.b.09.1.P.Seq	F	M00005382B:F08	CH02COH
1379	427346	RTA00002665F.a.24.3.P.Seq	F	M00028066C:D07	CH08LNH
1380	49540	RTA00002712F.e.01.1.P.Seq	F	M00023399C:E10	CH04MAL
1381	14440	RTA00002674F.e.14.2.P.Seq	F	M00039129C:D04	CH09LNL
1382	391401	RTA00002682F.k.11.1.P.Seq	F	M00040004D:B03	CH09LNL
1383	43782	RTA00002662F.d.21.2.P.Seq	F	M00007165B:G11	CH02COH
1384	212635	RTA00002666F.p.01.1.P.Seq	F	M00032688D:D11	CH08LNH
1385	15618	RTA00002710F.o.05.1.P.Seq	F	M0002268-A:C02	CH03MAH
1386	18501	RTA00002669F.g.23.3.P.Seq	F	M00033217B:H07	CH08LNH
1387	400310	RTA00002688F.b.05.2.P.Seq	F	M00040375C:B06	CH14EDT
1388	403796	RTA00002687F.h.17.1.P.Seq	F	M00040293 D:G04	CH14EDT
1389	452314	RTA00002694F.a.21.1.P.Seq	F	M00043416C:A02	CH20COHLV
1390	119179	RTA00002712F.k.20.1.P.Seq	F	M00027021A:G02	CH04MAL
1391	167451	RTA00002663F.j.11.1.P.Seq	F	M00022646.A:H10	СНОЗМАН
1392	450523	RTA00002691F.e.19.2.P.Seq	F	M00043401D:G08	CH17COHLV
1393	289535	RTA00002693F.f.06.1.P.Seq	F	M00043202B:F01	CH19COP
1394	374736	RTA00002673F.o.08.2.P.Seq	F	M00039112B:C05	CH09LNL
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1396	134877	RTA00002662F.d.05.2.P.Seq	F	M00007026B:H09	CH02COH
1397	372811	RTA00002670F.c.12.2.P.Seq	·F	M0003334TC:F02	CH09LNL
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1402	451013	RTA00002691F.f.08.1.P.Seq	F	M00043409B:B03	CH17COHLV
1403	212635	RTA00002666F.o.24.1.P.Seq	F	M00032688D:D11	CH08LNH
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1406		RTA00002713F.i.15.1.P.Seq	F	M00027462A:D07	CH04MAL
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1414	375589	RTA00002680F.f.06.1.P.Seq	F	M00039794A:E04	CH09LNL
1415	375789	RTA00002674F.a.16.1.P.Seq	F	M00039120C:H03	CH09LNL
1416	456227	RTA00002694F.c.16.1.P.Seq	F	M00043465C:C09	CH20COHLV
1417	455852	RTA00002694F.a.02.1.P.Seq	F	M00042592A:H10	CH20COHLV
1418	25169	RTA00002710F.m.05.1.P.Seq	F	M00022579C:C11	СНОЗМАН
1419	376524	RTA00002678F.h.23.2.P.Seq	F	M00039477A:B03	CH09LNL
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1421	449562	RTA00002690F.b.13.3.P.Seq	F	M00042515C:F08	CH16COP
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1423	286001	RTA00002690F.b.08.3.P.Seq	F	M00042511.A:H04	CH16COP
1424	380322	RTA00002683F.p.21.1.P.Seq	F	M00040106B:B09	CH09LNL
1425	401603	RTA00002685F.f.23.2.P.Seq	F	M00039510C:G02	CH12EDT
1426	376541	RTA00002678F.d.13.2.P.Seq	F	M00039456A:C08	CH09LNL
1427	449123	RTA00002690F.a.13.3.P.Seq	F	M00042435A:A11	CH16COP
1428	418358	RTA00002686F.m.07.1.P.Seq	F	M00040265D:B07	CHISEDT
1429	380263	RTA00002689F.a.22.1.P.Seg	F	M00042543C:G04	CHISCON
1430	455748	RTA00002694F.b.06.1.P.Seq	F	M00043428D:G08	CH20COHLV
1431	451679	RTA00002693F.a.04.2.P.Seq	F	M00042612D:F06	CH19COP
1432	396332	RTA00002686F.k.14.1.P.Seq	F	M00040252C:C06	CHISEDT
1433	377578	RTA00002683F.b.11.2.P.Seq	F	M00040037.A:E11	CH09LNL
1434	20061	RTA00002710F.m.14.1.P.Seq	F	M00022597D:A06	СНОЗМАН
1435	402494	RTA00002686F.h.16.1.P.Seq	F	M00040191A:B09	CHISEDT
1436	372798	RTA00002670F.c.18.2.P.Seq	F	M00033349D:F05	CH09LNL
1437	236295	RTA00002679F.a.19.2.P.Seq	F	M00039655B:H09	CH09LNL
1438	451570	RTA00002691F.c.03.3.P.Seq	F	M00043340B:H08	CH17COHLV
1439	35847	RTA00002708F.h.03.1.P.Seq	F	M00004239B:F11	CH01COH
1440	455706	RTA00002694F.b.10.1.P.Seq	F	M00043433B:G09	CH20COHLV
1441	346310	RTA00002684F.d.18.1.P.Seg	F	M00040122D:A02	CH09LNL
1442	189561	RTA00002676F.j.09.3.P.Seq	F	M00039308B:G08	CH09LNL
1443	403200	RTA00002687F.j.24.1.P.Seq	F	M00040318A:B02	CH14EDT
1444	401413	RTA00002685F.i.03.2.P.Seq	F	M00039530B:E02	CHIZEDT
1445	448680	RTA00002690F.b.02.3.P.Seq	F	M00042440B:E09	CH16COP
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1450	377055	RTA00002682F.k.13.1.P.Seq	F.	M00040005B:C11	CH09LNL
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1453	450366	RTA00002691F.c.06.3.P.Seq	F	M00027772C:E04	CH17COHLV
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1460	12270	RTA00002711F.f.23.1.P.Seq	F	M00023007C:E10	СНОЗМАН
1461	401013	RTA00002685F.o.16.1.P.Seq	F	M00039641.A:A05	CH12EDT
1462	74344	RTA00002661F.f.10.1.P.Seq	F	M00003902A:C03	CH01COH
1463	423432	RTA00002687F.I.10.2.P.Seq	F	M00040323C:G11	CH14EDT
1464	423432	RTA00002687F.I.10.1.P.Seq	F	M00040323C:G11	CH14EDT
1465	379560	RTA00002682F.g.18.1.P.Seq	F	M00039981A:E08	CH09LNL
1466	122669	RTA00002712F.f.22.1.P.Seq	F	M00026857D:G12	CH04MAL
1467	373319	RTA00002671F.c.17.2.P.Seq	F	M00038259B:A02	CH09LNL
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1469	376366	RTA00002677F.h.05.2.P.Seq	F	M00039397B:H09	CH09LNL
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1472	373647	RTA00002672F.d.04.1.P.Seq	F	M00038664C:E04	CH09LNL
1473	379721	RTA00002676F.b.20.2.P.Seq	F	M00039276B:H09	CH09LNL
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1475	403738	RTA00002687F.a.10.2.P.Seq	F	M00039748.4:F11	CH14EDT
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1477	373787	RTA00002677F.I.04.2.P.Seq	F	M00039414D:G03	CH09LNL
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1480	403232	RTA00002687F.g.20.2.P.Seq	F	M00040218C:C02	CH14EDT
1481	403232	RTA00002687F.g.20.1.P.Seq	F	M00040218C:C02	CH14EDT
1482	449080	RTA00002690F.a.04.2.P.Seq	F	M00042347D:H11	CH16COP
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1484	374742	RTA00002676F.c.12.2.P.Seq	F	M00039279B:C11	CH09LNL
1485	449741	RTA00002690F.e.23.2.P.Seq	F	M00042856B:H02	CH16COP
1486	45341	RT.A00002710F.k.19.1.P.Seq	F	M00022499A:B02	СНОЗМАН
1487	451220	RTA00002691F.f.07.2.P.Seq	F	M00043408B:D11	CH17COHLV
1488	22067	RTA00002708F.f.12.1.P.Seq	F	M00004140D:C03	CH01COH
1489	378952	RTA00002683F.h.11.2.P.Seq	F	M000400 T0B:B07	CH09LNL
1490	401435	RTA00002685F.n.14.2.P.Seq	F	M00039607D:E08	CH12EDT
1491	375284	RTA00002676F.g.21.2.P.Seq	F	M00039298D:B04	CH09LNL
1492	449080	RT.A00002690F.a.04.3.P.Seq	F	M00042347D:H11	CH16COP
1493	37897	RTA00002661F.b.15.1.P.Seq	F	M00001476B:G10	CH01COH
1494	7572	RTA00002709F.h.03.1.P.Seq	F	M00006S09B:B09	CH02COH
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1496	374828	RTA00002674F.m.10.2.P.Seq	F	M00039170A:B10	CH09LNL
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1572	174250	RTA00002689F.c.09.1.P.Seq	F	M00042697D:C07	CHISCON
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1766	376200	RTA00002693F.f.08.2.P.Seq	F	M00043203A:B09	CH19COP
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1771	378911	RTA00002672F.n.24.2.P.Seq	F	M00039042B:B02	CH09LNL
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1773	372886	RTA000026 OF.5.22.2.P.Seq	F	M00033343C:H08	CH09LNL
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1777	37372	RTA00002708F.f.20.1.P.Seq	F	M00004155D:A10	CH01COH
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6	42233	RT.A00002912F.g.24.1.P.Seq	F	M00027359B:A06	CH0+MAL
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9	3093	RTA00002923F.e.03.1.P.Seq	F	M00039225A:D11	CH09LNL
10	15806	RT.A00002894F.f.07.1.P.Seq	F	M00003991A:C11	CH01COH
11	19739	RT.A00002896F.d.12.1.P.Seq	F	M00004147C:E01	CH01COH
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356	18782	RTA00002905F.f.07.1.P.Seq	F	M00008021C:G12	CHOICOH
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868 4609 RTA00002919F.e.07.1.P.Seq F M00033037B:F04 CH08LNH 869 6889 RTA00002919F.e.06.1.P.Seq F M00033035D:D02 CH08LNH 870 15228 RTA00002904F.e.22.1.P.Seq F M00033035D:D02 CH02COH 871 20971 RTA0000293F.e.23.1.P.Seq F M0004313D:E09 CH17COHLV 872 5174 RTA0000293F.e.16.1.P.Seq F M0004313D:E09 CH17COHLV 873 15236 RTA0000293F.e.16.1.P.Seq F M0004198A:F12 CH13EDT 874 9223 RTA0000293F.g.10.P.Seq F M0004198A:F12 CH13EDT 875 24591 RTA0000293F.g.10.P.Seq F M00039121C:H12 CH01COH 876 36306 RTA00002838F.i.11.P.Seq F M00003916A:E04 CH01COH 877 3309 RTA00002891F.g.23.P.Seq F M00003916A:E04 CH01COH 879 9090 RTA0000289F.g.23.P.Seq F M0000374C:E11 CH01COH 880 11510		4270				
869 6889 RTA00002919Fe.06.1.P.Seq F M00033055D:D02 CH08LNH 870 15228 RTA00002919Fe.06.1.P.Seq F M00007158D:D03 CH02COH 871 20971 RTA0000293Fe.2.1.P.Seq F M0000413B.ED0 CH17COHLV 872 5174 RTA0000293Fe.16.1.P.Seq F M00040198.F12 CH13EDT 873 15236 RTA0000293Fe.16.1.P.Seq F M00040198.F12 CH13EDT 874 9223 RTA0000293Fe.g.10.1.P.Seq F M00004141A.D01 CH01COH 875 24591 RTA0000293Fe.g.10.1.P.Seq F M000039516A.E04 CH01COH 876 36306 RTA0000288FF.g.23.1.P.Seq F M00001485C.F06 CH01COH 877 3309 RTA0000293F.g.23.1.P.Seq F M00003746C.E11 CH01COH 878 186712 RTA0000293F.g.23.1.P.Seq F M00003746C.E11 CH01COH 879 9090 RTA0000293F.g. Seq. F. F M00003746C.E11 CH01COH 880 1510	868	4609	RTA00002935F.e.15.1.P.Seq			
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872 5174 RTA00002935F.a.23.1.P.Seq F M00043313D:99 CH1COLE. 873 15236 RTA00002928F.e.16.1.P.Seq F M00040198A:F12 CH15EDT 874 9223 RTA0000293F.e.16.1.P.Seq F M00004141A:D01 CH01COH 875 24591 RTA0000293F.g.10.1.P.Seq F M00003915C:H12 CH09LNL 876 36306 RTA0000288F.i.11.1.P.Seq F M00003916A:E04 CH01COH 877 3309 RTA00002891F.g.23.1.P.Seq F M00003916A:E04 CH01COH 878 186712 RTA00002911F.c.11.2.P.Seq F M00003746C:E11 CH01COH 879 9090 RTA00002389F.j.15.1.P.Seq F M00001467C:D04 CH01COH 880 11510 RTA00002389F.j.15.1.P.Seq F M00001467C:D04 CH01COH 881 9784 RTA00002389F.j.15.1.P.Seq F M00042554-E010 CH01COH 882 25618 RTA00002930F.d.9.F.Seq F M00040289D:C06 CH13EDT 883 12493	871	20971				
873 15236 RTA00002928F.E.Io.I.P.Seq F M00004141A:D01 CH01COH 874 9223 RTA00002936F.b.Io.I.P.Seq F M0003925IC:H12 CH09LNL 875 24591 RTA0000293F.g.Io.I.P.Seq F M0003925IC:H12 CH09LNL 876 36306 RTA0000288F.I.II.P.Seq F M00003916A:E04 CH01COH 877 3309 RTA0000289F.g.23.I.P.Seq F M00026809A:H08 CH04MAL 879 9090 RTA0000289F.g.23.I.P.Seq F M00003746C:E11 CH01COH 880 11510 RTA0000288F.i.D.P.Seq F M00001467C:D04 CH01COH 881 9784 RTA0000288F.j.I5.I.P.Seq F M00001554C:G19 CH01COH 882 25618 RTA00002930F.a.II.I.P.Seq F M00042554A:D01 CH15CON 883 12493 RTA0000293F.b.O.B.I.P.Seq F M00043134A:F05 CH19COP 884 24361 RTA0000293F.b.O.B.I.P.Seq F M00039747B:B06 CH15CON 885 12449	872	5174				
874 9223 RTA0000293FB: 10.1.P.Seq F M00039251C:H12 CH09LNL 875 24591 RTA0000293Fg: 10.1.P.Seq F M00001485C:F06 CH01COH 876 36306 RTA00002838F.I.11.I.P.Seq F M00003916A:E04 CH01COH 877 3309 RTA00002911F.c.11.2.P.Seq F M00003916A:E04 CH01COH 878 186712 RTA00002891F.g.23.1.P.Seq F M00003746C:E11 CH01COH 879 9090 RTA00002889F.j.15.1.P.Seq F M00001467C:D04 CH01COH 880 11510 RTA00002838F.j.15.1.P.Seq F M00001554C:G19 CH01COH 881 9784 RTA00002838F.j.15.1.P.Seq F M00042554A:D01 CH15CON 882 25618 RTA00002930F.a.11.1.P.Seq F M0004289D:C06 CH13EDT 884 24361 RTA0000293F.b.03.1.P.Seq F M00043134A:F05 CH19COP 885 12449 RTA0000293F.b.03.1.P.Seq F M00039747B:B06 CH14EDT 887 13204 <td>873</td> <td>15236</td> <td></td> <td></td> <td></td> <td></td>	873	15236				
875 24591 RTA0000293F.g.10.II.P.Seq F M00001483C:F06 CH01COH 876 36306 RTA00002888F.I.11.IP.Seq F M00003916A:E04 CH01COH 877 3309 RTA0000291IF.c.11.2.P.Seq F M000026809A:H08 CH04MAL 878 186712 RTA00002891F.g.23.I.P.Seq F M00003746C:E11 CH01COH 879 9090 RTA0000288F.i.07.I.P.Seq F M00001467C:D04 CH01COH 880 11510 RTA00002889F.j.15.I.P.Seq F M00001467C:D04 CH01COH 881 9784 RTA00002939F.a.11.I.P.Seq F M00001554C:G19 CH01COH 882 25618 RTA00002930F.a.11.I.P.Seq F M00042554A:D01 CH15CON 883 12493 RTA0000293F.b.08.I.P.Seq F M00043134A:F05 CH19COP 884 24361 RTA0000293F.b.02.I.P.Seq F M00039747B:B06 CH15CON 885 12449 RTA0000293F.c.19.I.P.Seq F M00055745B:A08 CH15CON 886 17894<	874	9223				
876 36306 RTA00002893F;1:11.F.seq F M00003916A:E04 CH01COH 877 3309 RTA00002891F;2:11.P.Seq F M00026809A:H08 CH04MAL 879 9090 RTA00002891F;g:23.1.P.Seq F M00003746C:E11 CH01COH 880 11510 RTA00002888F;i.07.1.P.Seq F M00001467C:D04 CH01COH 881 9784 RTA00002889F;j.15.1.P.Seq F M00001554C:G19 CH01COH 882 25618 RTA0000293F.a.11.1.P.Seq F M00042554A:D01 CH15CON 883 12493 RTA0000293F.a.11.1.P.Seq F M00040289D:C06 CH13EDT 884 24361 RTA0000293F.b.08.1.P.Seq F M00043134A:F05 CH19COP 885 12449 RTA0000293F.b.02.1.P.Seq F M00055468A:A08 CH15CON 886 17894 RTA00002930F.c.19.Seq F M00039747B:B06 CH14EDT 887 13204 RTA0000293F.f.09.1.P.Seq F M00055745B:A08 CH15CON 888 32119	875	24591				
877 3309 RTA00002893F.j.21.1.P.Seq F M00026809A:H08 CH04MAL 878 186712 RTA00002911F.c.11.2.P.Seq F M00003746C:E11 CH01COH 879 9090 RTA0000288Fi.07.1.P.Seq F M00001467C:D04 CH01COH 880 11510 RTA0000288Fi.07.1.P.Seq F M00001554C:G19 CH01COH 881 9784 RTA00002930F.a.11.1.P.Seq F M00042554A:D01 CH15CON 882 25618 RTA00002930F.a.11.1.P.Seq F M0004289D:C06 CH13EDT 884 24361 RTA0000293F.b.08.1.P.Seq F M00043134A:F05 CH19COP 885 12449 RTA00002930F.d.02.1.P.Seq F M00039747B:B06 CH14EDT 886 17894 RTA00002930F.d.91.P.Seq F M00039747B:B06 CH14EDT 887 13204 RTA00002930F.c.19.1.P.Seq F M0005548B:E05 CH15CON 889 5909 RTA00002935F.i.23.1.P.Seq F M0005593B:A03 CH17COHLY 890 24453	876	36306				
878 186712 RTA0000291F.C:11:2F.3cq F M00003746C:E11 CH01COH 879 9090 RTA00002888F.i.07.1.P.Seq F M00001467C:D04 CH01COH 880 11510 RTA00002888F.i.07.1.P.Seq F M00001554C:G19 CH01COH 881 9784 RTA00002930F.i.11.1.P.Seq F M00042554A:D01 CH15CON 882 25618 RTA00002930F.i.11.1.P.Seq F M0004289D:C06 CH13EDT 884 24361 RTA00002933F.b.08.1.P.Seq F M00043134A:F05 CH19COP 885 12449 RTA00002930F.d.02.1.P.Seq F M00035745B:A08 CH15CON 886 17894 RTA00002930F.f.09.1.P.Seq F M00039747B:B06 CH14EDT 887 13204 RTA00002930F.c.19.1.P.Seq F M00055745B:A08 CH15CON 888 32119 RTA00002930F.c.19.1.P.Seq F M0005548B:E05 CH15CON 889 5909 RTA00002935F.i.23.1.P.Seq F M00039526A:A08 CH12EDT 891 46982<	877	3309				
879 9090 RTA0000289FF.g.23.LP.Seq F M00001467C:D04 CH01COH 880 11510 RTA00002838Fi.107.1P.Seq F M00001467C:D04 CH01COH 881 9784 RTA00002838Fi.11.1P.Seq F M00042554A:D01 CH15CON 882 25618 RTA00002938Fi.11.1P.Seq F M0004259D:C06 CH13EDT 883 12493 RTA00002938Fi.08.1P.Seq F M0004239D:C06 CH13EDT 884 24361 RTA00002938Fi.08.1P.Seq F M00043134A:F05 CH19COP 885 12449 RTA00002930Fi.09.1P.Seq F M00039747B:B06 CH15CON 886 17894 RTA00002930Fi.09.1P.Seq F M00039747B:B06 CH14EDT 887 13204 RTA00002930Fi.09.1P.Seq F M00055745B:A08 CH15CON 888 32119 RTA00002930Fi.09.1P.Seq F M0005543B:E05 CH15CON 889 5909 RTA00002935Fi.23.1P.Seq F M000593B:A03 CH17COHL 890 24453 RTA0	878	186712				
880 11510 RTA00002889F.i.07.1P.Seq F M00001554C:G19 CH01COH 881 9784 RTA00002930F.a.11.1P.Seq F M000042554A:D01 CH15CON 882 25618 RTA00002938F.i.11.1P.Seq F M00042554A:D01 CH15CON 883 12493 RTA00002938F.i.11.1P.Seq F M00043134A:F05 CH19COP 884 24361 RTA00002930F.d.02.1P.Seq F M00055468A:A08 CH15CON 885 12449 RTA00002930F.d.02.1P.Seq F M00039747B:B06 CH14EDT 886 17894 RTA00002930F.d.09.1P.Seq F M00035745B:A08 CH15CON 887 13204 RTA00002930F.d.09.1P.Seq F M00055745B:A08 CH15CON 888 32119 RTA00002930F.d.1P.Seq F M00055448B:E05 CH15CON 889 5909 RTA0000293F.i.23.1P.Seq F M00039526A:A08 CH12EDT 891 46982 RTA0000293F.b.23.1P.Seq F M00055093B:A03 CH17COHLY 892 43888	879	9090	RTA00002891F.g.23.1.P.Seq			
881 9784 RTA00002839F.J.II.P.Seq F M00042554A:D01 CH15CON 882 25618 RTA00002938F.i.II.I.P.Seq F M00040289D:C06 CH13EDT 883 12493 RTA00002938F.i.D.08.I.P.Seq F M00043134A:F05 CH19COP 884 24361 RTA0000293F.b.08.I.P.Seq F M00055468A:A08 CH15CON 885 12449 RTA00002930F.d.02.I.P.Seq F M00039747B:B06 CH15CON 886 17894 RTA00002930F.d.01.P.Seq F M00055745B:A08 CH15CON 887 13204 RTA00002930F.c.19.I.P.Seq F M00055745B:A08 CH15CON 888 32119 RTA00002930F.c.19.I.P.Seq F M00055448B:E05 CH15CON 889 5909 RTA00002935F.i.23.I.P.Seq F M00039526A:A08 CH12EDT 890 24453 RTA00002935F.k.22.I.P.Seq F M00039526A:A08 CH12EDT 891 46982 RTA00002935F.b.23.I.P.Seq F M00055093B:A03 CH17COHL* 892 438	880	11510				
882 25618 RTA00002930F.3.11.1.P.Seq F M00040289D:C06 CH13EDT 883 12493 RTA00002938F.i.11.1.P.Seq F M00043134A:F05 CH19COP 884 24361 RTA00002933F.b.08.1.P.Seq F M00055468A:A08 CH15CON 885 12449 RTA00002930F.d.02.1.P.Seq F M00039747B:B06 CH14EDT 886 17894 RTA00002930F.f.09.1.P.Seq F M00055745B:A08 CH15CON 887 13204 RTA00002930F.c.19.1.P.Seq F M00055745B:A08 CH15CON 888 32119 RTA00002930F.c.19.1.P.Seq F M000554931D:E10 CH17COHL 890 24453 RTA00002935F.i.23.1.P.Seq F M00039526A:A08 CH12EDT 891 46982 RTA00002935F.k.22.1.P.Seq F M00055093B:A03 CH17COHL 892 43838 RTA0000293F.b.23.1.P.Seq F M000430-0A:C03 CH18CON 893 24580 RTA0000293F.b.21.1.P.Seq F M000393-4D:E05 CH12EDT 894 <td< td=""><td>881</td><td>9784</td><td></td><td></td><td></td><td></td></td<>	881	9784				
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884 24361 RTA00002933F.b.08.1.P.Seq F M00043134A;F03 CH19Col. 885 12449 RTA00002930F.d.02.1.P.Seq F M000353468A;A08 CH15CON 886 17894 RTA00002930F.d.09.1.P.Seq F M00039747B;B06 CH14EDT 887 13204 RTA00002930F.d.09.1.P.Seq F M00055745B;A08 CH15CON 888 32119 RTA00002930F.c.19.1.P.Seq F M00055448B;E05 CH15CON 889 5909 RTA00002935F.i.23.1.P.Seq F M00039526A;A08 CH12EDT 890 24453 RTA00002937F.d.15.1.P.Seq F M00039526A;A08 CH12EDT 891 46982 RTA00002937F.b.23.1.P.Seq F M00043070A;C03 CH18CON 892 43888 RTA00002937F.b.23.1.P.Seq F M00043070A;C03 CH18CON 893 24580 RTA00002937F.a.21.1.P.Seq F M00039364D;E05 CH12EDT 894 186495 RTA00002937F.b.21.1.P.Seq F M00032562C;F01 CH08LNH 896 <t< td=""><td>883</td><td>12493</td><td></td><td></td><td></td><td></td></t<>	883	12493				
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887 13204 RTA00002930F.t.93.t.P.Seq Indicates Indicates 888 32119 RTA00002930F.t.19.1.P.Seq F M00055448B:E05 CH15CON 889 5909 RTA00002935F.i.23.1.P.Seq F M00034931D:E10 CH17COHL 890 24453 RTA00002927F.d.15.1.P.Seq F M00039526A:A08 CH12EDT 891 46982 RTA00002935F.k.22.1.P.Seq F M00055093B:A03 CH17COHL 892 43888 RTA00002932F.b.23.1.P.Seq F M00043070A:C03 CH18CON 893 24580 RTA00002930F.c.24.1.P.Seq F M000393e4D:E05 CH12EDT 894 186495 RTA00002937F.a.21.1.P.Seq F M000393e4D:E05 CH12EDT 895 12420 RTA00002932F.b.21.1.P.Seq F M000325e2C:F01 CH08LNH 896 3833 RTA00002930F.j.13.1.P.Seq F M000325e2C:F01 CH15CON 897 10438 RTA00002937F.p.10.1.P.Seq F M00039133B:D06 CH09LNL	886	17894	RTA00002929F.a.04.1.P.Seq			
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	045 45585	RTA00002925F.e.18.1.P.	Seq F	M00039860B:E0	244001 171
<u> </u>	046 25025	RT.A00002919F.p.05.1.P	.SeqF	M00033274D:F0	
_	047 15715	RTA00002926F.c.07.2.P	.Seq I F	M00040078.A:C0	
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SEQ		SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
ID	CLUSTER		F	M00055676A:G02	CH15CON
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1054	21853	RTA00002896F.g.12.1.P.Seq	F	M00055402A:H01	CH17COHLV
1055	23439	RTA00002935F.p.01.1.P.Seq	F	M00033402141104 M00043529A:B08	CH20COHLV
1056	13060	RTA00002934F.a.19.1.P.Seq		M00055402.A:H01	CH17COHLV
1057	23439	RTA00002935F.o.24.1.P.Seq	F	M00042822A:H04	CH16COP
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1063	5631	RTA00002929F.e.16.1.P.Seq	F	M00040326B:G09	CH13EDT
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1088		RTA00002903F.m.18.1.P.Se		M00004160D:G05	CH01COH
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1090		RTA00002935F.h.21.1.P.Sec	<u> </u>	M00004053D:F09	CH01COH
1091	34112	RTA00002894F.o.19.1.P.Se	q F	M00003851B:A01	CH01COH
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1093		RTA00002890F.f.18.1.P.Sec	q F	M00001003D:C11	CHOICOH
109-		RTA00002S96F.k.07.1.P.Se	q F	M000041.3D.E00	СН02СОН
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1096		RTA00002930F.i.03.1.P.Se	q F	M00056035D:A08	CH02COH
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		RTA00002891F.f.07.1.P.Se	u F	M00001692C:C04	
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SEQ				CLONE ID	LIBRARY
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1101	11054	RTA00002915F.n.07.2.P.Seq	F	M00032504B:B10	CH08LNH
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1103	9301	RTA00002887F.f.22.1.P.Seq	F	M00001396D:H02	CH02COH
1104	13438	RTA00002901F.a.11.1.P.Seq	F	M00005422D:H10 M00005506C:E09	CH02COH
1105	23691	RTA00002901F.g.21.1.P.Seq	F	M00003306C:E09 M00022694A:F05	CH03MAH
1100	32788	RTA00002909F.m.04.1.P.Seq	F	M00022694A:1 05 M00032515A:B12	CH08LNH
1107	34364	RTA00002915F.o.09.2.P.Seq	F	M00032313A:B12 M00022452B:E06	СН03МАН
1103	24840	RTA00002908F.i.01.1.P.Seq	<u>F</u>	M00022432B.200	CH04MAL
	3416	RTA00002911F.j.17.1.P.Seq	F	M00027036A:B06 M00055724B:E04	CH15CON
1110	16889	RTA00002930F.f.04.1.P.Seq	F	M00055724B:E04	CH14EDT
1111	2159	RTA00002929F.f.15.1.P.Seq	F	M00040344C:D05	CH14EDT
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1113	10722	RTA00002921F.o.22.1.P.Seq	F	M00038304B:E02	CH01COH
1114		RTA00002887F.c.08.1.P.Seq	<u> </u>	M00001389B:E10	CHOICOH
1115	15046	RTA00002898F.g.18.1.P.Seq		M00004347B:E04	CH09LNL
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1117		RTA00002909F.1.06.1.P.Seq	F	M00022678B:C08	CH02COH
1118		RTA00002900F.1.02.1.P.Seq	F	M00005359B:D09	CH02COH
1119		RTA00002900F.d.08.1.P.Sec	F	M00004856D:F09	CH03MAH
1120		RTA00002905F.o.16.1.P.Sec	F	M00021678A:H03	CH03MAH
1121		RTA00002901F.h.12.1.P.Sec	F	M00005515D:F02	CH02COH
1122		RTA00002903F.p.20.1.P.Sec	g F	M00007141C:B05	CH17COHLV
1123		RTA00002935F.p.14.1.P.Se	q F	M00055424B:H06	CH09LNL
1124		RTA00002924F.i.09.1.P.Sec	F	M00039654C:C11	CHOICOH
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112		RTA00002929F.h.24.1.P.Se	g F	M00040391A:G05	CH09LNL
112		RTA00002924F.e.22.1.P.Se	g F	M00039471D:G10	CH09LNL
1129		RTA00002922F.n.11.1.P.Se	a F	M00039133C:F12	CHUSENE
113	0 1820	RTA000029221 III.TT. III.	eq F	M00042894C:A11	CH15CON
113		RTA00002930F.d.21.1.P.Se	a F	M00006907B:C06	CH02COH
113		RTA00002903F.d.21.11		M00032676C:C10	CH08LNH
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113		RTA00002898F.d.22.1.P.S	***************************************	M00004328.A:D01	CH01COH
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113		RTA00002888F.h.08.1.P.S		M00005511.A:F05	CH02COH
113		RTA00002901F.h.07.1.P.S		M00004155C:A10	CHOICOH
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114		RTA00002929F.f.22.1.P.S		M00033223C:G0-	CHOSLINA
114	42 3241	RTA00002919F.n.09.1.P.S		M00055925D:B0	CHISCON
11		RTA00002930F.h.02.1.P.S		M00055477D:B0	CH1/COHLV
_	44 2766	RTA00002935F.p.21.1.P.S		M00001340D:F0	CHOICOH
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	46 7223	RTA00002923F.i.06.1.P.S		M00032792C:B0	I CHOSLNH
	47 6786	RTA00002917F.o.05.1.P.		M00039219B:C0	S CHOSLNL
	48 186651	RTA00002923F.d.21.1.P.	~~	M00055724D:C0	7 CHISCON
	49 7878	RTA00002930F.f.05.1.P.S		M00055423A:B0	S CH17COHL
ننا	150 12624	RTA00002935F.p.11.1.P.	Sed I		

SEQ		250 31 345	ORIENTATION	CLONE ID	LIBR.ARY
ID	CLUSTER_	SEQ NAME		M00001351B:E11	CH01COH
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1153	4177	RT.A00002902F.h.07.1.P.Seq	F	M00003996B:H07	CH01COH
1154	10430	RTA00002894F.g.21.1.P.Seq	F	M00007007.A:E04	CH02COH
1155	31280	RTA00002903F.k.08.1.P.Seq	F	M00039861C:B12	CH09LNL
1156	19098	RTA00002925F.e.23.1.P.Seq	F	M00042585D:E10	CH18CON
1157	24105	RT.A00002932F.a.06.1.P.Seq	F	M00054856C:D03	CH17COHLV
1158	7750	RT.A00002935F.i.02.1.P.Seq		M00004324A:D05	CH01COH
1159	14582	RTA00002898F.d.07.1.P.Seq		M00032753A:C07	CH08LNH
1160	21356	RTA00002917F.j.19.1.P.Seq		M00056345D:A04	CH15CON
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1163	5391	RT.A00002909F.p.21.1.P.Seq		M00001338C:B02	CH01COH
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1165	16403	RT.A00002935F.p.15.1.P.Seg		M00001361A:C12	CHOICOH
1166	21920	RT.A00002886F.j.05.1.P.Seq		M00033374D:C07	CH09LNL
1167	7070	RT.A00002921F.e.06.1.P.Seq	F	M00005569D:G09	CH02COH
1168	45734	RTA00002901F.j.14.1.P.Seq	F	M00003369B:G05	CH14EDT
1169	12362	RT.A00002929F.i.01.1.P.Seg	F	M00003830C:D02	CH01COH
1170	9405	RT.A00002892F.k.04.1.P.Sec	F	M00003830C:D02	CH09LNL
1171	6507	RTA00002922F.o.05.1.P.Sec	F	M00039149A:1 03 M00039822A:H02	CH09LNL
1172	10735	RTA00002925F.b.24.1.P.Sec	F	M00054542B:A10	CH17COHLV
1173	21177	RTA00002935F.d.18.1.P.Sec	F	M00004047D:F12	CHOICOH
1174	14950	RTA00002894F.m.18.1.P.Se	q F	M00032793A:G06	CH08LNH
1175	10762	RT.A00002917F.o.08.1.P.Se	9 F	M00001396B:B01	CH01COH
1176	23170	RTA00002887F.f.15.1.P.Sec	F	M00001396B:B12	CH01COH
1177	8487	RTA00002887F.f.16.1.P.Sec	g F	M00001396B:B12 M00027050A:B02	CH04MAL
1178	185798	RT.A00002911F.k.06.1.P.Se	q F	M00027050A:B02 M00004161B:G07	CHOICOH
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1180		RTA00002930F.c.01.1.P.Se	q F	M00042894C:A11	CH18CON
1181	7788	RTA00002932F.b.13.1.P.Se	g F	M00043017C:D08	CH08LNH
1182		RT.A00002917F.d.09.1.P.Se	q F	M00032688C:A03	CH02COH
1183		RTA00002902F.k.19.1.P.Se	q F	M00006740B:A09	CHOICOH
1184		RTA00002891F.o.11.1.P.Se	eq F	M000037S2A:B02	CH09LNL
1185		RTA00002925F.I.17.1.P.Se	q F	M00039981D:B01	CH04MAL
1186		RTA00002911F.p.07.1.P.Se	eq F	M00027177B:D04	CH03MAH
1187		RTA00002908F.h.03.1.P.Se	eq F	M00022438C:H09	CH18CON
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1188		RTA00002889F.i.11.1.P.Se	q F	M00001550D:B11	CH17COHLV
_		RTA00002935F.i.06.1.P.Se	eq F	M00054866B:C08	CH17COHLV
1190		RTA00002935F.1.04.1.P.Sc	eq F	M0005510SB:A02	CH1/COREV
1191		RTA00002933F.b.17.1.P.S	eq F	M00043152C:B10	
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1193		RT.A00002901F.k.23.1.P.S	eq F	M00005606D:B12	CHOICOH
1194		RTA00002898F.j.19.1.P.S	eq F	M00004365A:B11	CHOICON
119:		RTA00002890F.d.14.1.P.S	eq F	M00001600B:G01	CH01COH
1190		RTA00002931F.c.06.1.P.S	eq F	M00042873D:F05	CH16COP
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119		RT.A00002896F.c.21.1.P.S		M00004146A:C11	CHOICOH
119		RTA00002897F.a.02.1.P.S		M00004207C:A04	CHOICOH
120	0 4408	K1.40000_3971.a.02.111.5			

SEQ	CLUSTED	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
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1202	185841	RTA00002912F.j.15.1.P.Seq	F	M00027459C:B10	CH04MAL
1203	1278	RTA00002912F.j.15.1.1.Seq	F	M0004038-B:E04	CH14EDT
1204	19677	RTA00002929F.h.10.1.P.Seq	F	M00022563B:C08	СНОЗМАН
1205	17539	RTA00002909Fic.08.1.P.Seq	F	M00003830B:C06	CHOICOH
1206	11390	RTA00002892F.c.01.1.P.Seq	F	M00039822.A:H02	CH09LNL
1207	10735	RT.A00002923F.c.01.11.5eq	F	M00001406D:F06	CH01COH
1208	3239	RTA00002905F.n.20.1.P.Seq	F	M00021668D:A03	CH03MAH
1209	181718	RTA00002903F.n.20.117.5eq RTA00002917F.n.18.1.P.Seq		M00032787D:C05	CH08LNH
1210	6957	RTA00002917F.n.18.11.1.5eq RTA00002930F.a.14.1.P.Seq	F	M00042557D:B06	CH15CON
1211	23673	RTA00002938F.b.13.1.P.Seq	F	M00032831A:E09	CH08LNH
1212	11405	RTA00002918F.b.13.1.1.1.Seq RTA00002888F.d.16.1.P.Seq		M00001449B:H10	CH01CCH
1213	10256	RTA00002888F.d.10.1.1.5eq RTA00002891F.b.23.1.P.Seq	F	M00001675B:D06	CH01COH
1214	25563	R1.400002891F.0.23.1.F.Seq	F	M00001368A:B07	CH01COH
1215	2669	RTA00002886F.I.03.1.P.Seq		M00023389A:G04	CH04MAL
1216	185877	RTA00002911F.b.11.2.P.Seq		M00054911D:E06	CH15CON
1217	1314	RT.A00002930F.c.08.1.P.Seq		M00022509.A:H02	CH03MAH
1218	25843	RTA00002908F.o.05.1.P.Seq		M00039560C:G06	CH09LNL
1219	1794	RTA00002924F.g.06.1.P.Seq		M00004136C:B12	CH01COH
1220	22038	RTA00002896F.a.20.1.P.Seq		M00039478C:B02	CH09LNL
1221	6011	RTA00002924F.f.12.1.P.Seq		M00005675D:D09	CH02COH
1222	41087	RTA00002901F.o.06.1.P.Seq		M00022512B:A09	CH03MAH
1223	18534	RTA00002908F.o.16.1.P.Sec		M00038389D:D10	CH09LNL
1224	1444	RTA00002922F.a.12.1.P.Sec	F	M000038389D:D10	CH01COH
1225	1078	RTA00002893F.p.24.1.P.Sec	F	M00003972C:109	CH01COH
1226	8632	RTA00002896F.h.09.1.P.Sec	F	M00032795C:A03	CH08LNH
1227	105042	RTA00002917F.o.11.1.P.Sec	F	M00032793C:A03	CH04MAL
1228	6878	RTA00002912F.1.11.1.P.Sec	F	M00027313B:B04	CH04MAL
1229	23639	RTA00002912F.i.05.1.P.Sec	F	M000027381B:B04	CHOICOH
1230		RT.A00002896F.c.15.1.P.Sec	F	M0004094B:C08	CH09LNL
1231		RT.A00002926F.d.18.2.P.Sec		M00040094B:C08	CH15CON
1232		RTA00002930F.g.04.1.P.Sec	g F		CH09LNL
1233		RTA00002921F.o.01.1.P.Se	q F	M00038290A:D12	CHOICOH
1234		RTA00002890F.e.21.1.P.Se	g F	M00001606D:D06	CH18CON
1235		RTA00002932F.a.07.1.P.Se	q F	M00042586A:B01	CH02COH
1236		RTA00002901F.g.18.1.P.Se	q F	M00005505B:E01	CH09LNL
1237		RTA00002921F.b.02.1.P.Se	9 F	M00033302B:F10	CHOICOH
1238		RTA00002887F.p.11.1.P.Se	q F	M00001430B:C01	CHISCON
1239		RTA00002930F.j.17.1.P.Se	9 F	M00056244A:B06	CH09LNL
1240		RTA00002922F.m.04.1.P.Se	eq F	M00039121D:E07	
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1242		RTA00002891F.j.23.1.P.Se	q F	M00003761B:B02	CH01COH
1242		RT.A00002930F.g.09.1.P.Se	q F	M00055818B:D01	CH15CON
1242		RT.A00002935F.f.21.1.P.Se	q F	M00054725C:D09	
		RT.A00002918F.p.11.1.P.Se	eq F	M00033006A:F10	
1245	10000	RTA00002888F.j.20.1.P.Se	eq F	M00001477D:G09	CH01COH
1246		RT.A00002927F.h.15.1.P.Se	eq F	M00039642C:F08	
1247		RTA00002889F.e.21.1.P.Se		M00001539C:F12	
1248	2.5001	RTA00002909F.p.23.1.P.S		M00022740C:H11 M00022383C:A12	CH03MAL CH03MAL
1249					1 61107111

SEQ D				, . <u>.</u>		
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1552 29413 RTA0000290FR.23.1.P.Seq F M00022069D.C12 CH03MAH 1253 12315 RTA00002907FL24.2.P.Seq F M000222-0D:B11 CH03MAH 1254 4930 RTA00002930Fg.04.2.P.Seq F M000536180C.D03 CH13CON 1255 12018 RTA00002934Fc.16.1.P.Seq F M0005502-1B-F09 CH13CON 1255 12018 RTA00002935Fk.03.1.P.Seq F M0005502-1B-F09 CH13CON 1256 10501 RTA00002935Fk.03.1.P.Seq F M0005502-1B-F09 CH13CON 1257 11314 RTA00002937Fb.15.1.P.Seq F M0005502-1B-F09 CH13CON 1258 6426 RTA00002937Fb.15.1.P.Seq F M0005907-1B-H09 CH12EDT 1259 2250 RTA00002907Fb.03.1.P.Seq F M0003907-1B-H09 CH12EDT 1259 2250 RTA00002907Fb.03.1.P.Seq F M0003907-1B-H09 CH12EDT 1261 11928 RTA00002907Fb.05.1.P.Seq F M0003907-1B-H09 CH12EDT 1262 28226 RTA00002907Fb.05.1.P.Seq F M0003907-1C-B11 1263 16059 RTA00002907Fb.05.1.P.Seq F M00022-6B-B-B06 CH03MAH 1264 2252 RTA00002935Ff.19.1.P.Seq F M0000349-3C-F01 CH17COHLV 1266 21795 RTA00002935Ff.19.1.P.Seq F M0000349-3C-F01 CH17COHLV 1266 21795 RTA00002935F.19.1.P.Seq F M0000349-3B-E12 CH17COHLV 1266 21795 RTA00002935F.10.1.P.Seq F M0000349-3B-E12 CH17COHLV 1268 2565 RTA00002935F.10.1.P.Seq F M0000349-3B-E12 CH17COHLV 1269 20493 RTA00002935F.10.1.P.Seq F M0000349-3B-E12 CH17COHLV 1269 20493 RTA00002935F.10.1.P.Seq F M000349-3B-E12 CH17COHLV 1270 10509 RTA00002935F.00.1.P.Seq F M000349-3B-E12 CH17COHLV 1271 16392 RTA00002935F.00.1.P.Seq F M000349-3B-E12 CH17COHLV 1272 15797 RTA00002935F.00.1.P.Seq F M000349-3B-E12 CH17COHLV 1273 1811 RTA00002935F.00.1.P.Seq F M000354-3B-E0 CH19CON 1274 17503 RTA00002935F.00.1.P.Seq F M000354-3B-E0 CH19CON 1275 14639 RTA00002935F.00.1.P.Seq F M000429-3B-E0 CH19CON 1276 14639 RTA00002935F.00.1.P.Seq F M000429-3B-E0 CH19CON 1276 14639 RT	ID	CLUSTER				
1253 12315	1251	20412				
1254 4930	1252	29413				
1255 12018		12315				
1256	1254	4930				
1537 11314	1255	12018				
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1.536	1257	11314				
1.556 6991 RTA00002927F.j.12.1.P.Seq F M000390S1B:C04 CH09LNL	1258	6426				
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1962 28226 RTA00002907Fn.20.1.P.Seq F M00022262B:B06 CH03MAH 1263 16059 RTA00002935F, i.13.1.P.Seq F M0003497SC:F01 CH17COHLV 1264 2252 RTA00002886Fk.24.1.P.Seq F M0003497SC:F01 CH17COHLV 1265 4059 RTA00002935F, i.13.1.P.Seq F M0003497L4B:G10 CH17COHLV 1266 21795 RTA00002935F, i.10.1.P.Seq F M0003497L4B:G10 CH02COH 1267 15049 RTA00002935F, i.0.1.P.Seq F M0003497L4B:G10 CH02COH 1268 5565 RTA00002935F, i.0.1.P.Seq F M0003497L4B:G10 CH17COHLV 1269 20493 RTA00002935F, i.0.1.P.Seq F M0003497L4B:G10 CH17COHLV 1270 20257 RTA00002934Fa.141.P.Seq F M0004307TC:D12 CH17COH 1271 16392 RTA00002934Fa.141.P.Seq F M0004349SC:H05 CH20COHLV 1272 15797 RTA00002934Fa.141.P.Seq F M0003449SC:H05 CH20COHLV 1273 1811 RTA00002934Fa.121.P.Seq F M000349SC:H05 CH20COHLV 1274 17503 RTA00002935F, i.0.1.P.Seq F M0005455C:H06 CH15CON 1275 14639 RTA00002905F, i.12.1.P.Seq F M0005467:SD:G03 CH17COHLV 1275 14639 RTA00002934Fa.10.1.P.Seq F M0003405C:H01 CH00COHLV 1276 10689 RTA00002936Fb.19.1.P.Seq F M000360C-B:C05 CH15CON 1278 11596 RTA00002936Fb.19.1.P.Seq F M0000360C-B:C05 CH15CON 1278 11596 RTA00002936Fb.19.1.P.Seq F M000360C-B:C05 CH15CON 1278 11596 RTA00002936Fb.19.1.P.Seq F M0003585C:B04 CH01COH 1279 23731 RTA00002936Fb.19.1.P.Seq F M0003585C:B04 CH01COH 1281 1610 RTA00002936Fb.10.1.P.Seq F M0004345SC:G11 CH16COP 1282 1176 RTA00002936Fb.10.1.P.Seq F M0004385SC:G11 CH16COP 1283 125378 RTA00002936Fb.10.1.P.Seq F M0004285SC:G11 CH16COP 1284 17238 RTA00002936Fb.10.1.P.Seq F M0004385SC:G11 CH16COP 1285 1610 RTA00002936Fb.10.1.P.Seq F M0004385SC:G11 CH16COP 1286 16366 RTA00002936Fb.10.1.P.Seq F M0004385SC:G11 CH16COP 1290 23731 RTA00002936Fb.10.1.P.Seq F M0004365CB. CH11 CH16C	1260	6991				
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1264 2252	1262	28226				
1265 4059 RTA00002935F.f.I9.I.P.Seq F M00054714B:G10 CH17COHLV 1266 21795 RTA00002901F.b.I6.I.P.Seq F M00005412A:B10 CH02COH 1267 15049 RTA00002930F.c.02.I.P.Seq F M00054973B:I2 CH17COHLV 1268 5565 RTA0000293F.a.I4.I.P.Seq F M0004308:A:F09 CH15CON 1269 20493 RTA0000293F.a.I4.I.P.Seq F M0004307:C:D12 CH19COP 1270 20257 RTA0000293F.a.I4.I.P.Seq F M0004307:C:D12 CH19COP 1271 16392 RTA0000293F.a.I4.I.P.Seq F M00043495C:H05 CH20COHLV 1272 15797 RTA0000293F.a.IP.Seq F M000043495C:H05 CH20COHLV 1273 1811 RTA0000293F.a.IP.Seq F M000055456C:H06 CH15CON 1274 17503 RTA0000293F.b.I2.I.P.Seq F M00005605B:D100 CH03MAH 1276 9146 RTA0000293F.h.I2.I.P.Seq F M00005605B:D100 CH03MAH 1276 9146 RTA0000293F.h.I9.I.P.Seq F M000043465C:H11 CH20COHLV 1277 10689 RTA0000293F.h.I9.I.P.Seq F M00005600-B:O5 CH15CON 1278 11596 RTA0000293F.h.I9.I.P.Seq F M00005600-B:O5 CH15CON 1279 23731 RTA0000293F.h.I9.I.P.Seq F M00005600-B:O5 CH15CON 1280 25429 RTA0000293F.h.I0.I.P.Seq F M0000558SC:B04 CH15CON 1281 1610 RTA0000293F.h.I0.I.P.Seq F M0000558SC:B04 CH15CON 1282 1176 RTA0000293F.h.I0.I.P.Seq F M000428SC:G11 CH16COP 1283 13578 RTA0000293F.h.I0.I.P.Seq F M000428SC:G11 CH16COP 1284 17238 RTA0000293F.h.I0.I.P.Seq F M000425SSC:G11 CH16COP 1285 1610 RTA0000293F.h.I0.I.P.Seq F M000425SSC:G11 CH16COP 1286 16366 RTA0000293F.h.I0.I.P.Seq F M000425SSC:G11 CH16COP 1287 1790 RTA0000293F.h.I0.I.P.Seq F M000425SSC:G11 CH16COP 1288 17238 RTA0000293F.h.I0.I.P.Seq F M000425SSC:G11 CH16COP 1289 23451 RTA0000293F.h.I0.I.P.Seq F M000425SSC:G11 CH16COP 1280 16366 RTA0000293F.h.I0.I.P.Seq F M000425SSC:G11 CH16COP 1290 23731 RTA0000293F.h.I0.I.P.Seq F M000425SSC:G11 CH16COP 1291 47898 RTA000	1263	16059				
1266 21795 RTA00002901F.b.16.1.P.Seq F M0000544_2.A:B10 CH02COH 1267 15049 RTA00002931F.b.10.1.P.Seq F M00005497_3B:E12 CH17COHLV 1268 5565 RTA00002933F.a.14.1.P.Seq F M00042905.A:F09 CH15CON 1269 20493 RTA00002933F.a.14.1.P.Seq F M0004307_7C:D12 CH19COP 1270 20257 RTA00002934F.a.14.1.P.Seq F M000431495C:H05 CH20COHLV 1271 16392 RTA00002939F.a.05.1.P.Seq F M00043495C:H05 CH20COHLV 1272 15797 RTA00002939F.a.23.1.P.Seq F M0000414:Ba:A11 CH01COH 1273 1811 RTA00002931F.a.21.1.P.Seq F M0000168-D:E04 CH01COH 1274 17503 RTA00002931F.a.12.1.P.Seq F M00005467_5D:G03 CH17COHLV 1275 14639 RTA00002935F.1.12.1.P.Seq F M00005465C:H06 CH03MAH 1276 9146 RTA00002934F.a.10.1.P.Seq F M00005465C:H10 CH03MAH 1277 10689 RTA00002930F.h.19.1.P.Seq F M00005600-B:C05 CH15CON 1278 11596 RTA00002930F.a.19.1.P.Seq F M00005600-B:C05 CH15CON 1278 11596 RTA00002930F.a.19.1.P.Seq F M00005600-B:C05 CH15CON 1281 1610 RTA00002930F.a.110.1.P.Seq F M00005598:C:B04 CH15CON 1281 1610 RTA00002931F.a.12.1.P.Seq F M00004285SC:G11 CH16COP 1282 1176 RTA00002930F.a.110.1.P.Seq F M0004295SC:G04 CH15CON 1283 23578 RTA00002930F.a.110.1.P.Seq F M0004295SC:G04 CH15CON 1284 17238 RTA00002931F.a.11.P.Seq F M0004295SC:G01 CH16COP 1285 1610 RTA00002931F.a.11.P.Seq F M0004295SC:G01 CH16COP 1286 16366 RTA00002931F.a.11.P.Seq F M0004295SC:G01 CH16COP 1287 17970 RTA00002931F.a.19.P.Seq F M0004295SC:G01 CH16COP 1288 11027 RTA00002931F.a.11.P.Seq F M0004295SC:G01 CH16COP 1289 23451 RTA00002931F.a.19.P.Seq F M0004295SC:G01 CH18CON 1289 23451 RTA00002931F.a.19.P.Seq F M0004295SC:G01 CH18CON 1290 23731 RTA00002931F.a.19.P.Seq F M0004295SC:G01 CH18CON 1290 23731 RTA00002931F.a.19.P.Seq F M0004301SB:G03 CH1	1264	2252				
1267 15049 RTA00002935F.j.10.1.P.Seq F M000549^3B.E12 CH17COHLV 1268 5565 RTA00002935F.j.10.1.P.Seq F M00042908.A:F09 CH15CON 1269 20493 RTA00002933F.a.14.1.P.Seq F M000430^7C.D12 CH19COP 1270 20257 RTA00002934F.a.14.1.P.Seq F M0004319^5C.H05 CH20COHLV 1271 16392 RTA00002934F.a.14.1.P.Seq F M0004319^5C.H05 CH20COHLV 1272 15797 RTA00002930F.c.23.1.P.Seq F M0000441\$B.A11 CH01COH 1273 1811 RTA00002930F.c.23.1.P.Seq F M0000168-D.E04 CH15CON 1274 17503 RTA00002935F.08.1.P.Seq F M0000168-D.E04 CH01COH 1275 14639 RTA00002935F.08.1.P.Seq F M0000361-D.E04 CH01COH 1276 9146 RTA00002935F.h.12.1.P.Seq F M000080^7.D.D01 CH03MAH 1276 9146 RTA00002930F.h.12.1.P.Seq F M00043465C.H11 CH20COHLV 1277 10689 RTA00002930F.h.19.P.Seq F M00043465C.H11 CH20COHLV 1278 11596 RTA00002930F.g.18.1.P.Seq F M0000160^-A:E04 CH01COH 1279 23731 RTA00002930F.h.10.1.P.Seq F M0000558^*.D:C02 CH15CON 1280 25429 RTA00002930F.g.18.1.P.Seq F M000558^*.D:C02 CH15CON 1281 1610 RTA00002931F.h.10.1.P.Seq F M0004365*C:B04 CH15CON 1282 1176 RTA00002935F.a.10.1.P.Seq F M00042858C:G11 CH16COP 1283 13578 RTA00002935F.a.18.1.P.Seq F M00042858C:G11 CH16COP 1284 17238 RTA00002935F.a.22.1.P.Seq F M0004257*C:B00 CH15CON 1285 1610 RTA00002931F.c.01.1.P.Seq F M0004255*C:B04 CH15CON 1286 16366 RTA00002931F.c.01.1.P.Seq F M0004255*C:B04 CH15CON 1287 19709 RTA00002931F.c.01.1.P.Seq F M0004255*C:B01 CH18CON 1288 1027 RTA00002931F.c.01.1.P.Seq F M0004255*C:B01 CH18CON 1289 23451 RTA00002931F.c.01.1.P.Seq F M0004555*3.D:C02 CH15CON 1291 47898 RTA00002931F.c.01.1.P.Seq F M0004555*3.D:C02 CH15CON 1292 32581 RTA00002931F.c.01.1.P.Seq F M0004555*3.B:D:C01 CH19COHLV 1294 1447 RTA00002935F.d.14.1.P.Seq F M0004555	1265	4059	RTA00002935F.f.19.1.P.Seq			
1268	1266	21795				
1269 20493 RTA00002933F.a.14.1.P.Seq F M00043077C:D12 CH19COP 1270 20257 RTA00002934F.a.14.1.P.Seq F M00043495C:H05 CH20COHLV 1271 16392 RTA00002939F.a.05.1.P.Seq F M0000441SB:A11 CH01COH 1272 15797 RTA00002930F.c.23.1.P.Seq F M00053456C:H06 CH15CON 1273 1811 RTA0000293F.d.03.1.P.Seq F M0000168-D:E04 CH01COH 1274 17503 RTA00002935F.d.03.1.P.Seq F M0000168-D:E04 CH01COH 1275 14639 RTA00002935F.d.03.1.P.Seq F M0000807:D:D01 CH03MAH 1276 9146 RTA00002935F.h.12.1.P.Seq F M00043465C:H11 CH20COHLV 1277 10689 RTA00002930F.h.19.1.P.Seq F M0003600-B:C05 CH15CON 1278 11596 RTA00002930F.a.19.1.P.Seq F M00005600-B:C05 CH15CON 1278 1279 23731 RTA00002930F.a.18.1.P.Seq F M0000587:D:C02 CH15CON 1280 25429 RTA00002930F.h.10.1.P.Seq F M00005587:D:C02 CH15CON 1281 1610 RTA00002931F.b.24.1.P.Seq F M00042457:CB04 CH16COP 1282 1176 RTA00002935F.a.10.1.P.Seq F M00042457:CB06 CH17COHLV 1283 23578 RTA00002935F.a.10.1.P.Seq F M0004257:CB06 CH17COHLV 1284 17238 RTA00002931F.a.10.1.P.Seq F M0004257:CB06 CH17COHLV 1285 1610 RTA00002931F.a.10.1.P.Seq F M0004257:CB01 CH18CON 1286 16366 RTA00002931F.a.10.1.P.Seq F M0004257:CB01 CH18CON 1287 19709 RTA00002931F.a.10.1.P.Seq F M0004257:CB01 CH18CON 1288 11027 RTA00002931F.a.10.1.P.Seq F M0004257:CB01 CH18CON 1289 23451 RTA00002931F.a.10.1.P.Seq F M0004257:CB01 CH18CON 1291 47898 RTA00002931F.a.10.1.P.Seq F M0004257:CB01 CH18CON 1292 32581 RTA00002931F.a.10.1.P.Seq F M0004257:CB01 CH18CON 1293 42 RTA00002931F.a.10.1.P.Seq F M0004257:CB01 CH19COP 1294 1447 RTA00002931F.a.10.1.P.Seq F M0004257:CB01 CH19COP 1295 30451 RTA00002935F.a.10.1.P.Seq F M0004257:CB01 CH19COP 1296 35359 RTA00002935F.a.10.1.P.Seq F M0004257:CB01 CH19COP	1267	15049				
1270 20257 RTA00002934F.a.14.I.P.Seq F M00043495C:H05 CH20COHLV 1271 16392 RTA00002899F.a.05.I.P.Seq F M00004418B.A11 CH01COH 1272 15797 RTA00002891F.d.21.I.P.Seq F M00055456C:H06 CH15CON 1273 1811 RTA00002891F.d.21.I.P.Seq F M000560-ED4 CH01COH 1274 17503 RTA00002935F.f.08.I.P.Seq F M00054675D:G03 CH17COHLV 1275 14639 RTA00002935F.f.08.I.P.Seq F M00008073D:D01 CH03MAH 1276 9146 RTA00002934F.a.10.I.P.Seq F M000434675D:G05 CH15CON 1277 10689 RTA00002930F.h.19.I.P.Seq F M0005600-B:C05 CH15CON 1278 11596 RTA00002930F.h.19.I.P.Seq F M00005600-B:C05 CH15CON 1279 23731 RTA00002930F.a.18.I.P.Seq F M00055873D:C02 CH15CON 1280 25429 RTA00002930F.h.10.I.P.Seq F M00055873D:C02 CH15CON 1281 1610 RTA00002931F.b.24.I.P.Seq F M00055873D:C02 CH15CON 1282 1176 RTA00002931F.b.24.I.P.Seq F M00042855C:B04 CH16COP 1283 23578 RTA00002935F.a.10.I.P.Seq F M0004285C:B04 CH16COP 1284 17238 RTA00002931F.a.18.I.P.Seq F M0004285C:B04 CH16CON 1285 1610 RTA00002931F.a.18.I.P.Seq F M0004285C:G11 CH16COP 1286 16366 RTA00002931F.a.19.I.P.Seq F M0004285C:G11 CH16COP 1287 19709 RTA00002931F.a.19.I.P.Seq F M0004285C:G11 CH16COP 1288 11027 RTA00002931F.a.04.I.P.Seq F M0004285C:G11 CH16COP 1289 23451 RTA00002931F.a.04.I.P.Seq F M0004295:D:G12 CH18CON 1291 47898 RTA00002931F.a.09.I.P.Seq F M0004295:D:G12 CH18CON 1291 47898 RTA00002931F.a.09.I.P.Seq F M0004295:D:G12 CH18CON 1291 47898 RTA00002931F.a.09.I.P.Seq F M0004295:D:G12 CH18CON 1293 42 RTA00002931F.a.09.I.P.Seq F M0004295:D:G12 CH19CON 1294 1447 RTA00002931F.a.09.I.P.Seq F M0004295:D:G12 CH19CON 1295 10449 RTA00002935F.a.14.I.P.Seq F M00055395:D:D11 CH17COHLV 1295 10449 RTA00002935F.a.19.I.P.Seq F M00055395:D:D11 CH17COHLV	1268	5565				
1271 16392 RTA00002899F.a.05.1.P.Seq F M000441\$B:A11 CH01COH 1272 15797 RTA00002930F.c.23.1.P.Seq F M0005545cC:H06 CH15CON 1273 1811 RTA00002931F.d.21.1.P.Seq F M000016\$-D:E04 CH01COH 1274 17503 RTA00002935F.f.08.1.P.Seq F M0000546*5D:E03 CH17COHLV 1275 14639 RTA00002905F.h.12.1.P.Seq F M0000546*5D:E03 CH17COHLV 1276 9146 RTA00002935F.h.12.1.P.Seq F M000360*2B:C05 CH17COHLV 1277 10689 RTA00002930F.h.19.1.P.Seq F M000360*2B:C05 CH15CON 1278 11596 RTA00002930F.h.19.1.P.Seq F M000016*A:E04 CH01COH 1279 23731 RTA00002930F.e.23.1.P.Seq F M000016*A:E04 CH01COH 1280 25429 RTA00002930F.h.10.1.P.Seq F M000558*3D:C02 CH15CON 1281 1610 RTA00002931F.b.24.1.P.Seq F M0004285*C:G11 CH16COP 1282 1176 RTA00002935F.a.10.1.P.Seq F M0004285*C:G11 CH16COP 1283 23578 RTA00002930F.a.22.1.P.Seq F M000425*C:B06 CH17COHLV 1283 23578 RTA00002935F.a.18.1.P.Seq F M000425*C:B06 CH17COHLV 1284 17238 RTA00002935F.a.18.1.P.Seq F M000425*C:B01 CH18CON 1285 1610 RTA00002935F.a.18.1.P.Seq F M000425*C:B01 CH18CON 1286 16366 RTA00002935F.a.18.1.P.Seq F M000425*C:B01 CH18CON 1287 19709 RTA00002935F.a.18.1.P.Seq F M000425*C:B01 CH18CON 1288 11027 RTA00002935F.a.19.1.P.Seq F M000425*C:B01 CH18CON 1298 23451 RTA00002935F.b.10.1.P.Seq F M000425*C:B01 CH18CON 1299 23731 RTA00002935F.b.10.1.P.Seq F M000425*C:B01 CH18CON 1291 47898 RTA00002935F.b.10.1.P.Seq F M000425*C:B01 CH19COP 1290 23731 RTA00002935F.b.10.1.P.Seq F M000425*C:B01 CH19COP 1291 47898 RTA00002935F.b.10.1.P.Seq F M000425*C:B01 CH19COP 1294 1447 RTA00002935F.b.10.1.P.Seq F M000545*C:B01 CH19COP 1295 10449 RTA00002935F.b.10.1.P.Seq F M000545*C:B01 CH17COHLV 1296 35359 RTA00002935F.b.10.1.P.Seq F M000545*C:B01 CH17COHLV	1269	20493				
1272 15797 RTA00002930Fc.23.1.P.Seq F M0005545eC:H06 CH15CON 1273 1811 RTA00002891F.d.21.1.P.Seq F M0000168-D.E04 CH01COH 1274 17503 RTA00002935F.f.08.1.P.Seq F M000367-D.E04 CH17COHL V 1275 14639 RTA00002935F.h.12.1.P.Seq F M000367-D.E001 CH17COHL V 1276 9146 RTA00002934Fa.1.01.P.Seq F M000360-B:C05 CH17COHL V 1277 10689 RTA00002930F.h.19.1.P.Seq F M0003600-B:C05 CH15CON 1278 11596 RTA00002930F.h.19.1.P.Seq F M000560-B:C05 CH15CON 1279 23731 RTA00002930F.h.10.1.P.Seq F M000558*3-D:C02 CH15CON 1280 25429 RTA00002930F.h.10.1.P.Seq F M000558*3-D:C02 CH15CON 1281 1610 RTA00002931F.b.24.1.P.Seq F M0004285*SC:G11 CH16COP 1282 1176 RTA00002931F.b.24.1.P.Seq F M0004285*SC:G11 CH16COP 1283 23578 RTA00002930Fa.18.1.P.Seq F M0004285*C:B04 CH15CON 1284 17238 RTA00002931Fa.18.1.P.Seq F M0004295*C:B01 CH15CON 1285 1610 RTA00002931Fa.04.1.P.Seq F M0004295*C:B01 CH15CON 1286 16366 RTA00002931Fa.04.1.P.Seq F M0004295*C:B01 CH18CON 1287 19709 RTA00002932Fa.10.1.P.Seq F M0004295*C:B01 CH18CON 1288 11027 RTA00002932Fa.10.1.P.Seq F M0004295*C:B01 CH18CON 1289 23451 RTA00002932Fa.10.1.P.Seq F M0004205*C:B01 CH18CON 1290 23731 RTA00002932Fa.10.1.P.Seq F M0004205*C:B01 CH18CON 1291 47898 RTA00002932Fa.10.1.P.Seq F M0004205*C:B01 CH18CON 1291 47898 RTA00002932Fa.10.1.P.Seq F M0004205*C:B01 CH19COP 1294 1447 RTA00002935Fa.10.1.P.Seq F M0004205*C:B01 CH19COP 1295 10449 RTA00002935Fa.14.1.P.Seq F M0004205*C:B01 CH17COHLV 1295 10449 RTA00002935Fa.11.1.P.Seq F M0004205*C:B01 CH17COHLV 1296 35359 RTA00002935Fa.11.1.P.Seq F M000555*C:B01 CH17COHLV 1297 19657 RTA00002935Fa.11.1.P.Seq F M0005516*C:D10 CH17COHLV 1298 10449 RTA00002935Fa.21.1.P.Seq F M0005516*C:D10 CH17COHLV	1270	20257				
1273 1811 RTA0000293FF.08.1.P.Seq F M000168±D:E04 CH01COHL 1274 17503 RTA0000293FF.08.1.P.Seq F M000546±D:E03 CH17COHL 1275 14639 RTA0000293FF.08.1.P.Seq F M000546±D:E03 CH17COHL 1276 9146 RTA0000293FF.1.12.1.P.Seq F M000546±D:E01 CH03MAH 1276 9146 RTA0000293FF.1.12.1.P.Seq F M000540±B:C05 CH15CON 1277 10689 RTA0000293FF.1.12.1.P.Seq F M000560±B:C05 CH15CON 1278 11596 RTA0000293FF.23.1.P.Seq F M000560±B:C05 CH15CON 1279 23731 RTA0000293F.2.13.1.P.Seq F M000558±D:C02 CH15CON 1280 25429 RTA0000293FF.1.10.1.P.Seq F M000558±C:B04 CH15CON 1281 1610 RTA0000293FF.2.1.P.Seq F M0004285±C:G01 CH16COP 1282 1176 RTA0000293FF.2.1.P.Seq F M0004285±C:G01 CH16COP 1283 23578 RTA0000293F.2.1.P.Seq F M0004285±C:B06 CH17COHLV 1283 23578 RTA0000293F.2.1.P.Seq F M0004285±C:B01 CH18CON 1284 17238 RTA0000293F.2.2.1.P.Seq F M0004285±C:B01 CH18CON 1285 1610 RTA0000293F.2.0.1.P.Seq F M0004285±C:B01 CH18CON 1286 16366 RTA0000293F.2.1.P.Seq F M0004285±C:G11 CH16COP 1287 19709 RTA0000293F.2.1.P.Seq F M0004285±D:G12 CH18CON 1288 11027 RTA0000293F.2.1.P.Seq F M0004285±D:G12 CH18CON 1289 23451 RTA0000293F.2.1.P.Seq F M0004285±D:G12 CH18CON 1291 47898 RTA0000293F.2.1.P.Seq F M0004285±D:G12 CH18CON 1292 32581 RTA0000293F.2.1.P.Seq F M0004285±D:D03 CH18CON 1293 42 RTA0000293F.0.02.1.P.Seq F M0004285±D:D03 CH18CON 1294 1447 RTA0000293F.0.1.P.Seq F M000535395±D10 CH17COHLV 1295 10449 RTA0000293F.0.21.P.Seq F M000535395±D10 CH17COHLV 1296 35359 RTA0000293F.1.20.1.P.Seq F M000535395±D10 CH17COHLV 1296 35359 RTA0000293F.1.20.1.P.Seq F M000536±C=D10 CH17COHLV 1297 19657 RTA0000293F.1.20.1.P.Seq F M0005613±A:E11 CH17COHLV 1298 12659 RTA0000293F.1.20.1.P.Seq F M0005613±A:E1	1271	16392				
17503	1272	15797				
1275	1273	1811				
1276	1274	17503				
1277 10689 RT A00002930F.h.19.I.P.Seq F M0003600-B:C05 CH15CON 1278 11596 RT A00002890F.e.23.I.P.Seq F M0000160^-A:E04 CH01COH 1279 23731 RT A00002930F.g.18.I.P.Seq F M000558^-3D:C02 CH15CON 1280 25429 RT A00002930F.h.10.I.P.Seq F M000558^-3D:C02 CH15CON 1281 1610 RT A00002931F.b.24.I.P.Seq F M0004285^-C:B04 CH15CON 1282 1176 RT A00002931F.a.10.I.P.Seq F M000425^-C:B06 CH17COHLV 1283 23578 RT A00002935F.a.10.I.P.Seq F M000425^-C:B06 CH17COHLV 1284 17738 RT A00002930F.a.22.I.P.Seq F M000425^-C:B01 CH18CON 1285 1610 RT A00002931F.c.01.I.P.Seq F M000425^-C:B01 CH18CON 1286 16366 RT A00002932F.a.104.I.P.Seq F M000425^-C:B01 CH18CON 1287 19709 RT A00002932F.a.04.I.P.Seq F M000425^-C:B01 CH18CON 1288 11027 RT A00002932F.b.10.I.P.Seq F M000425^-C:B01 CH18CON 1289 23451 RT A00002930F.g.10.I.P.Seq F M000426^-C:B01 CH18CON 1290 23731 RT A00002930F.g.18.2.P.Seq F M000426^-C:B01 CH19COP 1290 23731 RT A00002930F.g.18.2.P.Seq F M000426^-C:B01 CH19COP 1291 47898 RT A00002930F.g.18.2.P.Seq F M000426^-C:B00 CH19CON 1292 32581 RT A00002930F.g.18.2.P.Seq F M000426^-C:B00 CH19CON 1293 42 RT A00002930F.d.14.I.P.Seq F M0004301-B-C:B00 CH3CON 1294 1447 RT A00002935F.d.14.I.P.Seq F M000436^-C:B00 CH3CON 1295 10449 RT A00002935F.d.14.I.P.Seq F M00055395^-D:D11 CH17COHLV 1296 35359 RT A00002935F.d.12.I.P.Seq F M0005518^-C:D10 CH17COHLV 1297 19657 RT A00002935F.d.12.I.P.Seq F M0005613^-A:E11 CH15CON 1298 12659 RT A00002935F.d.12.I.P.Seq F M0005613^-A:E11 CH15CON 1299 9081 RT A00002934F.a.22.I.P.Seq F M0005613^-A:E11 CH15CON 1299 9081 RT A00002934F.a.22.I.P.Seq F M0005613^-A:E11 CH15CON 1298 12659 RT A00002934F.a.22.I.P.Seq F M0005613^-A:E11 CH15CON 1299 9081 RT A00002934F.a.	1275	14639				
1278	1276	9146				
1279 23731 RTA00002930F.g.18.1.P.Seq F M000558~3D:C02 CH15CON 1280 25429 RTA00002930F.h.10.1.P.Seq F M0005598C:B04 CH15CON 1281 1610 RTA00002931F.b.24.1.P.Seq F M00042858C:G11 CH16COP 1282 1176 RTA00002935F.a.10.1.P.Seq F M00042858C:G11 CH16COP 1283 23578 RTA00002930F.a.22.1.P.Seq F M0004257°C.B06 CH17COHLV 1284 17238 RTA00002932F.a.18.1.P.Seq F M0004257°C.B01 CH18CON 1284 17238 RTA00002931F.c.01.1.P.Seq F M0004257°C.B01 CH18CON 1285 1610 RTA00002931F.c.01.1.P.Seq F M00042585.C:G11 CH16COP 1286 16366 RTA00002932F.a.12.1.P.Seq F M00042585.A:H11 CH18CON 1287 19709 RTA00002932F.a.12.1.P.Seq F M0004295.D:G12 CH18CON 1288 11027 RTA00002932F.b.10.1.P.Seq F M0004295.D:G12 CH18CON 1289 23451 RTA00002933F.a.091.P.Seq F M0004261°B:E01 CH19COP 1290 23731 RTA00002930F.g.18.2.P.Seq F M00042085.D:G02 CH15CON 1291 47898 RTA00002931F.k.071.P.Seq F M0005587.3D:C02 CH15CON 1293 422 RTA00002934F.a.11.1.P.Seq F M0004298.D:E03 CH18CON 1294 1447 RTA00002935F.b.02.1.P.Seq F M0004304.C:A:B10 CH004M.AL 1295 10449 RTA00002935F.d.14.1.P.Seq F M00055395.D:D11 CH17COHLV 1296 35359 RTA00002935F.h.11.1.P.Seq F M0005516.C:D10 CH17COHLV 1297 19657 RTA00002935F.h.11.1.P.Seq F M000516.C:D10 CH17COHLV 1298 12659 RTA00002935F.l.20.1.P.Seq F M000513.A:E11 CH15CON 1299 9081 RTA00002934F.a.22.1.P.Seq F M000561.3.A:E11 CH15CON 1299 9081 RTA00002935F.a.22.1.P.Seq F M0000561.3.A:E11 CH15CON 1200 RTA00002935F.a.22.1.P.Seq F M0000561.3.A:E11 CH1	1277	10689				
1280 25429 RTA00002930F.h.10.1.P.Seq F M0005598CC:B04 CH15CON 1281 1610 RTA00002931F.b.24.1.P.Seq F M00042858C:G11 CH16COP 1282 1176 RTA00002935F.a.10.1.P.Seq F M00042858C:G11 CH16COP 1283 23578 RTA00002930F.a.22.1.P.Seq F M0004245^**C.B06 CH17COHLV 1284 17238 RTA00002930F.a.22.1.P.Seq F M0004257C*A.D09 CH15CON 1284 17238 RTA00002931F.c.01.1.P.Seq F M0004297CC:B01 CH18CON 1285 1610 RTA00002931F.c.01.1.P.Seq F M00042858C:G11 CH16COP 1286 16366 RTA00002932F.a.04.1.P.Seq F M00042585A:H11 CH18CON 1287 19709 RTA00002932F.a.12.1.P.Seq F M0004295*D:G12 CH18CON 1288 11027 RTA00002932F.b.10.1.P.Seq F M00043013B:E03 CH18CON 1289 23451 RTA00002933F.a.09.1.P.Seq F M0004261*B:E01 CH19COP 1290 23731 RTA00002930F.g.18.2.P.Seq F M00004561*B:E01 CH19COP 1291 47898 RTA00002931F.k.07.1.P.Seq F M0002705*A:E10 CH04MAL 1292 32581 RTA00002934F.a.11.1.P.Seq F M0004298*D:E03 CH18CON 1293 42 RTA00002934F.a.11.1.P.Seq F M000434*C:A:C10 CH20COHLV 1294 1447 RTA00002935F.d.14.1.P.Seq F M000553*95*D:D11 CH17COHLV 1295 10449 RTA00002935F.d.14.1.P.Seq F M000551*6C*D10 CH17COHLV 1296 35359 RTA00002935F.1.20.1.P.Seq F M000551*6C*D10 CH17COHLV 1297 19657 RTA00002935F.1.20.1.P.Seq F M000561*3*A:E11 CH15CON 1298 12659 RTA00002935F.1.20.1.P.Seq F M000436*C.a.B01 CH20COHLV 1299 9081 RTA00002934F.a.22.1.P.Seq F M000436*C.a.B01 CH20COHLV 1299 9081 RTA00002935F.22.1.P.Seq F M000436*	1278	11596				
1281 1610 RTA00002931F.b.24.1.P.Seq F M00042858C:G11 CH16COP 1282 1176 RTA00002935F.a.10.1.P.Seq F M0004245TC:B06 CH17COHLV 1283 23578 RTA00002930F.a.22.1.P.Seq F M000425TC:B06 CH15CON 1284 17238 RTA00002932F.a.18.1.P.Seq F M000425TC:B01 CH18CON 1285 1610 RTA00002931F.c.01.1.P.Seq F M00042858C:G11 CH16COP 1286 16366 RTA00002932F.a.04.1.P.Seq F M000425S5A:H11 CH18CON 1287 19709 RTA00002932F.a.12.1.P.Seq F M0004295:D:G12 CH18CON 1288 11027 RTA00002932F.b.10.1.P.Seq F M0004295:D:G12 CH18CON 1289 23451 RTA00002933F.a.09.1.P.Seq F M0004261*B:E01 CH19COP 1290 23731 RTA00002935F.a.12.P.Seq F M0004261*B:E01 CH19COP 1291 47898 RTA00002931F.k.07.1.P.Seq F M00027052.A:E10 CH04MAL 1292 32581 RTA00002932F.b.02.1.P.Seq F M0004298*D:E03 CH18CON 1293 42 RTA00002934F.a.11.1.P.Seq F M0004347C.A:C10 CH20COHLV 1294 1447 RTA00002935F.d.14.1.P.Seq F M00055395D:D11 CH17COHLV 1295 10449 RTA00002935F.o.20.1.P.Seq F M0005516*C:D10 CH17COHLV 1296 35359 RTA00002935F.b.11.1.P.Seq F M0005516*C:D10 CH17COHLV 1297 19657 RTA00002935F.l.20.1.P.Seq F M0005516*C:D10 CH17COHLV 1298 12659 RTA0000293F.a.22.1.P.Seq F M00056153.A:E11 CH15CON 1299 9081 RTA0000293F.a.22.1.P.Seq F M0004364*C.A:B01 CH20COHLV 1200 1200 1200 1200 1200 1200 1200 1200 1200 1200 1200 1200 1200 1200 1200 1200 1200 1200 1						
1281 1810		25429				
1282 1176 RTA00002930F.a.22.1.P.Seq F M0004257°C.a:D09 CH15CON 1283 23578 RTA00002930F.a.22.1.P.Seq F M0004297°C:B01 CH18CON 1284 17238 RTA00002931F.c.01.1.P.Seq F M0004297°C:B01 CH18CON 1285 1610 RTA00002931F.c.01.1.P.Seq F M00042858C:G11 CH18CON 1286 16366 RTA00002932F.a.12.1.P.Seq F M0004295°D:G12 CH18CON 1287 19709 RTA00002932F.a.12.1.P.Seq F M0004295°D:G12 CH18CON 1288 11027 RTA00002932F.b.10.1.P.Seq F M0004295°D:G12 CH18CON 1289 23451 RTA00002933F.a.09.1.P.Seq F M0004261°B:E01 CH19COP 1290 23731 RTA00002930F.g.18.2.P.Seq F M000558°C.DC02 CH15CON 1291 47898 RTA00002931F.b.02.1.P.Seq F M0004298°C.DE03 CH18CON 1293 42 RTA0000293F.b.02.1.P.Seq F M000434°C.A.C10 CH20COHLV 1294	1281	1610				
1284 17238 RTA00002932F.a.18.1.P.Seq F M0004297CC:B01 CH18CON 1285 1610 RTA00002931F.c.01.1.P.Seq F M00042858C:G11 CH16COP 1286 16366 RTA00002932F.a.04.1.P.Seq F M00042585A:H11 CH18CON 1287 19709 RTA00002932F.a.12.1.P.Seq F M0004295:D:G12 CH18CON 1288 11027 RTA00002932F.b.10.1.P.Seq F M00043013B:E03 CH18CON 1289 23451 RTA00002933F.a.09.1.P.Seq F M000426:TB:E01 CH19COP 1290 23731 RTA00002930F.g.18.2.P.Seq F M0002705:2.A:E10 CH04MAL 1291 47898 RTA00002931F.k.07.1.P.Seq F M0004298cD:E03 CH18CON 1293 42 RTA00002934F.a.11.1.P.Seq F M000434TCA:C10 CH20COHLV 1294 1447 RTA00002935F.d.14.1.P.Seq F M000543*C:B:B01 CH17COHLV 1296 35359 RTA00002935F.b.11.1.P.Seq F M000543*C:C:D10 CH17COHLV 1298<						
1285 1610 RTA00002931F.c.01.1.P.Seq F M00042858C:G11 CH16COP 1286 16366 RTA00002932F.a.04.1.P.Seq F M00042585A:H11 CH18CON 1287 19709 RTA00002932F.a.12.1.P.Seq F M0004295:D:G12 CH18CON 1288 11027 RTA00002932F.b.10.1.P.Seq F M00043013B:E03 CH18CON 1289 23451 RTA0000293F.a.09.1.P.Seq F M0004261 B:E01 CH19COP 1290 23731 RTA0000293F.g.18.2.P.Seq F M00055873D:C02 CH15CON 1291 47898 RTA0000293F.b.02.1.P.Seq F M00027052A:E10 CH04MAL 1292 32581 RTA0000293F.b.02.1.P.Seq F M0004298cD:E03 CH18CON 1293 42 RTA0000293F.b.02.1.P.Seq F M0004347CA:C10 CH20COHLV 1294 1447 RTA00002935F.d.14.1.P.Seq F M000553cB:B01 CH17COHLV 1295 10449 RTA00002935F.b.11.1.P.Seq F M000553cC:D10 CH17COHLV 1297	1283	23578				
1286 16366 RTA0000293E.a.04.1.P.Seq F M00042585.A:H11 CHISCON 1287 19709 RTA0000293E.a.12.1.P.Seq F M0004295.D:G12 CHISCON 1288 11027 RTA0000293E.b.10.1.P.Seq F M00043013B:E03 CHISCON 1289 23451 RTA0000293F.a.09.1.P.Seq F M0004261 B:E01 CH19COP 1290 23731 RTA0000293F.g.18.2.P.Seq F M00055873D:C02 CH15CON 1291 47898 RTA0000293F.g.18.2.P.Seq F M00027052A:E10 CH04MAL 1292 32581 RTA0000293F.b.02.1.P.Seq F M0004298cD:E03 CH18CON 1293 42 RTA0000293F.b.11.1.P.Seq F M0004347CA:C10 CH20COHLV 1294 1447 RTA00002935F.d.14.1.P.Seq F M00055395D:D11 CH17COHLV 1295 10449 RTA00002935F.b.11.1.P.Seq F M00055395D:D11 CH17COHLV 1296 35359 RTA00002935F.b.20.1.P.Seq F M0005516cC:D10 CH17COHLV 1298	1284	17238				
1287 19709 RTA00002932F.a.12.1.P.Seq F M0004295:D:G12 CH18CON 1288 11027 RTA00002932F.b.10.1.P.Seq F M00043013B:E03 CH18CON 1289 23451 RTA00002933F.a.09.1.P.Seq F M00042617B:E01 CH19COP 1290 23731 RTA0000293F.g.18.2.P.Seq F M00055873D:C02 CH15CON 1291 47898 RTA0000293F.b.02.1.P.Seq F M00027052A:E10 CH04MAL 1292 32581 RTA0000293F.b.02.1.P.Seq F M0004298cD:E03 CH18CON 1293 42 RTA0000293F.b.02.1.P.Seq F M0004347CA:C10 CH20COHLV 1294 1447 RTA00002935F.d.14.1.P.Seq F M0005453cB:B01 CH17COHLV 1295 10449 RTA00002935F.b.11.1.P.Seq F M00055395D:D11 CH17COHLV 1296 35359 RTA00002935F.b.20.1.P.Seq F M0005518cC:D10 CH17COHLV 1298 12659 RTA00002935F.l.20.1.P.Seq F M00056183A:E11 CH15CON 1299	1285	1610				
1287 19709 RTA00002932F.b.10.1.P.Seq F M00043013B:E03 CH18CON 1288 11027 RTA00002932F.b.10.1.P.Seq F M00043013B:E03 CH18CON 1289 23451 RTA00002933F.a.09.1.P.Seq F M00042617B:E01 CH19COP 1290 23731 RTA00002930F.g.18.2.P.Seq F M00025873D:C02 CH15CON 1291 47898 RTA00002911F.k.07.1.P.Seq F M00027052A:E10 CH04MAL 1292 32581 RTA00002932F.b.02.1.P.Seq F M0004298cD:E03 CH18CON 1293 42 RTA00002934F.a.11.1.P.Seq F M0004347CA:C10 CH20COHLV 1294 1447 RTA00002935F.d.14.1.P.Seq F M0005453cB:B01 CH17COHLV 1295 10449 RTA00002935F.b.11.1.P.Seq F M00055395D:D11 CH17COHLV 1296 35359 RTA00002935F.l.20.1.P.Seq F M0005516cC:D10 CH17COHLV 1298 12659 RTA00002935F.l.20.1.P.Seq F M0005613A:E11 CH15CON 1299 <td>1286</td> <td>16366</td> <td></td> <td></td> <td></td> <td></td>	1286	16366				
1288 11027 RTA00002932F.B.10.1.F.Seq F M0004261 B:E01 CH19COP 1289 23451 RTA00002933F.a.09.1.P.Seq F M0004261 B:E01 CH19COP 1290 23731 RTA00002930F.g.18.2.P.Seq F M0002705 2A:E10 CH15CON 1291 47898 RTA0000291F.k.07.1.P.Seq F M0004298 D:E03 CH18CON 1292 32581 RTA0000293F.b.02.1.P.Seq F M0004298 D:E03 CH18CON 1293 42 RTA00002934F.a.11.1.P.Seq F M000434 T:CA:C10 CH20COHLV 1294 1447 RTA00002935F.d.14.1.P.Seq F M0005453 B:B01 CH17COHLV 1295 10449 RTA00002935F.b.11.1.P.Seq F M00055395 D:D11 CH17COHLV 1296 35359 RTA00002935F.b.20.1.P.Seq F M0005516cC:D10 CH17COHLV 1297 19657 RTA00002935F.b.20.1.P.Seq F M0005516cC:D10 CH17COHLV 1298 12659 RTA00002936F.i.21.1.P.Seq F M0005613 A:E11 CH15CON 12						
1290 23731 RTA00002930F.g.18.2.P.Seq F M000558T3D:C02 CH15CON 1291 47898 RTA0000291F.k.07.1.P.Seq F M00027052.A:E10 CH04MAL 1292 32581 RTA00002932F.b.02.1.P.Seq F M0004298cD:E03 CH18CON 1293 42 RTA00002934F.a.11.1.P.Seq F M000434TCA:C10 CH20COHLV 1294 1447 RTA00002935F.d.14.1.P.Seq F M0005453cB:B01 CH17COHLV 1295 10449 RTA00002935F.o.20.1.P.Seq F M00055395D:D11 CH17COHLV 1296 35359 RTA00002935F.h.11.1.P.Seq F M0005481 D:A11 CH17COHLV 1297 19657 RTA00002935F.l.20.1.P.Seq F M0005613:A:E11 CH17COHLV 1298 12659 RTA00002930F.i.21.1.P.Seq F M0005613:A:E11 CH15CON 1299 9081 RTA00002934F.a.22.1.P.Seq F M0004364:CA:B01 CH20COHLV	1288	11027	RTA00002932F.b.10.1.P.Seq			
1290 23731 RTA00002931F,8.07.1.P.Seq F M00027052A;E10 CH04MAL 1291 47898 RTA0000291F,8.07.1.P.Seq F M0004298;D:E03 CH18CON 1292 32581 RTA0000293F,6.02.1.P.Seq F M0004298;D:E03 CH18CON 1293 42 RTA0000293F,6.11.1.P.Seq F M000434T;A:C10 CH20COHLV 1294 1447 RTA00002935F,0.20.1.P.Seq F M0005453;B:B01 CH17COHLV 1295 10449 RTA00002935F,0.20.1.P.Seq F M000548;D:A11 CH17COHLV 1296 35359 RTA00002935F,1.20.1.P.Seq F M000548;D:A11 CH17COHLV 1297 19657 RTA00002935F,1.20.1.P.Seq F M0005613;A:E11 CH17COHLV 1298 12659 RTA00002930F,1.21.1.P.Seq F M0004364;A:B01 CH20COHLV 1299 9081 RTA00002934F,a.22.1.P.Seq F M0004364;A:B01 CH20COHLV	1289	23451				
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1304	113291	RTA00002935F.m.15.1.P.Seq	F	M00054693A:E11	CH17COHLV
1305	13224	RTA00002935F.f.15.1.P.Seq	F	M00056320B:A03	CH15CON
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1308	16869	RTA00002889F.c.21.1.P.Seq		M00042449B:F05	CH17COHLV
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1317	13193	RTA00002886F.1.16.1.P.Seq		M00033149B:E10	CH08LNH
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1324	94859	RTA00002909F.i.23.1.P.Seq	·F		CH03MAH
1325	12315	RTA00002907F.m.01.1.P.Se	q F	M00022240D:B11 M00022690.A:A07	CH03MAH
1326	4822	RTA00002909F.1.16.1.P.Sec	F	M00022690A:A07	CH03MAH
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1334		RTA00002907F.i.09.2.P.Sec	q <u>F</u>	M00022200B:B05	CH08LNH
1335		RTA00002916F.b.19.1.P.Se	q F	M00032541C:G03	CH08LNH CH04MAL
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		RTA00002887F.a.09.1.P.Se	q F	M00001385A:E07	CH01COH
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1339		RTA00002917F.g.15.1.P.Se	g F	M00032727A:E04	CH08LNH
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134:		RTA00002897F.d.03.1.P.Sc		M00004225D:E03	CH01COH
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134		RTA00002933F.K.TT.T.S.		M00026900A:H07	CH04MAL
134		RTA00002911F.t.01.117.50		M00033434D:F05	CH09LNL
134		KIA00002921F.g.24.1.F.S		M00022474B:C08	
[135	0 25844	RTA00002908F.k.23.1.P.S	<u> </u>		

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SEQ	at tramen	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
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1356	5741	RTA00002887F.c.19.1.P.Seq	F	M00001330D:202	CH02COH
1357	17264	RTA00002900F.a.18.1.P.Seq	F	M00039871C:G05	CH09LNL
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1360	13903	RTA00002923F.c.18.1.P.Seq	F	M00039646.A:E06	CH12EDT
1361	10673	RTA00002927F.h.23.1.P.Seq	F	M000330-EH:200	CH18CON
1362	17412	RTA00002932F.b.11.1.P.Seq	F	M0003302SC:A02	CH08LNH
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1366	8050	RTA00002900F.n.04.1.P.Seq	F	M00040329.A:H05	CH14EDT
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1370	123823	RTA00002905F.h.08.1.P.Seq	F	M00005445D:D04	CH02COH
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1376	15353	RTA00002910F.e.11.1.F.Seq		M0003861SD:D08	CH09LNL
1377	6314	RTA00002922F.8.00.1.F.Seq	F	M00022662C:H04	CH03MAH
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1380	16572	RTA00002890F.p.21.1.P.Seq		M00001663A:A12	CH01COH
1381	74821	RTA00002889F.d.12.1.P.Seq		M00001535B:B10	CH01COH
1382	11315	RTA00002894F.c.18.1.P.Seq		M00003980D:C06	CHOICOH
1383	10859	RTA00002914F.f.04.1.P.Seq		M00028193B:E07	CH08LNH
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1387	17156	RTA00002934F.a.08.1.P.Seq RTA00002896F.o.18.1.P.Seq		M0000420CC:A04	CHOICOH
1388		RT.A00002901F.m.08.1.P.Seq		M00005626D:G11	CH02COH
1389		RT.A0000_901F.m.08.1.F.Seq		M00043213.A:D05	CH19COP
1390		RTA00002907F.a.18.1.P.Seq		M00022103C:D05	СН03М.АН
1391		RTA00002907F.a.13.1.F.Seq		M000333+-A:B06	CH09LNL
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1393		RTA00002S97F.i.20.1.P.Seq		M00004269 A:F11	CH01COH
1394		RTA00002597F.1.20.1.P.Seq RTA00002916F.d.12.1.P.Seq		M000032553.A:A07	CH08LNH
1395				M0000501-B:F02	CH02COH
1396		RTA00002900F.h.07.1.P.Seq		M0000301=5:102	CH03MAH
1397		RTA00002905F.c.13.1.P.Seq		M00007361C:F07	CH03MAH
1398		RTA00002907F.d.24.1.P.Seq		M0002772-D:D04	CH04MAL
1399		RTA00002913F.b.07.1.P.Seq RTA00002906F.b.20.1.P.Seq		M00021866C:H08	СНОЗМАН
1400	12657	TK (A0000 1 A00 P.D. 10. 11 P. 250	1	1	

					
SEQ		GEO NAME	ORIENTATION	CLONE ID	LIBRARY
ID	CLUSTER	SEQ NAME		M00039024D:E12	CH09LNL
1401	2033	RTA00002922F.e.08.2.P.Seq	F	M00033024D:E12	CH08LNH
1402	24229	RTA00002920F.b.04.1.P.Seq	F	M00001338C:F05	CHOICOH
1403	20664	RTA00002886F.a.07.1.P.Seq	F.	M00001538C:105	CH02COH
1404	3656	RTA00002902F.f.20.1.P.Seq	F	M0000641B:F03	CH16COP
1405	10998	RTA00002931F.c.07.1.P.Seq	F	M00042373D:G00 M00039081B:G07	CH09LNL
1406	1150	RTA00002922F.j.14.1.P.Seq	F	M00039081B:007 M00005013D:H05	CH02COH
1407	45221	RTA00002900F.h.06.1.P.Seq	F	M00005423C:A10	CH02COH
1408	34505	RTA00002901F.a.16.1.P.Seq	F	M00003423C:A10 M00039472B:E05	CH09LNL
1409	8175	RTA00002924F.f.01.1.P.Seq	F	M00039472B:E05	CH09LNL
1410	8175	RTA00002924F.e.24.1.P.Seq	F		CH02COH
1411	19375	RTA00002903F.n.02.1.P.Seq	F	M00007081B:C08	CH14EDT
1412	10866	RTA00002929F.c.15.1.P.Seq	F	M00040219B:B07	CH01COH
1413	24166	RTA00002891F.k.07.1.P.Seq	F	M00003763A:B02	CHOICOH
1414	15333	RTA00002888F.c.12.1.P.Seq	F.	M00001442C:G12	
1415	44436	RTA00002907F.b.17.1.P.Seq		M00022117C:A02	CH03MAH
1416	9247	RTA00002930F.a.16.1.P.Seq		M00042560C:G06	CH15CON
1417	12317	RTA00002908F.g.13.1.P.Seq	F	M00022430C:C06	CH03MAH
1418	11968	RTA00002890F.i.24.1.P.Seq		M00001625D:B04	CH01COH
1419	14181	RTA00002908F.n.09.2.P.Seq	F	M00022499D:D08	CH03MAH
1420		RTA00002909F.1.02.1.P.Seq	F	M00022677C:C01	CH03MAH
1421	46675	RTA00002916F.h.03.1.P.Seq	F	M0003258-1A:D06	CH08LNH
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1426		RTA00002894F.e.20.1.P.Seq	F	M00003988D:B01	CH01COH
1427		RTA00002914F.h.10.1.P.Seq		M00028210B:H03	CH08LNH
1428		RTA00002890F.j.15.1.P.Seq		M00001632C:A10	CH01COH
1429		RTA00002896F.h.05.1.P.Seq		M00004162D:F02	CH01COH
1430		RT-A00002908F.b.06.1.P.Seq		M00022367D:G11	CH03MAH
1431		RTA00002921F.h.01.1.P.Seq		M00033434D:F05	CH09LNL
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1433		RTA00002919F.f.13.1.P.Seq		M00033071D:E08	CH08LNH
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1439		RT.A00002909F.a.07.1.P.Sec	F	M00022530B:C04	CH03MAH
		RTA00002910F.k.22.1.P.Sec		M00022992B:G12	СН03МАН
1440		RT.A00002908F.p.07.1.P.Sec		M00022516B:C05	CH03MAH
		RTA00002387F.o.06.1.P.Sec		M00001426C:F06	CH01COH
1442		RTA00002900F.b.07.1.P.Sec		M00004836B:C02	CH02COH
1443		RTA00002907F.n.19.1.P.Sec		M00022262A:F06	CH03MAH
1444		RTA00002926F.c.10.2.P.Sec		M00040079B:F06	CH09LNL
1445		RTA00002928F.d.07.1.P.Sec		M00040173D:A04	CH13EDT
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1450	773	TK1.400002889F.J.02.1.F.360	11	<u> </u>	

SEQ		CEO NAME	ORIENTATION	CLONE ID	LIBRARY
ID	CLUSTER	SEQ NAME	F	M00039630D:B07	CH12EDT
1451	142367	RTA00002927F.h.11.1.P.Seq	F	M00001537B:H10	CHOICOH
1452	19284	RTA00002889F.e.10.1.P.Seq	F	M00039440C:G06	CH09LNL
1453	24011	RTA00002924F.c.17.1.P.Seq	F	M00035410B:G06	CH04MAL
1454	5930	RTA00002911F.f.08.1.P.Seq	F	M00005822C:A04	СН02СОН
1455	21581	RTA00002902F.c.05.1.P.Seq	F	M00039826D:E04	CH09LNL
1456	3662	RTA00002925F.c.07.1.P.Seq	F	M00042719.A:G08	CH15CON
1457	4873	RTA00002930F.b.05.1.P.Seq	F	M00004161A:E08	CH01COH
1458	11214	RTA00002896F.h.01.1.P.Seq	F	M00003837C:D10	CH01COH
1459	22888	RTA00002892F.1.09.1.P.Seq	F	M00039932B:A07	CH09LNL
1460	15490	RTA00002925F.k.08.1.P.Seq	F	M00031676C:G03	CH03MAH
1461	112819	RTA00002905F.o.13.1.P.Seq	F	M00004179D:A12	CHOICOH
1462	19688	RTA00002896F.1.02.1.P.Seq	F	M00039138B:G05	CH09LNL
1463	15132	RTA00002922F.n.20.1.P.Seq	F	M000371303:005 M00028219B:H05	CH08LNH
1464	25022	RTA00002914F.i.21.1.P.Seq		M00001438.A:E01	CHOICOH
1465	16303	RTA00002888F.b.12.1.P.Seq		M00004214.A:E05	CH01COH
1466	16828	RTA00002897F.b.04.1.P.Seq		M00033296C:C11	CH09LNL
1467	14295	RTA00002921F.a.18.1.P.Seq	F	M00055725D:D09	CH15CON
1468	1979	RTA00002930F.f.06.1.P.Seq		M00001460C:E10	CH01COH
1469	36248	RTA00002888F.g.05.1.P.Seq		M00040075B:A05	CH09LNL
1470	5676	RTA00002926F.b.22.2.P.Seq		M00001428B:C10	CHOICOH
1471	1239	RTA00002887F.o.21.1.P.Seq		M00032728D:F01	CH08LNH
1472	7937	RTA00002917F.g.22.1.P.Seq		M00026856B:G03	CH04MAL
1473	4483	RTA00002911F.d.22.2.P.Seq		M00039826B:F09	CH09LNL
1474	7796	RT.A00002925F.c.05.1.P.Seq		M00033616C:D09	CH08LNH
1475	17330	RTA00002915F.a.03.1.P.Seq		M00006631C:A04	CH02COH
1476	25620	RTA00002902F.f.09.1.P.Seq		M00039326A:G07	CH09LNL
1477		RTA00002923F.1.20.1.P.Seq		M00039258C:C01	CH09LNL
1478		RTA00002923F.g.21.1.P.Seq		M0002773+D:C03	CH04MAL
1479		RTA00002913F.b.16.1.P.Seq		M00022435B:G12	СН03МАН
1480		RTA00002908F.g.17.1.P.Seq		M00033264B:E06	CH08LNH
1481	30321	RTA00002919F.o.17.1.P.Seq		M00027688C:C01	CH04MAL
1482		RTA00002913F.a.16.1.P.Seq		M00021649B:A02	СНОЗМАН
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1484		RTA00002908F.i.21.1.P.Seq		M00055254A:H03	CH17COHLV
1485		RT.A00002935F.m.24.1.P.Sec	1	M00032828.A:A06	CH08LNH
1486		RTA00002918F.a.22.1.P.Sec		M00055254.A:H03	CH17COHLV
1487		RTA00002935F.n.01.1.P.Sec		M0003251 C:E10	CH08LNH
1488		RTA00002915F.o.19.2.P.Sec	1	M0000378CA:G01	CH01COH
1489		RTA00002891F.o.03.1.P.Sec		M00005003D:C02	CH02COH
1490		RTA00002900F.g.10.1.P.Sec		M00039820B:F06	CH09LNL
1491		RTA00002925F.b.18.1.P.Sec		M000037026B:H07	CH01COH
1492		RTA00002897F.g.15.1.P.Sec		M0000434-A:G11	CH01COH
1493		RTA00002898F.g.06.1.P.Sec		M00003314cD:A03	CH08LNH
1494		RTA00002919F.i.09.1.P.Sec	1	M0000331465:103	CHOICOH
1495		RT.A00002898F.c.14.1.P.Sec		M00040003.A:G10	CH09LNL
1496		RTA00002925F.m.06.1.P.Se		M0003250 D:G08	CH08LNH
149		RTA00002915F.n.13.2.P.Sec		M0003258eC:B04	CH08LNH
1498		RTA00002916F.h.11.1.P.Se		M0003238CC:B04	CH04MAL
1499		RTA00002911F.p.08.1.P.Se		M00039710B:A01	CH09LNL
1500	25605	RTA00002924F.m.22.1.P.Se	9	1 Mood // Te S Tot	

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SEQ		T			
D	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
1501		RTA00002906F.m.24.1.P.Seq	F	M00022070B:B04	CH03MAH
1502	9668	RTA00002908F.g.02.1.P.Seq		M00022421A:F12	CH03MAH
1503	29446	RTA00002906F.n.01.1.P.Seq		M00022070B:B04	CH03MAH
1504	7171	RTA00002887F.m.22.1.P.Seg		M00001421B:E07	CH01COH

Table 3

$\neg \tau$	Nearest N	eighbor (BlastN vs. G	enbank)	Nearest Neighb	or (BlastX vs. Non-Redundant Prot	eins)
EQ	T				1	
1	ACCESSION	DESCRIPTION	PVALUE	ACCESSION		VALUE
-	<none></none>	<none></none>	<none></none>	<none></none>	1.01.E	<none></none>
\ \	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>
$\frac{2}{3}$	<none></none>	<none></none>	<none></none>	<none></none>	V.101.02	<none></none>
4	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>
5	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>
6	<none></none>	<none></none>	<none></none>	<none></none>	V.101.22	<none></none>
7	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>
3	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>
9	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>
10	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>
11	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>
12	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>
13	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>
14	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>
15	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>	
16	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>
17	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>	
18	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>
19	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>
20	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>	<none< td=""></none<>
21	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>	<none< td=""></none<>
22	<none></none>	<none></none>	<:NONE>	<none></none>	<none> GENOME POLYPROTEIN</none>	KNONE
			NOVE	548562	[CONTAINS: RNA REPLICASE; HELICASE: COAT PROTEIN] 2.7.7.48) - apple stem grooving virus (strain P-209)	9.2
23	<none></none>	<none></none>	<none></none>	348302	EXCISION REPAIR PROTEIN ERCC-6 DNA repair helicase ERCC6 - human >gi 182181 (L04791) excision repair protein	
		NONE	<none></none>	416959	[Homo sapiens]	8.9
24	<none></none>	<none></none>	1	<u> </u>	(AB014541) KIAA0641 protein	
~~	<none></none>	<none></none>	<none></none>	3327096	[Homo sapiens]	8.7
25	SINUINES	CHOILE			(U28741) F35D2.1 gene product [Caenorhabditis	7.9
26	<none></none>	<none></none>	<none></none>	861293	elegans] (AL031032) extensin-like	
	1		_		· · · · · · · · · · · · · · · · · · ·	5.5
27	<none></none>	<none></none>	<none></none>	3297821	protein	
					transforming growth factor-beta type III receptor - chicken >gi 511843 (L01121) transforming growth factor-beta	}
28	<none></none>	<none></none>	<none></none>	2119692	type III receptor [Gallus gallus]	5.0
29		<none></none>	<none></none>	2136028	protein-kinase PRK1 - human	+

PCT/US00/18374 WO 01/02568

					Marrest Neighb	or (BlastX vs. Non-Redundant Pro	oteins)
		Nearest Ne	eighbor (BlastN vs. G	enbank)	Nearcatition		\$ 1
EQ		{	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	PVALUE
ID	ACC	CESSION	DESCREE -	1		(AF040659) No definition line	1
						(AF040039) No definition into	4.6
	Γ^-			<none></none>	2746912	found [Caenorhabditis elegans]	1
30	<	NONE>	<none></none>	anomis		(AF010404) ALR [Homo	4.5
	 			<none></none>	2358287	sapiens)	
31	ے ا	NONE>	<none></none>	ZNUNES		(Z96048) predicted using	1 1
	╁╌			i		Genefinder: cDNA EST	_1
	Į.		υ		1	EMBL:D65516 comes from thi	`
	1			1		gene; cDNA EST yk191a5.5	1
	1			1	1	comes from this gene	
	1		}		2077016	(Caeporhabditis elegans)	4.4
	1	NONTE	<none></none>	<none></none>	3877816	(Y14953) SRCR domain,	1
32	4	<none></none>					4.1
	1		· <none></none>	<none></none>	4140268	(U51183) transposase [Hydra	
33	1	<none></none>	4-01-01	•	1	vulgaris)	4.0
			<none></none>	<none></none>	1708663	(U45958) pistil extensin-like	
34	. 1 _	<none></none>	ZNUNES			(U45958) pistit extensiti	3.9
	Т			<none></none>	1184100	protein [Nicotiana alata]	
3.5	; [<none></none>	<none></none>	- \ \\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	1	GLUCOCORTICOID	3.9
	_			<none></none>	121073	RECEPTOR (GR)	
30	5	<none></none>	<none></none>	-1-000		ONE 15: contains a	n l
۳	+			1	1	(U75698) ORF 45; contains a	; }
1	- 1			1	1	extended acidic domain; EBV	
	- 1		1	1	1	BKRF4 homolog [Kaposi's	
1	1					carcoma-associated herpesvir	usi
1	- 1			}		homolog, conserved in other	1
1	t			- ł _	> 1718298	gamma-herpesviruses	2.6
١.	_ [NONES	<none></none>	<none< td=""><td>> 1/18298</td><td>(AF006564) alcohol</td><td>1</td></none<>	> 1/18298	(AF006564) alcohol	1
	37	<none></none>			1	dehydrogenase [Drosophila	
1	- }			1		persimilis] persimilis]	1.4
1	1		<none></none>	<none< td=""><td>> 2352538</td><td>(AF066071) SP85; PsB</td><td></td></none<>	> 2352538	(AF066071) SP85; PsB	
L	38	<none:< td=""><td>ANONE</td><td></td><td></td><td>[Dictyostelium discoideum]</td><td>1.4</td></none:<>	ANONE			[Dictyostelium discoideum]	1.4
			<none></none>	<non!< td=""><td>> 3192897</td><td>Dictyosterium disco-</td><td></td></non!<>	> 3192897	Dictyosterium disco-	
1	39	<none:< td=""><td>> ANONE</td><td></td><td></td><td>[</td><td>1</td></none:<>	> ANONE			[1
Г			1			(L33421) This CDS feature	is
- {		l		1	1	included to show the transla	tion
1		1	1	l		included to show the dataset	ion.
		l		l	Į.	of the corresponding V_reg	ers
Ì		!		1	1	Presently translation qualifi	egal 1.0
Ì		l		<non< td=""><td>ES 561645</td><td>on V region features are ill</td><td></td></non<>	ES 561645	on V region features are ill	
	40	<non!< td=""><td><none></none></td><td>- KINOIN</td><td></td><td></td><td>l</td></non!<>	<none></none>	- KINOIN			l
H		 		1	1	Genefinder: cDNA EST	n this
		1		1	. }	EMBL:D35016 comes from	
l		l		l		gene; cDNA EST	m this
- 1		1	1	ļ	1	EMBL:D32583 comes from	ווו נוווס
ł		1		l	1	I cONA EST	1
I		1	t t	1	1	EMBL:D35258 comes fro	m this
1		1	\	l	l l	L CONA EST	1
l		1	-	1	1	EMBL:C11471 comes fro	m this
1		1	1	l			C 1.
		}	VE> <none< td=""><td><no< td=""><td>NE> 387885</td><td>7 Igene; CDINA EST DATE</td><td></td></no<></td></none<>	<no< td=""><td>NE> 387885</td><td>7 Igene; CDINA EST DATE</td><td></td></no<>	NE> 387885	7 Igene; CDINA EST DATE	
	41	<non< td=""><td>TEL I KNUNE</td><td></td><td></td><td></td><td></td></non<>	TEL I KNUNE				

PCT/US00/18374 WO 01/02568

11011 11000111	r (Blasty vs. radiist	Magreet Neighbor					
Non-Redundant Proteins)		Nearest Neighbor	nk)	or (BlastN vs. Gen	est Neigh	Nearest	
CRIPTION P VALU		ACCESSION	VALUE	1	· ·		EQ
3T1A7 [Rattus	(U75903) UGT1A7		1,7202	SCRIPTION /	ION D	ACCESSION	D
1.0	nominations)	1450533	NONE>				
putative immediate	(AF005370) putati		NONES	<none></none>	E>	<none></none>	42
(Alcelaphine	early protein [Alce		1				
11 0.80	hamacuirus II		NONE>		l		
KIAA0595 protein	(AB011167) KIAA		NONE	<none></none>	E>	<none></none>	43
ens] 0.42	[Homo sapiens] HYPOTHETICAL	3043714	NONE>	· · · · · · · · · · · · · · · · · · ·			
TICAL 92.7 RD	HYPOTHETICAL		NONE	<none></none>	E>	<none></none>	44
N ASNZ-PHB1	PROTEIN IN ASI		ı	1			
IIC REGION	INTERGENIC RE		i	1	1	\$	
3 pir S64439	>gi 2131678 pir S		1	Į.	1	1	
l protein YGR130c -	hypothetical prote		1	·	1	ł	
naromyces	yeast (Saccharom)	•	1	. [l	Ì	
	cerevisiae)		. 1	İ	- 1	t	
5 gn1 PID e243523	>gi 1323215 gnl F		1		1	1	
)RF YGR130c	(Z72915) ORF Y	•	t		İ	1	
	[Saccharomyces of	1723710	<none></none>		1	Ĭ.	
TICAL 92.7 KD	HYPOTHETICA		21101112	<none></none>	NE>	<none:< td=""><td>45</td></none:<>	45
IN ASNZ-PROT	PROTEIN IN AS		- 1			1	
NIC REGION	INTERGENIC R		1			1	
/8 pir 504439	>gi 2131678 pir		1			1	
al protein YGR130c -	hypothetical prot		1			Ì	
	yeast (Saccharon				1	į	
)	cerevisiae)		l		- 1	\	
15 gnl PID e243523	>gi 1323215 gnl		ł		}	,	
ORF YGRISOC 0.	(Z72915) ORF		l.		1	1	
myces celeviside	[Saccharomyces	1723710	<none></none>	NOTE:	1	1	l
(5) immediate early 2	(AF046125) imr		VIII.	<none></none>	NE>	<non< td=""><td>46</td></non<>	46
neo310VIIUSI <u>I</u>	[Rat cytomegalo	2996117	<none></none>	MONE			
55) synaptic SAPAP-	(AF102855) syn		410.12	<none></none>	ONE>	/ <non< td=""><td>47</td></non<>	47
g protein Synamon 0.	interacting prote	4151809	<none></none>	NONE.	!		
- u a santaia			<u> </u>	<none></none>	ONE>	8 <non< td=""><td>4</td></non<>	4
54) putative protein	(AF040954) put	•			ì	1	
ase I nuclear targeting Detrois porvegicus 0.	phosphatase 1 n				l		1
Kallus IIOI regions	subunit [Rattus	2773341	<none></none>	<none></none>		ì	1
) hypothetical protein 36 HETICAL 100.6 KD	(D90914) hypo	1653522	<none></none>	<none></none>	ONE>		4
AETICAL 100.0 KB	HYPOTHETIC			ZNUNES	ONE>	0 <non< td=""><td>5</td></non<>	5
NING PROTEIN	TRP-ASP REP	İ			1	1	1
INING PROTEIN C IN CHROMOSOME	CONTAINING				\	Ţ	1
C IN CHROMOSOME	C2C6.04C IN C	l			1	1	1
		3219965	<none></none>	<none></none>			1
180) cAMP-dependent		1		CHOILE	IONE>	51 <non< td=""><td>1.5</td></non<>	1.5
180) CAIVIT -dependent	(AF115480) c.		ŀ			1	1
anine-nucleotide e factor (Mus musculus)	Rapl guanine-	1				1	1
	levchange facto	4185567	<none></none>			ł	ı.

		leighbor (BlastN vs. Ge	nbank)	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
Mir.	Nearest N	leignbor (Blasus vs. Ge			1	ł	
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION		VALUE	
<u> </u>	ACCESSION		T		HYPOTHETICAL 43.2 KD		
					PROTEIN C34E10.1 IN		
		1	1		CHROMOSOME III		
		1			>gi 500724 (U10402) C34E10.1		
		· ·	i		gene product (Caenorhabditis		
		<none></none>	<none></none>	1176527	elegans)	3e-20	
53_	<none></none>	G.pallida repetitive			beta-globin - chimpanzee	0.6	
	7505444	DNA element	5.0	2118936	(fragment)	8.6	
54	X85444	DIVA Eleticit			MICROTUBULE-		
	1	i l			ASSOCIATED PROTEIN IA		
	Į.	Synechococcus sp.			microtubule-associated protein		
	}	cpeB, cpeA genes and			MAP1A - rat >gi 205538	2.2	
~ ~	X72961	ORF3	5.0	462569	norvegicus]	2.2	
55	X/2901	0.013					
	1	Human WD repeat					
	1	protein HAN11		ł	(Z67990) similar to cuticle	1.3	
56	U94747	mRNA. complete cds	5.0	3875538	collagen		
30	1-0/2/-				\ `		
	1	Homo sapiens			1		
	1	integrin alpha-7			collagen - Paralvinella grasslei	0.002	
57	AF032108	mRNA, complete cds	5.0	2147194	ASPARTYL-TRNA		
	120000			1	SYNTHETASE synthetase		
	1	G.gallus mRNA for	1		[Bacillus subtilis]	3e-11	
58	Z50798	p52	5.0	3122885	(Bacillus subtilis)		
		Human mRNA for	j	1 .	(Y15513) Prodos protein		
1	ł	KIAA0386 gene,		2632098	[Drosophila melanogaster]	9e-12	
59	AB002384	complete cds	5.0	2032096	(Drosopinia money)		
			_1	1	Ì	}	
	5	Thermofilum pendens	`\		1	1	
l	ì	DNA for 16S and		1	l l	ļ	
ţ	1	23S ribosomal RNA,	J				
1	Ì	tRNA-Met, and tRNA	4.9	<none></none>	<none></none>	<none< td=""></none<>	
60	X14835	Gly	4.5		NONSTRUCTURAL	1	
	į.		1	1	PROTEIN NS-S spotted wilt	1	
Ì		Hordeum vulgare	i	1	virus (strain CPNH1) non-	1	
1	1		1	1	structural protein [Tomato		
1		nucellin gene,	4.9	128578	spotted wilt virus]	2.8	
61	U87149	complete cds Mus musculus gene	+	1		1	
	i	for integrin alpha v	ł	1	HYPOTHETICAL PROTEIN	}	
1	}	subunit, promoter	1	1	UL61 cytomegalovirus (strain	0.030	
	2 D87541	region	4.9	136956	AD169) cytomegalovirus]	0.038	
1 .	2 U0/341	10 KION	1		1	1	
6				•	i i	ı	
6:		Mus musculus mena	1			. 1	
6:		Mus musculus mena protein (Mena)		3413892	(AB007934) KIAA0465 protein [Homo sapiens]	6e-07	

	Negrect N	leighbor (BlastN vs. Ge	nbank)	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
	Nearest N	leighbor (Blasa vs. 55				j	
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
		enzymatic	1	•	}	ì	
		glycosylation-	1		Ì	Į.	
	1	regulating gene [rats.	1		1	1	
		Sprague-Dawley,			1	1	
	1	streptozotocin				1	
		diabetic, heart,	_		<none></none>	<none></none>	
64	S79797	mRNA, 5010 nt]	4.8	<none></none>	RECEPTOR RECOGNIZING		
			ļ		PROTEIN gp38 - phage Ox2		
					>gi 15126 (X05675) gene 38		
	ŀ	Homo sapiens mRNA			(AA 1-266); pid:g15126	·	
	ł	for KIAA0530	4.0	138022	[Bacteriophage Ox2]	3.6	
65	AB011102	protein, partial cds	4.8	136022	(Dacter teproep		
	1	Penaeus monodon					
l	1	phosphopyruvate	,		(D16221) endochitinase {Oryza		
ŀ		hydratase mRNA.	4.8	500615	satival	2.8	
66	AF100985	complete cds	4.0	3000.5	(AL021471) similar to		
1	į.	Bacillus subtilis			Eukaryotic aspartyl proteases	1	
	1	į.	İ		[Caenorhabditis elegans]	ļ	
ļ .	· ·	gamma- aminobutyrate	}		Eukaryotic aspartyl proteases		
	1121756	permease cds	4.8	3880699	[Caenorhabditis elegans]	2.8	
67	U31756	permease cus				l	
1	1	Pisum sativum	1			l	
	1	chloroplast					
1	1	processing enzyme				1	
1	1	mRNA, nuclear gene	1			Ì	
	l l	encoding chloroplast		1	(U83658) FH1/FH2 protein	1.6	
68	U25111	protein, complete cds	4.8	1800145	homolog [Emericella nidulans]	1.0	
	· · · · · · · ·	Mus musculus Cdx-2		{			
	1	homeobox protein	1		<none></none>	<none></none>	
69	U00454	gene, complete cds.	4.7	<none></none>	RENIN-BINDING PROTEIN		
		Hamster c-Ha-ras	1		(RNBP) protein [Rattus		
1	i i	protein gene,	1	1710606	norvegicus]	0.88	
70	M84166	complete cds.	4.7	1710000	Hot vegicus		
		Mus musculus major	Ì				
1	§	sperm fibrous sheath	}	1		1	
1	1	protein Pro-	ł			1	
1	1	mAKAP82 gene,	4	1			
		alternative splice	4.6	<none></none>	<none></none>	<none:< td=""></none:<>	
71	AF087516	M.esculenta mRNA	1	1			
1	1	for granule-bound	1	[1	1	
	V74160	starch synthase	4.6	<none></none>	<none></none>	<none:< td=""></none:<>	
7:	2 X74160	Haloferax volcanii	 	 		1	
1	1	superoxide dismutas	e	1 .	1	{	
1	}	(sod2) gene, complete	tel	i	(AC002409) putative ubiquitin	1	
7	3 M97487		4.6	2623307	protease [Arabidopsis thaliana]	3.4	
	3 1417/48/						

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	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
	Nearest :	leighbor (Blastin vs. Ge	IIU4IIK)		1	1	
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
		Drosophila			 		
		melanogaster				ł	
	İ	suppressor of sable		NONE	<none></none>	<none></none>	
74	M57889	gene, complete cds.	4.5	<none></none>			
		Rattus norvegicus					
	1	mRNA for RNA		<none></none>	<none></none>	<none></none>	
75	D49708	binding protein	4.5	GIONE			
				§	1		
	l .	Yeast GTS1 gene for			(U42580) NETTF (7x), DETTS		
	l .	glycin-threonin/serine		1	(4x) [Paramecium bursaria		
	ì	repeat protein,	4.5	2447195	Chlorella virus 1]	3.3	
76	D31853	complete cds	4.3				
	I	Human partial cDNA		ł	1		
Ĺ	}	sequence, clone	2.9	<none></none>	<none></none>	<none></none>	
77	Z47036	bs613;	4.5	 			
		Rattus norvegicus	1	Į.		j	
ł	1	gastric inhibitory	Ļ	1		ţ	
Į	1	gastric milibitory	1 .	1	(AF007871) torsinA [Homo	2e-07	
1		peptide receptor mRNA, complete cds	2.7	2358279	sapiens]		
78	L19660	mRNA, complete cus	 		immediate-early protein E110 -		
1	1		1	1.	human herpesvirus I (strain	8.4	
\		A.thaliana Aco gene	2.6	483212	HFEM) (fragment)	- 8.4	
79	X82841	A.thanana Aco gone	 			1'	
1	1	ţ			Ĺ	1 .	
1		S.purpurascens fam A	. [1	1	1	
1	1	and famB genes for	1	i	l		
ļ	1	FAS domain and acy	1-	1	(U95031) sublingual gland		
1		CoA-dehydrogenase	s.		mucin [Homo sapiens]	0.47	
8	X61931	respectively	2.6	2290534	mucin (riomo sapiens)		
۳		Human lactate	1	\$	\	1	
	ł	dehydrogenase-C	1	•	(AB007874) KIAA0414 [Hom	0	
	1	(LDH-C) mRNA,		2007440	[sapiens]	3.1	
8	1 U13680	complete cds.	2.5	2887449	Japiensj		
٣		Homo sapiens		1	(AB008859) pheromone	}	
		KIAA0409 mRNA.	1	3130157	receptor [Fugu rubripes]	5.4	
8	2 AB00786	59 partial cds	2.4	3130137			
		H.sapiens mas proto)-	<none></none>	<none></none>	<none< td=""></none<>	
8	3 X97479	oncogene. 5' region	2.1				
			.	1	}		
-	1	R.norvegicus mRN	1.9	<none></none>	<none></none>	<none< td=""></none<>	
	34 X98374	4 for KIS protein				1	
		10		1		l l	
1	1	Aquifex aeolicus	<i>,</i>]	į	l	NON	
	1	section 42 of 109 o		<none></none>	<none></none>	<non< td=""></non<>	
- 1	85 AE0007	10 the complete genor	1.5				

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				Noighb	or (BlastX vs. Non-Redundant Pro	teins)
400	Nearest N	leighbor (BlastN vs. Ge	nbank)	Nearest Neight	of (Blasce vs. rvoir res	
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
	7.002	Homo sapiens mRNA			 	
86	D30612	for repressor protein, partial cds	1.9	<none></none>	<none></none>	<none></none>
80_	D30012	Homo sapiens PMP69 gene, exons		<none></none>	<none></none>	<none></none>
87	Y14321	8,9,10 & 11 E.coli genomic DNA,	1.9	CITOLICE	(D78305) DNA binding protein	5.0
88	D90773	Kohara clone #262(30.3-30.5 min.)	1.9	1536816	[Chlorella virus]	7.9
	. 5000001	Archaeoglobus fulgidus section 116 of 172 of the complete genome	1.9	520645	(X79095) pyruvate,orthophosphate dikinase [Flaveria trinervia]	2.7
89	AE000991	Rattus norvegicus p95 Vav (Vav) proto- oncogene mRNA. complete cds.	1.9	4158178	(AL023496) hypothetical	1.6
90	U39476	Human transcription factor TFIIIB 90 kD	1.9	2495730	HYPOTHETICAL PROLINE- RICH PROTEIN KIAA0269 >gi 1665805 gnl PID d1014089 (D87459) Similar to Volbox carteri extensin (S22697) [Homo sapiens]	0.23
91		Rattus norvegicus synaptotagmin VII mRNA, complete cd	s. 1.9	478380	UL47h protein - Marek's diseas	e 0.23
	3 AF07101	Mouse mammary tumor virus putative integrase, env polyprotein, and superantigen mRNA		2781386	(AC004010) similar to Leucine rich transmembrane proteins; 44% similarity to U42767 (PID:g1736918) [Homo sapiens]	4e-33
	04 AF06188	Mesocricetus auratu c-fos proto-oncoger protein (c-fos) gene complete cds	ne }	<none></none>	<none></none>	<none:< td=""></none:<>
		Plasmodium falciparum chromosome 2. section 34 of 73 of the complete	1	NONES	<none></none>	<none< td=""></none<>
- 1	95 AE0013	97 sequence	1.8	<none></none>		

. A-77- E	No	leighbor (BlastN vs. Ge	nbank)	Nearest Neighbo	r (BlastX vs. Non-Redundant Prot	
。 EQ	Nearest		1	ACCESSION	DESCRIPTION	VALUE
	ACCESSION	DESCRIPTION	PVALUE	ACCESSION		
=	ACCEDOTO	Horseshoe crab				
		mRNA for			Į.	
		coagulation factor B,			<none></none>	<none></none>
	D14701	complete cds	1.8	<none></none>	4407.25	
96	D14701	P.falciparum				
	1	multidrug resistance				
	i .	(MDR) gene,	l i		<none></none>	<none></none>
		complete cds.	1.8	<none></none>	CHOILE	
97	M29154	Rattus norvegicus				
	1	(clone pCNPII) 2',3'-		Į	i i	
	1	cyclic nucleotide 3'-	1	į.		
	i	phosphodiesterase			· ·	ļ
	1	(CNPII) mRNA,	}	i	<none></none>	<none></none>
	1		1.8	<none></none>	<nunes< td=""><td>1</td></nunes<>	1
98	L16532	complete cds. Plasmodium	+			
			1	1	1	l
	1	falciparum chromosome 2,	l	1	ì	1
	1 .	section 71 of 73 of	1	ł	į	Ì
	l l		1	1		<none></none>
		the complete	1.8	<none></none>	<none></none>	121011
99	AE001434	sequence				1
		D.melanogaster gen	٠		·	<none:< td=""></none:<>
1	İ	for protamine	1.8	<none></none>	<none></none>	SHOWE
10	0 Z46785	(mst35Bb).	1.0			
T		P.sylvestris mRNA	1		(D90452) I-caldesmon I [Homo	9.7
1	1	for glutamine	1.8	219896	sapiens	
10	1 X69822	synthetase	- 1.0		INSULIN-LIKE GROW IH	4
				}	FACTOR BINDING PROTEIN	`\
1	1		1		4 (IGFBP-4) (IBP-4) (IGF-	ì
1	1	\	1		BINDING PROTEIN 4) factor	-
1	ł	1	1	1	binding protein-4 - sheep	
1	ł		1	1 .	(fragment) factor-binding	1
1	1	Rattus norvegicus	.,	1	protein-4, IGFBP-4 (sheep,	
1	I	CTD-binding SR-I	ike	· •	liver, Peptide, 237 aa] [Ovis	2.5
1.	1.	protein rA8 mRNA	1.8	2497252	aries]	- 2.3
1	02 U4905	5 complete cds	1.8			
		Homo sapiens		1	_	1
Ţ	1	kallistatin (PI4) ge	ne.		(AC005223) 55585	1 24
1	1	exons 1-4, comple	10	4204267	[Arabidopsis thaliana]	2.4
1	103 L2810	1 cds	1.8			1
			1			
1	1	Pandorina morum	ا بي		\	}
- 1		internal transcribe	·u	ł.	1	1
1	1	spacer 1. 5.8S	į.	1		
١	i	ribosomal RNA g	ene.	1		
1	1	and internal	. 1	1	(Z99121) permease [Bacillus	٠.
1	ļ	transcribed space	r 2.	2635909	subtilis)	1.9
- }	104 U669	87 complete sequent	ce 1.8	2033707		

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	Nonest N	eighbor (BlastN vs. Ge	nbank)	Nearest Neight	oor (BlastX vs. Non-Redundant Pro	
EQ			P VALUE	ACCESSION	DESCRIPTION	P VALUE
מו	ACCESSION	DESCRIPTION	PVALUE	ACCESSION		
$\overline{}$		Human polymorphic			keratin KAP5.5 - sheep	_
		Mspl site DNA		2136878	(fragment) >gi 313722	0.65
105	X58033	(D3S3 locus)	8.1	2130010		
					(AC004877) sco-spondin-mucin-	
		Human p82 (ST5)			like; similar to P98167 uncertain	
	t	mRNA, alternatively		3638957	(Homo saniens)	0.64
106	U15780	spliced, complete cds	1.8	3030731	(U00690) calcium channel alpha	i
		Homo sapiens	1	l	1 subunit [Drosophila	1
	1	synaptotagmin VII	1.8	457927	melanogaster]	0.51
107	AF038535	mRNA, partial cds	1.0	1		
		Homo sapiens clone	1	1 .	HOMEOBOX PROTEIN HOX-	0.00
	1	23585 mRNA	1.8	232263	D1 (HOX-4.9)	0.28
108	AF052134	sequence	1.0]
		H.sapiens HEK2	1	1	GROWTH-ARREST-SPECIFIC	-1
	}	mRNA for protein	l	Ì	PROTEIN 1 gene product	0.00
	i .	tyrosine kinase	1.8	1730198	[Homo sapiens]	0.22
109	X75208	receptor.	1.0		T. CTOR	}
	T-	Xenopus laevis	1	ì	TRANSCRIPTION FACTOR	0.17
		mRNA for SOX-D.	1.8	2494501	FKH-4 factor [Mus musculus]	0.17
110	AB013896	complete cds Human HepG2 3'	+		222 . 10454	
	1	Human nepoz 3	1	i	(AB007923) KIAA0454 protein	0.002
	1	region cDNA, clone	1.8	3413870	[Homo sapiens]	0.002
111	D16947	hmd6b10	+			}
	l l	Mouse DNA, T early	,	1	(AL031174) hypothetical	5e-08
l	212512	alpha (TEA) region	1.8	3393018	protein HYPOTHETICAL 11.3 KD	
113	2 D13547	alpha (TEA) region			PROTEIN C2C6.07 IN	1
1	1		1		CHROMOSOME I	i
}	1	}	Ì		>gi 2370504 gnl PID e339194	- }
1	l l	}	1	ì	pombe]	1
1	1	1	\	1	pomoe >gi 3451305 gnl PID e1316730	
ļ	1		t	,	(AL031324) very hypothetical	}
1	i i			.1	protein [Schizosaccharomyces	. [
1	1	Woodchuck c-myc			pombe]	8e-10
111	3 M35498	protein gene, exon	1. 1.8	3183405	pontuej	
1	17155450	Hamster c-Ha-ras		· I	(AC004665) unknown protein	. 1
-	1	protein gene.	1	2207722	[Arabidopsis thaliana]	2e-10
1,	14 M84166	complete cds.	1.8	3386622	[Autologics and	
一		Mychodea carnosa	. 1		<u> </u>	1
1	t	18S ribosomal RN	4		(AC005306) R27216_1 [Hom	10
1	1	gene, complete	1	3334982	sapiens)	3e-22
١,	15 U3313	sequence	1.8	3334982		7
+		Homo sapiens	1	1		1
	j	putative tumor	1			-
1	Ţ	suppressor (BIN1)		<none></none>	<none></none>	<non< td=""></non<>
- 1	16 U8400		1.7	<inuine></inuine>		

			, ,, , , , , , , , , , , , , , , , , ,	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
TY _n I.	Nearest N	leighbor (BlastN vs. Ge	nbank)	Nearest Neighbo	(Diaset) street		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
		Borrelia burgdorferi				1 1	
		(section 7 of 70) of				NONE	
117	AE001121	the complete genome	1.7	<none></none>	<none></none>	<none></none>	
11,	712001727	Archaeoglobus			!	1 1	
<u> </u>	1	fulgidus section 165				į	
	1	of 172 of the				NONTES	
118	AE001114	complete genome	1.7	<none></none>	<none></none>	<none></none>	
	11200111	Angiostrongylus					
•	1	cantonensis adult-			-	1	
ł	Į.	specific muscle			-		
	}	protein-1 gene, partial		·		<none></none>	
119	U82064	cds	1.7	<none></none>	<none></none>	< NONES	
1		Buchnera aphidicola				1	
1	1	plasmid pLeu-Sg.				1	
ļ	ŧ	complete plasmid		•		<none></none>	
120	AF041836	sequence	1.7	<none></none>	<none></none>	ENONES	
1.50	+	Lymnaea stagnalis			i	1	
1	}	FMRFamide gene.	1	1	NOTE:	<none></none>	
121	M87479	mature peptides.	1.7	<none></none>	<none></none>	CHOILE	
T	T			1	į	- 1	
1	1	Xenopus laevis			\$	İ	
]	1	fibroblast growth	1	,	1	l	
	1	factor receptor		1	<none></none>	<none></none>	
122	M55163	mRNA, complete cds.	1.7	<none></none>	ENONES	- CANOLINE	
		histamine H2-	1	· .	l	ľ	
		receptor [rats,	ļ		<none></none>	<none></none>	
123	S57565	Genomic, 1928 nt]	1.7	<none></none>	ROND		
	1	Simian	i	,	į.	1	
1	1	immunodeficiency	1			ì	
ļ.	ļ	virus (SIV) pol	1	NO.	<none></none>	<none></none>	
124	M27256	region.	1.7	<none></none>	1		
		Human chromosome	1	•		4	
1	} `	8 anonymous clone	1	<none></none>	<none></none>	<none></none>	
125	U31516	pBS8-165	1.7	KNUNES			
	1	Human gene for	Ì	1		Ì	
Į.	1	heterogeneous	1	l l	\	1	
Į.	Į.	nuclear		1	1	4	
1	1	ribonucleoprotein	l .	ţ			
į.	Į.	(hnRNP) core proteir		<none></none>	<none></none>	<none></none>	
120	6 X12671	Al	1.7	CHOINE			
	1	Paeonia suffruticosa	1:		1	1	
	1	ssp. spontanea	1	1	· I	j	
1	ł	alcohol	1		1	1	
	1	dehydrogenase IB	.1	1	}	Ţ	
	_	(Adh1B) gene, partia	1.7	<none></none>	<none></none>	<none:< td=""></none:<>	
12	7 AF00905	cds	<u> </u>			_	

				Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
- 12 m	Nearest N	eighbor (BlastN vs. Ge	nbank)	Nearest ivergnoor	(1) (1)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
<u> </u>	ACCESSION				·		
		Mus musculus				1 1	
		transketolase gene,				<none></none>	
	. 5046017	exon 6 and partial cds	1.7	<none></none>	<none></none>	- KINOIVIE	
128	AF046917	Homo sapiens mRNA				1 1	
	<u> </u>	for Acyl-CoA	'	į		1	
		synthetase 3,		i i	NONE	<none></none>	
	D89053	complete cds	1.7	<none></none>	<none></none>	-1010111	
129	D89033	Staphylothermus			· 	1 1	
	Y	marinus surface layer-	ł			1 1	
	ì	associated STABLE	ł	1		1 . 1	
		protease gene,	!		NOTE:	<none></none>	
	1157068	complete cds.	1.7	<none></none>	<none></none>	-1310112	
130	U57968	Bovine herpesvirus 1	<u> </u>		· ·	1 1	
	1	(clone p95) UL24	1	1		1	
	1	homologue gene.	ļ	· ·	, vo. 75.	<none></none>	
	L39072	complete cds.	1.7	<none></none>	<none></none>	- (1101122	
131	L39072	Drosophila simulans			1	,	
		retrotransposon 297	٠.	1]	1 .	
	1	5'-LTR and flanks	}		1101Te	<none></none>	
٠.,	X04980_	(pWK1020)	1.7	<none></none>	<none></none>	- CANOLINE	
132	X04980_	Archaeoglobus				1	
	ŀ	fulgidus section 165	1	1	Į.		
1	1	of 172 of the	1	,	NONTES	<none></none>	
١.,	3 AE001114	i	1.7	<none></none>	<none></none>		
13	3 AEOUTTA	Human mRNA for			•	1	
1	1 .	insulin-like growth	1		<none></none>	<none></none>	
13	4 X04434	factor I receptor	1.7	<none></none>	ZNONES		
13	* NOT-154	Mus musculus			1		
1	l	C57BL/6J epiderma	1 {	}		ł	
		surface antigen	1	•		l	
1		(mesa) mRNA,	Ĭ		<none></none>	<none></none>	
13	15 U07890	complete cds.	1.7	<none></none>	ZNONE		
1	007050	Human tyrosinase			ł	1	
1	.	gene, 5'-flanking	1	1	· I	1	
1	1	region cell-specific	Ì		<none></none>	<none:< td=""></none:<>	
1.0	36 D26163	transcription)	1.7	<none></none>	- CHOINES		
1	D20103	Panorpa nipponensi	S	ł	l	1	
1	1	NADH	.		1	ì	
1	1	dehydrogenase			}	1	
1	l l	subunit 5 gene.	Į.	\	1		
1	1	mitochondrial gene	ļ	1	1	l	
1	1	encoding	1	1		į	
1	1	mitochondrial	1		<none></none>	<none< td=""></none<>	
1.	37 AF09381	1	1.7	<none></none>	2110112		

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		Colonia Coloni	nhank)	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
	Nearest N	Neighbor (BlastN vs. Ge	Hodik)	1 Carest 1 Congress			
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
		Xenopus laevis					
		mRNA for					
		cytochrome P-450,	1		NO.	<none></none>	
138	D50560	complete cds	1.7	<none></none>	<none></none>	410112	
	·	Mus musculus	1				
		phospholipase D1			}		
	1	(PLD1) gene, exons			1		
	1	18 and 19, complete		ANONTES	<none></none>	<none></none>	
139	AF083488	sequence	1.7	<none></none>	GNONE		
	1	Mus musculus			1		
		Pontin52 mRNA,	1.7	<none></none>	<none></none>	<none></none>	
140	AF100694	complete cds	. 1./	· CHOILES			
I	i	Streptococcus			,		
	1	salivarius		,	1	i i	
	1	thermophilus beta-D-		į	1		
	Ţ	galactose (lacZ) gene.					
	1	complete cds. > ::					
	1	gb[M63636]STRLAC		1			
	h	ZZ Streptococcus	į	l .	1		
	ì	thermophilus beta-D-		Ì			
	1	galactosidase (lacZ)	1	Į .			
141	M73749	gene, complete cds.	1.7	<none></none>	<none></none>	<none></none>	
171	1473777	Archaeoglobus				<u> </u>	
}	Į.	fulgidus section 165	1	1		} ·	
	1	of 172 of the	Ì	l	(U84971) unknown [Homo	9.2	
142	AE001114	complete genome	1.7	2183023	sapiens] GENOME POLYPROTEIN	9.2	
	1				CONTAINS: N-TERMINAL	ł	
	I		1		PROTEIN (P1); HELPER		
	1		i	1	COMPONENT PROTEINASE	1	
Ī	1	}		1	INCLUSION PROTEIN (CI); 6	l	
1	1				KD PROTEIN 2 (6K2):	}	
]]	ļ.,		1 .	GENOME-LINKED PROTEIN	1	
1	1 .	Human type IV	1	l	(VPG); NUCLEAR virus	1	
]		sodium channel alpha		130504	(strain D)	9.2	
143	L01983	polypeptide	1.7	130304	(Strain 2)		
1		Plecotus rafinesquii	1	1	1	ł	
1	1	mitochondrial	.	l	(AB014541) KIAA0641 protein	{	
1		cytochrome b gene. 5	1.7	3327096	[Homo sapiens]	9.1	
144	L19731	end. Archaeoglobus	 	332.033			
1	1	fulgidus section 165		_		1	
1	1	of 172 of the		1	(U84971) unknown [Homo	1	
145	AE001114		1.7	2183023	sapiens)	8.8	
143	AEUU1114	Complete genome					

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: 1950g	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
	1.carest i	Totalloon (Diabat 15) O					
SEQ ID	A COTONI	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
	ACCESSION	DESCRIPTION	I VALUE	ACCESSION			
					 		
		Bos taurus serum					
1		amine oxidase					
	•	mRNA, complete cds.			SIGNAL TRANSDUCER AND		
		> oxidase=amiloride-			ACTIVATOR OF		
		binding protein			TRANSCRIPTION 6 (IL-4	1	
		homolog [cattle, liver,			STAT) >gi 559855 (U16031) IL-		
146	L27218	mRNA, 2664 nt]	1.7	1174459	4 Stat [Homo sapiens]	7.1	
		Caenorhabditis					
		elegans cosmid			·		
	•	W07E11, complete			,	(
		sequence			(AC005223) 40409	·	
147	740060	[Caenorhabditis elegans]	1.7	4204263	[Arabidopsis thaliana]	6.7	
147	Z49868	elegansj	1./	4204203	1.1.0.00		
	:			٠	PERIPLASMIC NITRATE	j ;	
ì				·	REDUCTASE PRECURSOR		
!					>gi 1086107 pir \$50163 nitrate)	
1		Caenorhabditis			reductase large chain precursor.	ŀ	
	1	elegans cosmid			periplasmic - Thiosphaera		
		F32F2, complete			pantotropha >gi 600093		
Į.		sequence			(Z36773) periplasmic nitrate reductase large subunit	1	
1		[Caenorhabditis		2497969	[Paracoccus denitrificans]	6.7	
148	AL022271	elegans] Mus musculus cyclin	1.7	249/909	(Faracoccus demaricans)		
1		D3 gene, complete			(AF062037) capsid protein		
149	U43844	cds	1.7	3861490	precursor [Thosea asigna virus]	5.1	
17/	043844	S.cerevisiae UNF1,					
1	ì	LTV1, MRP8, CYB3	[(U53151) weak similarity to		
1	[and TGL1 genes,			cytochrome b [Caenorhabditis		
150	Z25464	complete CDS's	1.7	1255404	elegans	4.1	
		Human elastin gene,		,			
	l	partial cds and partial			(AL031124) putative secreted	4.0	
151	U77846	3'UTR	1.7	3355682	lyase	4.0	
}	1	S.scrofa mRNA for	}		(AB014533) KIAA0633 protein)	
1,	V	calcium release	1.7	3327080	(Homo sapiens)	4.0	
152	X62880	channel (CRC)	1-/	3321000	(tronto apreno)		
	[ļ i		heterogeneous ribonuclear	j	
	1	•	}		particel protein homolog -	1	
	i	Human gene for	1		Caenorhabditis elegans]	
	l	neurofilament subunit	!		similarity to RNA recognition		
153	Y00067	M (NF-M)	1.7	. 479829	motifs [Caenorhabditis elegans]	3.9	

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13-16	Nearest N	leighbor (BlastN vs. Go	enbank)	Nearest Neigh	oor (BlastX vs. Non-Redundant Pro	oteins)
SEO						
ID ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION .	DESCRIPTION	P VALUE
	ACCESSION.				†	
\vdash					(AC000106) Contains similarity	
		D.melanogaster gene	1		to Rattus AMP-activated protein	1
1		for Beta-tubulin,	1		kinase (gb X95577).	
154	X68393	exons 1 and 2	1.7	2342682	[Arabidopsis thaliana]	3.8
		·			POL POLYPROTEIN	
1			1		(ORFIA/IB) [CONTAINS:	1
] !		Shuttle vector			RNA-DIRECTED RNA	
}		pAUR 123 gene for			POLYMERASE; HELICASE;	
155	AB012284	Aur.I-C, complete cds	1.7	417704	PROTEASE]	3.8
1 1			1		1	}
,		Rattus norvegicus	1		•]
1 1		mitochondrial			·	}
1		intermediate			(AE000613) H. pylori predicted	1
156	M96633	peptidase (MIP) mRNA, complete cds.	1.7	2314209	coding region HP1054	3.1
130	M90033	mikiva, complete cus.		2314203	INSULIN-LIKE GROWTH	
1		·	1		FACTOR BINDING PROTEIN	!
i			1		4 (IGFBP-4) (IBP-4) (IGF-	j .
1					BINDING PROTEIN 4) factor-	}
}					binding protein-4 - sheep	} 1
1		Rattus norvegicus			(fragment) factor-binding	[]
1		CTD-binding SR-like			protein-4, IGFBP-4 (sheep,	}
1		protein rA8 mRNA,		•	liver, Peptide, 237 aa] [Ovis	
157	U49055	complete cds	1.7	2497252	aries}	3.0
					identification of the control of the	. !
1	1	Mus musculus mRNA			iduronate-2-sulfatase, IDS (EC	
1		for myc-intron-		010776	3.1.6.13) Peptide Mutant, 550	3.0
158	Y15907	binding protein-l	1.7	912776	aal	- 3.0
1	1	Methanococcus jannaschii section 142			}	
1	j	of 150 of the			(AF052252) fork head domain	
159	U67600	complete genome	1.7	2982355	protein FKD9 [Danio rerio]	3.0
129	007000	complete genome		2702333		
1	1	Homo sapiens			}	}
1	Ì	calumein (Calu)			(AF052252) fork head domain	
160	AF013759	mRNA, complete cds	1.7	2982355	protein FKD9 [Danio rerio]	2.9

and the second	Nearest N	leighbor (BlastN vs. Go	enbank)	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEQ						1	
ъ	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
					(. Costoo) similarly to		
					Human mRNA product		
		·			KIAA0077 (TR:Q14997);	ł	
}					cDNA EST yk243h8.5 comes	İ	
l					from this gene; cDNA EST	1	
					yk243h8.3 comes from this	ļ	
1					gene; cDNA EST yk359h4.5	1	
					comes from this gene		
}		,		i	[Caenorhabditis elegans]	j	
1				i	>gi 3880318 gnl PID e1349839]	
					(Z81133) Similarity to Human	ł	
<u> </u>					mRNA product KIAA0077	ĺ	
]					(TR:Q14997); cDNA EST		
Į.			•		yk243h8.5 comes from this	•	
1		Arabidopsis thaliana			gene: cDNA EST yk243h8.3	l	
ł		putative transcription			comes from this gene; cDNA		
İ		factor (MYB90)		2050265	EST yk359h4.5 comes from this	2.3	
161	AF062915	mRNA, complete cds	1.7	3878065	gene (AC004877) sco-spondin-mucin-		
1	1	H.sapiens genomic			like; similar to P98167 uncertain	j	
	3202506	DNA (chromosome	1.7	3638957	[Homo sapiens]	2.3	
162	X87526	3; clone NL3003R)	1.7	3030337	(ITOMO SEPICIO)		
l l		Homo sapiens			(AF005632) phosphodiesterase	l	
		chromosome 5, PAC			Unucleotide pyrophosphatase	j	
163	AC005573	clone 202e13	1.7	2465540	beta [Homo sapiens]	1.8	
		Homo sapiens gene					
1	ľ	for prostacyclin			1	l	
{	i	synthase, exon 10 and			steroid hormone receptor TR3 -		
164	D83402	complete cds	1.7	627608	human sapiens]	1.7	
		Homo sapiens deltex					
	}	(Dx) mRNA,			(AB007864) KIAA0404 [Homo		
165	AF053700	complete cds	1.7	2662089	sapiens}	1.7	
					1	ŀ	
].		Mus musculus 6-		,		}	
	<u> </u>	pyruvoyl-			(AF006564) alcohol	}	
	1	tetrahydropterin			dehydrogenase [Drosophila	1	
	A F0 43225	synthase (Pts)	1.7	2352538	persimilis) persimilis)	1.4	
166	AF043225	mRNA, complete cds	1.7	2332338	(berginning) berginning)	1 1:7	

- 1	Nearest	Neighbor (BlastN vs. C	ienbank)	Nearest Neigh	ibor (BlastX vs. Non-Redundant Pr	roteins)
SEQ	1					1
ID	ACCESSION	DESCRIPTION	PVALUE	ACCESSION	DESCRIPTION	P VALUE
		Thermus aquaticus				
1		thermophilus NADH	}			
i	i	dehydrogenase I	1			
1	ł	subunits NQO7		ı	1	1
1	1	NQ06, NQ05,	·		1	•
İ		NQ04, NQ02,			\	1
l	l	NQ01, NQ03,			\$	i '
{		NQ08, NQ09,			Ì	
		NQ010, NQ011,				
		NQO12, NQO13, and			(AB006631) The human	
[:	-	NQO14, complete		•	homolog of mouse Cux-2	
167	U52917	cds.	1.7	2564334	[Homo sapiens]	1.0
		•			(Z/3425) Similarity to Yeast	
	;				hypothetical YIK9 protein	
					(SW:YIK9_YEAST); cDNA	
		·			EST EMBL:T01252 comes from this gene; cDNA EST	
·			j		EMBL:D33205 comes from this	
			1		gene; cDNA EST	
			1		EMBL:D33955 comes from this	
		M.musculus gene for	1		gene; cDNA EST	
168	X72222	serotonin 2 receptor	1.7	3875796	EMBL:D35484 co	1.0
					(X83413) DR5 [Human	
		Crotalus scutulatus	į		herpesvirus 6] >gi 853972	
169	i	PLA2-like			(X83413) DR5 [Human	
109	U23186	pseudogene	1.7	853971	herpesvirus 6]	0.99
1	j	Mus musculus factor	j		1	j
ſ	. 1	VIII-associated	1			ľ
ı		protein (f8a) mRNA,	}		(AC004669) hypothetical	!
170	M83118	complete cds.	1.7	3201617	protein [Arabidopsis thaliana]	0.80
į	. i	ì			(AL031282) dJ283E3.3.2 (Cell	
J	•]		Division Cycle 2-Like 2	· i
ł	Ì,	E.coli ATP-	ł		(PITSLRE, p58/GTA,	ľ
· 1	£**	dependent proteinase	•		Galactosyltransferase Associated Protein Kinase))	ţ
ł		(lon) gene, complete	1		(isoform beta 2-2) [Homo	i
171		eds.	1.7	4140322	(Isolorm beta 2-2) [Homo	0.78
					HYPOTHETICAL PROLINE-	<u> </u>
- 1	}		1		RICH PROTEIN KIAA0269	1
- !	Ì		1		>gi 1665805 gnl PID d1014089	1
		Human transcription	1		(D87459) Similar to Volbox]
,	1-	actor TFIIIB 90 kDa	1		carteri extensin (S22697)	İ
172	U28838 s	ubunit	1.7	2495730	[Homo sapiens]	0.62

	Nearest N	Neighbor (BlastN vs. G	enhank)	Nearest Neigh	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
	remestr	Teighoor (Diasut vs. O	Cilounky	TVCarcst TVCigit	The state of the s)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE		
173	U72487	Rattus norvegicus calcium-independent alpha-latrotoxin receptor mRNA, complete cds	1.7	544411	GLYCOPROTEIN GP100 PRECURSOR (P29F8) discoideum]	0.35		
		Aquifex aeolicus section 50 of 109 of			FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (FGFR-3) (HEPARIN-BINDING GROWTH FACTOR RECEPTOR) >gi 2117851 pir 155363 fibroblast growth factor receptor 3 - mouse >gi 199145 (M81342) fibroblast growth factor receptor			
174	AE000718	the complete genome	1.7	2497569	3 [Mus musculus]	0.34		
175	AF016897	Oryza sativa GDP dissociation inhibitor protein OsGDI2 (OsGDI2) mRNA, complete cds	1.7	125362	MACROPHAGE COLONY STIMULATING FACTOR I RECEPTOR PRECURSOR (CSF-1-R) (FMS PROTO- ONCOGENE) (C-FMS) factor 1 receptor - cat >gi 163855 (J03149) M-CSF receptor [Felis domesticus]	0.34		
		Xenopus laevis mitotic phosphoprotein 90			muscarinic acetylcholine receptor - fruit fly acetylcholine receptor [Drosophila			
176	U95102	mRNA, complete cds	1.7	85058	melanogaster] ACROSOMAL PROTEIN SP-	0.20		
		Chlamydomonas reinhardtii myosin			10 PRECURSOR SP-10 - western baboon >gi 298488 bbs 127113 (S56458) SP-10=intraacrosomal protein [Papio papio=baboons, Peptide, 285 aa] [Papio			
177		heavy chain Caenorhabditis	1.7	728901	hamadryas]	0.20		
170		elegans cosmid F53B8, complete sequence [Caenorhabditis	, -	74517	(U23517) D1022.7 [Caenorhabditis elegans]	0.068		
178	Z92788	elegans]	1.7	746516	>gi 3258651 elegans]	0.068		

				Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
rein di rein di	Nearest N	leighbor (BlastN vs. Ge	ndank)	Nearest Neigh	The state of the s		
SEQ	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
	ACCESSION			<u></u>	(X87883) mitochondrial capsule		
		Ralstonia eutropha			selenoprotein [Rattus norvegicus] >gi 1354135		
		megaplasmid pHG1	1		(U48702) mitochondia	1	
		nitric oxide reductase	i i		associated cysteine-rich protein	· ·	
		(norB) gene.				0.039	
179	AF002217	complete cds	1.7	1143538	SMCP	0.000	
					(D83776) The KIAA0191 gene		
			1		is expressed ubiquitously.; The		
				•	KIAA0191 protein retains the		
	l	Rat mRNA for			C2H2 zinc-finger at its N-	1	
٠.	1	protein tyrosine	} ,,	1228035	terminal region. [Homo sapiens]	0.008	
180	D30749	phosphatase	1.7 -	1228033	terminar region. (210110 capacity)		
		Rat fast skeletal TnT				ł	
	1	gene encoding			SKIN SECRETORY PROTEIN		
	1	troponin T isoforms.		731172	XP2 PRECURSOR	4e-04	
181	M15202	complete cds.	1.7	731172	A 21 lesections		
	ł		i :			1	
1	ľ	Human peroxisome	1	•	1	1	
}	l	proliferator activated			PUTATIVE IMPORTIN BETA	4	
	1	receptor mRNA,	1.7	4033414	4 SUBUNIT	2c-06	
182	L07592	complete cds.	1./	4033414	4 3 3 2 3 1 1 1		
1	l .	Dendrobium crumenatum ACC	1		ASPARTYL-TRNA	1	
1	į .				SYNTHETASE synthetase	1	
		synthase gene.	1.7	3122885	[Bacillus subtilis]	2e-11	
183	U64031	Complete cds Homo sapiens	 '	3.22005			
	1	docking protein	}	1	(U78737)	1	
1		(DOK-2) mRNA,	ļ		alpha(1,3)fucosyltransferase	!	
١	. 500 1000	complete cds	1.7	2289097	[Cricetulus griseus]	8e-12	
184	AF034970	L.longiflorum mRNA		220303.			
l	1	encoding calmodulin.		t		1	
1	1	> ::	1				
1	1	gb L18912 LILCALM	al	1	1		
1	1	ODU Lilium	7	1 4			
	ľ		1		1.	1	
1	1	longiflorum calmodulin mRNA.		1	(AF023270) probable	1	
	7,000	complete cds.	1.7	2511747	transcriptional regulator dre4	4e-12	
185	Z12839	Complete cus.	1 1				

i nggasa	Noneact N	leighbor (BlastN vs. Ge	nbank)	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
100	Nearest	eignoof (Diasus vs. Oc					
SEQ	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
					(270683) Weak similarity to		
					Human tyrosine-protein kinase		
					CSK (SW:CSK_HUMAN);		
					cDNA EST EMBL:C10908		
		Equine arteritis virus	,		comes from this gene; cDNA		
		(EAV) RNA genome			EST EMBL:C12822 comes		
		> :: emb[A45589]A45589	,		from this gene; cDNA EST		
	i	Sequence 1 from			yk408c2.3 comes from this		
		Patent WO9519438 >			gene; cDNA EST yk408c2.5		
					Human tyrosine-protein kinase		
	ĺ	emb A58849 A58849			CSK (SW:CSK_HUMAN);	.*	
	ľ	Sequence 1 from			cDNA EST EMBL:C10908		
	l	Patent WO9700963 >	, ·		comes from this gene; cDNA		
	1	::	1		EST EMBL:C12822 comes	ì	
		gb AR013959 AR013	1	′	from this gene; cDNA EST	1	
		959 Sequence 1 from			yk408c2.3 comes from this	1. 14	
186	X53459	patent US 5773235	1.7	3979817	gene; cDNA EST yk408c2.5	le-14	
					(Z70310) predicted using	,	
	ľ		1		Genefinder; Similarity to Mouse		
	ł		}		ankyrin (PIR Acc. No. S37771);	1	
1	1		l		cDNA EST EMBL:T01923	}	
	}	1			comes from this gene; cDNA		
	ļ	į	ļ		EST EMBL:D32335 comes		
1	<u>l</u>	1	i		from this gene; cDNA EST		
	i .		ł		EMBL:D32723 comes from this		
	1		į	ł	gene; cDNA ES Genefinder;	1	
i		}	}	ļ.	Similarity to Mouse ankyrin	ł	
			1		(PIR Acc. No. S37771); cDNA	}	
1		E. coli ddl gene	[1	EST EMBL:T01923 comes	}	
Ì	1	encoding D-alanine:D	·	·	from this gene; cDNA EST	1	
	1	alanine ligase and	i	i .	EMBL:D32335 comes from this	ŀ	
	1	ftsQ and ftsA genes.	1	ł	gene; cDNA EST EMBL: D32723 comes from this	l	
	1	complete cds, and		2070121	gene; cDNA ES	2e-19.	
187	K02668	ftsZ gene, 5' end.	1.7	3879121	Igene, CONA ES	1	
1	I		1	Ī	HYPOTHETICAL 55.9 KD		
	1	Homo sapiens mRNA	J	1	PROTEIN EEED8.6 IN	1	
1	1	for osteoblast specific			CHROMOSOME II >gi 733603	1	
1		cysteine-rich protein.		1	(U23484) No definition line	ł	
188	AB008375	1 7	1.7	2496945	found [Caenorhabditis elegans]	1e-19	
	1						
1	I	Pseudomonas cepacia			İ		
1	1	(clone Psudom70-1)	J	1	l		
1	1	heat shock protein 70	'	1	(Y15732) DNA polymerase bet	a	
	12000	(hsp70) gene,	1.7	2661842	[Xenopus laevis]	6e-20	
189	L36603	complete cds	1		г		

೯೩೩ ಕಾ	Nanaga- N	leighbor (BlastN vs. Ge	nhank)	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
4.47.67.187	Nearest N	leighbor (Blasul Vs. Oc					
SEQ			274115	ACCESSION	DESCRIPTION	P VALUE	
А	ACCESSION	DESCRIPTION	PVALUE	ACCESSION	THYPOTHETICAL 75.5 KD		
					PROTEIN C14A4.3 IN		
					CHROMOSOME II	1	
					>gi 3874230 gnl PID e1351618	1 1	
					protein (Swiss Prot accession	1	
			1		number P38376); cDNA EST	}	
} '		P.blakesleeanus			yk220e10.5 comes from this	!!	
		mRNA GTP		1731181	gene [Caenorhabditis elegans]	3e-21	
190	Z49760	cyclohydrolase I	1.7	1/31181	(AF125443) contains similarity	 	
Γ	1				to S. pombe phosphatidyl	i l	
1	ļ	Human fatty acid			synthase (GB:Z28295)		
l	l .	synthase gene, partial	1.7	4226073	[Caenorhabditis elegans]	6e-25	
191	U52428	cds	1./	4220013	[Capitol Hardens		
ł		Human mitogen				1 1	
		induced nuclear	1.6	<none></none>	<none></none>	<none></none>	
192	U12767	orphan receptor	1.0	410112			
1	l	H.sapiens CpG DNA.] [
į.	ļ.	clone 85a12. forward	·			1	
	700.00	read cpg85a12.ftla.	1.6	<none></none>	<none></none>	<none></none>	
193	Z63478	Homo sapiens	1.0			· .	
1	1	inversin protein,	l			<u> </u>	
194	AF084375	exons 8 and 9	1.6	<none></none>	<none></none>	<none></none>	
194	AF084373	Archaeoglobus				1	
1		fulgidus section 165	Ì		1	1	
1	1	of 172 of the		Ì		1 1	
195	AE001114	complete genome	1.6	<none></none>	<none></none>	<none></none>	
133	7	Homo sapiens	1			1	
	1	inversin protein.	İ	1		,,,,,,,,,,	
196	AF084375	exons 8 and 9	1.6	<none></none>	<none></none>	<none></none>	
1	+			I			
	1	Kluyveromyces lactis	1				
1	}	RNA polymerase II	1				
1	1	largest subunit gene,	1		NO. T.	<none></none>	
197	U24217	partial cds	1.6	<none></none>	<none></none>	CHOINES	
	1.	Helicobacter pylori		1	1		
	1	26695 section 58 of			1		
1		134 of the complete			NONE	<none></none>	
198	AE000580	genome	1.6	<none></none>	<none></none>	TAIONES	

1. feet . 0	Nearest N	leighbor (BlastN vs. Ge	nbank)	Nearest Neighb	or (BlastX vs. Non-Redundant Pro	(eins)
SEQ		DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
Ð	ACCESSION	DESCRIPTION 1				
					·	
1		H.sapiens mRNA for	1		[]	
		Drosophila female			1	
		sterile homeotic	1		ļ	•
		(FSH) homologue > ::				
		gb M80613 HUMFS				
		HG Human homolog			}	
	l	of Drosophila female			į	
	Į.	sterile homeotic		NONE	<none></none>	<none></none>
199	X62083	mRNA, complete cds.	1.6	<none></none>	110.12	
		Plasmodium		. '		
		brasilianum DNA				l
	I	homologous to the	l			
	1	histidine-rich knob protein region of		ł		
	1	Plasmodium			(M26647) ORF X	
	1,00064	falciparum.	1.6	457495	[Saccharomyces cerevisiae]	8.4
200	M28064	Streptomyces albus				
	1	lipase precursor (lip)	1	1	1	
	1	gene, complete cds,	1		(AC004877) sco-spondin-mucin-	
	i	and unidentified 5'	i		like; similar to P98167 uncertain	
	1	ORF and 3' ORF.	Ì		I .	7.8
201	U03114	partial cds.	1.6	3638957	[Homo sapiens]	
				1		ł
	1	Strix varia oocyte			VITAMIN D3 RECEPTOR	}
	1 .	maturation factor	1		(VDR) receptor [Rattus	1
		Mos (c-mos) proto-	1.6	137618	norvegicus	6.4
202	U88422	oncogene, partial cds Human pulmonary	1.0			1
	1	surfactant-associated		1		1
1	1	protein SP-A				1
	1	(SFTP1) gene,		1	(Z38112) E03A3.6	4.9
203	M68519	complete cds.	1.6	3875423	[Caenorhabditis elegans]	1 7.7
ٽٽ	+	Homo sapiens		1	GABA transport protein -	
1	1	transcription factor		2122626	tobacco hornworm	4.7_
20	AF044575		1.6	2133625	tobacco normania	
		Homo sapiens	_	1		1
1	1	(subclone 3_e10 from	n	[(AJ005588) 5-epi-aristolochene	. [
1		P1 H21) DNA	1.6	3687297	cynthase	4.6
20	5 L48476	sequence.	+		(Z81133) Similarity to Human	
	1	Rat CNS 2',3'-cyclic		1	mRNA product KIAA0077	1
i		nucleotide 3-		1	(TR:Q14997) [Caenorhabditis	3.7

W. 12	Names N	leighbor (BlastN vs. Ge	nbank)	Nearest Neight	oor (BlastX vs. Non-Redundant Pro	iteins)
	Nearest	leignboi (Blaset V3: O				
SEQ				ACCESSION	DESCRIPTION	P VALUE
D	ACCESSION	DESCRIPTION	P VALUE	ACCESSION		
		Arabidopsis thaliana				
		cellulose synthase	1			
		catalytic subunit (Ath-			TUMOR-ASSOCIATED	
		B) mRNA, complete		0/70/0	ANTIGEN L6	3.6
207	AF027174	cds	1.6	267068	(U53155) strong similarity to	
		Babesia microti heat			the carboxyl two-thirds of valyl-	
1		shock protein 70			tRNA synthetases	}
	1	(hsp70) gene.		1055420	[Caenorhabditis elegans]	2.2
208_	U53448	complete cds	1.6	1255429	PROBABLE	
			}		SERINE/THREONINE-	}
	,				PROTEIN KINASE CY49.28	
	1	Homo sapiens			>gi 1370255 gnl PID e247094	[
	l .	inversin protein		1770076	(Z73966) pknJ	1.2
209	AF084367	mRNA, complete cds	1.6	1730076	(273900) pkiis	
		Yeast dis 1+ gene for	1	}	(AF010496) maltose transport	}
	ļ	p93dis1, complete		3128353	inner membrane protein	1.2
210	D55635	cds	1.6	3126333	Intel memorate	
		Streptomyces sp. 2-	ł		(X83413) DR5 [Human	
	1	dehydro-3-	1	1.	herpesvirus 6] >gi 853972	1
	1	deoxyphosphohepton			(X83413) DR5 [Human	1
		ate aldolase gene.	1.6	853971	herpesvirus 6]	0.97
211	AF035756	partial cds	1.0	05577.	(Y17034) Bassoon [Mus	
	1	O.cuniculus rPTPA	1.6	3413810	musculusl	0.94
212	X73479	mRNA	1.0	3413010	(U95142) putative G-protein-	
	1		1		coupled receptor G-protein-	
]	TY CONTRACTOR		İ	coupled receptor [Arabidopsis	
		H.sapiens mRNA for	1.6	2072986	thalianal	0.73
213	X98330	ryanodine receptor 2	1.0	20,2500	NECDIN >gi 91129 pir JN0148	
	!	1			necdin, brain - mouse	1
	Į.	P.anserina FMR1	1		>gi 200020 (M80840) necdin	1
	3/44104	gene exons 1 and 2	1.6	128014	[Mus musculus]	0.42
214	X64194	Caenorhabditis				1.
	ł	elegans cosmid	1	1	Į.	1
		F53B8, complete	1	•		1
	1	sequence			(U23517) D1022.7	
	Ī	[Caenorhabditis			[Caenorhabditis elegans]	1
١ ,,,	702700	elegans	1.6	746516	>gi 3258651 elegans]	0.19
215	Z92788	[CIESTIP]	1	1		
1	Ī	Methanobacterium			INTERFERON-ALPHA/BETA	`
]	1	thermoautotrophicum	n l		RECEPTOR ALPHA CHAIN	
1	1 .	from bases 1098908			PRECURSOR (IFN-ALPHA-	1
1	1	to 1112186 (section	1	i	REC) >gi 346520 pir S27387	1
1		94 of 148) of the	1	1	interferon alpha receptor type 1	0.001
1					bovine >gi 432	1 0 001

1.00 (F)	Nonrest N	leighbor (BlastN vs. Ge	nbank)	Nearest Neigh	bor (BlastX vs. Non-Redundant Pro	(ems)
EQ	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
<u> </u>	ACCESSION	District				
-		Homo sapiens mRNA			HYPOTHETICAL 55.9 KD PROTEIN EEED8.6 IN CHROMOSOME II >gi 733603	
		for osteoblast specific cysteine-rich protein.			(U23484) No definition line found [Caenorhabditis elegans]	1e-18
217	AB008375	complete cds	1.6	2496945	(Z70750) similar to vanadate	
		Orang-utan involucrin			resistance protein transmembranous domains [Caenorhabditis elegans]	3e-26
218	M25312	gene, complete cds.	1.6	3875131	(Caenornaoditis elegans)	3433
		Cyprinus carpio mRNA for MyoD,	1.5	<none></none>	<none></none>	<none></none>
219	AB012882	complete cds Caenorhabditis				1
220	U29487	elegans cosmid	1.5	<none></none>	<none></none>	<none></none>
221	X74760	M.musculus mRNA for Notch 3	1.5	1364094	integral membrane protein - Streptomyces pristinaespiralis >gi 872306 (X84072) integral membrane protein [Streptomyces pristinaespiralis] EXOGLUCANASE II	4.3
		Lycopersicon esculentum class II small heat shock protein Le-HSP17.6	1.5	121855	PRECURSOR cellulose 1,4-beta cellobiosidase (EC 3.2.1.91) II precursor - fungus (Trichoderma reesei) 1,4-beta-cellobiosidase (EC 3.2.1.91) II - fungus cellobiohydrolase II [Trichoderma reesei]	
222	U72396	mRNA, complete cds	1.5			
223	3 U42391	Human myosin-IXb mRNA, complete cds	1.5	3688428	(AJ011534) sucrose synthase	4.2
224		Pongo pygmaeus gamma-1 and gamma 2 globin genes. complete cds.	1.5	186413	(M13144) inhibin A [Homo sapiens]	0.22
	5 X94144	C.japonica mRNA fo	or 1.5	2745737	Gal:betaGlcNAc beta 1,3- galactosyltranferase-II [Mus musculus]	3e-08

**************************************	Nearest N	eighbor (BlastN vs. Ge	nbank)	Nearest Neighb	or (BlastX vs. Non-Redundant Pro	teins)
##=	Nearest IV	eighloof (Diage]	
EQ	i	- magnerion	P VALUE	ACCESSION	DESCRIPTION	P VALUE
D]	ACCESSION	DESCRIPTION	PVALUE	ACCESSION		
					(X90568) Protein sequence and	
			i		annotation available soon via	
			Į.		Swiss-Prot; available at present	
			1	•	via e-mail from	
	•	Homo sapiens mRNA			LABEIT@EMBL-	
		for KIAA0657	1	1212992	Heidelberg.DE [Homo sapiens]	4e-13
226	AB014557	protein, partial cds	1.5	1212992	Treaters.g.== [
		Borrelia burgdorferi	1		1	
	}	oligopeptide				
	1	permease homolog				
	1	OppAIV (oppAIV)		<none></none>	<none></none>	<none></none>
227	AF000948	gene, complete cds	1.3	ENONE	MYC PROTO-ONCOGENE	
	1	Mus musculus			PROTEIN (C-MYC) proto-	
	ł	RAB/Rip protein		2498005	oncogene [Sus scrofa]	2.6
228	AF057287	mRNA, partial cds.	1.3	2498003	01.00 20.00 1	Ī
		Drosophila				
	1	melanogaster	1	1	ļ	İ
	ł	vacuolar ATPase	1.1	<none></none>	<none></none>	<none></none>
229	U38951	subunit E	 		(U90209) RNA polymerase II	ł
	ì	Homo sapiens			largest subunit [Bonnemaisonia	1
	1	myogenic	1.1	3172134	hamifera]	2.3
230	AF027148	determining factor 3 Mus musculus histone		31,213		1
	1	deacetylase 3	1	l .	1	}
		(Hdac3) gene, exons	i	}		
	1		1	.	(U66220) unknown	
		4 through 15 and	1.0	1657601	[Nannocystis exedens]	0.25
231	AF079310	complete cds P.radiata lac gene for			(X91638) BRM protein [Gallus	١ , , ,
	7/50104	P.radiata fac gene for	0.95	996020	gallus]	0.31
232	X52134	Human mRNA for	1			1
1		Neuroblastoma,	1	1		<none:< td=""></none:<>
	Denois	complete cds	0.93	<none></none>	<none></none>	KNUNE
23:	D89016	C.familiaris VIP36	1		(AL022238) dJ1042K10.2.1	1
ì	1	(vesicular integral-	1	1	(novel protein with probable	1
ŀ	1	membrane protein of		1	rabGAP domains and Src	7. 01
	, V76300	36 kDa) mRNA	0.93	4176446	homology domain 3)	7e-81
23	4 X76392	Mus musculus	 			1
1		Pontin52 mRNA.	1	I		<none< td=""></none<>
١	5 AF100694		0.90	<none></none>	<none></none>	KNONE

				Manage Naight	oor (BlastX vs. Non-Redundant Pro	teins)
2.	Nearest N	leighbor (BlastN vs. Ge	nbank)	Nearest Neight	To the second se	
SEQ	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
10	ACCESSION	1			EG12 PROTEIN PRECURSOR	
					(EARLY GI TRANSCRIPT 2)	
			ŀ		>gi 1362345 pir S55862	
1			ł		probable membrane protein	
			1		YNL327w - yeast	
Į .			ł		(Saccharomyces cerevisiae)	
į.		Archaeoglobus	I		cerevisiae]	
1	ł	fulgidus section 116	1		>gi 1302445 gnl PID e239572	
j	1	of 172 of the			(Z71603) ORF YNL327w	
	. 5000001	complete genome	0.90	1176579	[Saccharomyces cerevisiae]	6.9
236	AE000991	S.cerevisiae				
1.		chromosome II	,			
İ	i	reading frame ORF		-		
237	Z35922	YBR053c	0.86	<none></none>	<none></none>	<none></none>
1 237	233922	TBRosse				į
į.	•	Rattus norvegicus				
1	ł	metabotropic				
		glutamate receptor 4b	•		(Z80225) hypothetical protein	
238	U47331	mRNA, complete cds.	0.82	1550703	Rv2662	4.1
238	04,331	index.iv			1	
1		H.sapiens Ig germline		1	. management of a carefulation	1
1	1	kappa-chain gene	}	}	(AF052587) F14 [Xylella	6.7
239	X72810	variable region (L3)	0.69	3023063	fastidiosa]	0.7
	1					1
-	1	Escherichia coli	l	}		
1	1	genes facG, faeH,	į .	1	!	
	ı	fael, fael and IS629-	ł			1
í	i	like insertion	ļ	1		
1	ì	sequence. > ::	1	1		
1	1	emb Z11710 ECFAE	1	· ·		1
- }	i	HIJ E.coli faeH, faeI	1	1		1
1.		and fael genes	1	'	(AC002338) laccase isolog	1
	i	encoding FaeH, FaeI	0.00	2347188	[Arabidopsis thaliana] thaliana]	3.9
240	Z11700	and FaeJ proteins	0.69	234/100	[Alabidopsis Bianasa]	1
		Phrynosoma	. }	ļ	I	1
	1	douglassii NADH	}	1		
	1	dehydrogenase	}	}	·	1
	1	subunit 4 (ND4)	1	1	1	
	i	gene, mitochondrial	·	1		
	1	gene encoding	1			
	1	mitochondrial	0.65	<none></none>	<none></none>	<none:< td=""></none:<>
24	1 U71597	protein, partial cds	1 0.05	1		

	Nearest N	eighbor (BlastN vs. Ge	nbank)	Nearest Neighl	oor (BlastX vs. Non-Redundant Pro	neins)
EQ		DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
D	ACCESSION	DESCRIPTION	TVALUE		IGLUTAMYL-TRNA	
					SYNTHETASE glutamate	
			1		tRNA ligase (EC 6.1.1.17) -	i
1			1		Haemophilus influenzae (strain	
1			i	•	Rd KW20) >gi 1573240	
ł		Ammonia species			(U32713) glutamyl-tRNA]
1	·	LSU rRNA gene	1		synthetase (gltX) [Haemophilus	
- 1		(partial; isolate Tr S	0.44	1174506	influenzae Rd]	1.2
242	Z77798	5: clone 16)	0.64	1174300	Introduzio 1457	
		Human mRNA for				
		golgi antigen gcp372,			ultra-high-sulfur keratin 1 -	1
	205542	complete cds	0.64	111230	mouse	1e-05
243	D25542	complete cus			(Z99709) similar to Elongation	
	}			'	factor Tu family (contains	
	Ĭ	}			ATP/GTP binding P-loop);	
	ì		ĺ	1	cDNA EST EMBL:D76223	1
	1		1		comes from this gene; cDNA	ł
	1	Cow dopamine	ļ		EST yk478c5.5 comes from this	
		transporter mRNA,			gene [Caenorhabditis elegans]	8e-06
244	M80234	putative cds.	0.64	3874972	EPIDERMAL GROWTH	+ 30.55
			1	1	FACTOR RECEPTOR	
	į		I		KINASE SUBSTRATE EPS8	
	1	1	1	į	>gi 530823 (U12535) epiderma	d l
	l .	Homo sapiens mRNA		İ	growth factor receptor kinase	1
	1	for KIAA0449	1	000000	substrate [Homo sapiens]	2e-14
245	AB007918	protein, partial cds	0.64	2833239	substrate (Figure 5-4-7)	
		Human U266	1	ł		
	1	rearranged DNA for	1		(U95102) mitotic	ļ
	1	lambda-	}	ł	phosphoprotein 90 [Xenopus	
1	I	immunoglobulin ligh	0.63	2072301	laevisl	1.5
246	X51754	chain	0.63	2012301	100-101	
	1	Helicobacter pylori,		1	1	
	ı	strain J99 section 11:	'[,		
	1	of 132 of the	0.62	<none></none>	<none></none>	<none:< td=""></none:<>
247	AE001554	complete genome	0.02	4.0		1
1	1	H.sapiens CpG DNA]			Ì
1.	1	clone 96e7, reverse]	21027	<none< td=""></none<>
248	Z64067	read cpg96e7.rtla.	0.62	<none></none>	<none></none>	CHONE
240	204007	Pinus sylvestris	T	1	[
]	1	microsatellite DNA,			NONES	<none< td=""></none<>
249	AJ223768	1	0.62	<none></none>	<none></none>	

			-book) I	Nearest Neighb	oor (BlastX vs. Non-Redundant Pro	teins)
-	Nearest N	eighbor (BlastN vs. Ge	noank)	11cm cst 11c. gird		
SEQ		DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
ID.	ACCESSION	DESCRIPTION				
					PHOTOSYSTEM II 10 KD	
		İ			PHOSPHOPROTEIN deltoides	
		1	- 1		>gi 2143326 gnl PID e319090	
			1		(Y13328) 10kDa	1
					phosphoprotein [Populus	l
	<u> </u>	Bacteriophage P1 ban	0.62	2493689	deltoides]	7.9
250	AJ011592	gene	0.02	21,7000		
		Xenopus laevis				
	ł .	survival of motor			(AL034463) putative single-	1
	1	neuron protein			strand polynucleotide binding	1
	1	interacting protein 1		l	protein (Schizosaccharomyces	
	1	(SIP1) mRNA.	0.62	4007790	nombel	2.0
251	AF027151	complete cds	0.02		(U40763) CARS-Cyp [Homo	
		Helobdella triserialis	0.62	1117968	anienel capienel	0.90
252	AJ000376	mRNA for actin	0.02	1	(AC005058) similar to calcium-	· [
				1	independent phospholipase A2;	
1	1	1 .	1	1	similar to AC004392	
1	1	1		1	(PID:g3367519) [Homo	1
1	1	Rat thymosin beta 4	0.62	4176370	sapiens]	6e-51
253	M69231	gene (pTB4G).intron.		41,03.0		İ
		Homo sapiens X11L2	i	1		1
1		mRNA for X11-like		}]	
1		protein 2, complete	0.61	<none></none>	<none></none>	<none:< td=""></none:<>
25	4 AB021638	cds	0.01	-	·	
	7	Bacteroides	1	Í	<u> </u>	
1	1	gingivalis DNA for	1		1	1
1	1	arginyl	l			
1	1	endopeptidase.	0.61	<none></none>	<none></none>	<none:< td=""></none:<>
25	5 D26470	complete cds	0.01			
		A.thaliana ATPase	0.61	<none></none>	<none></none>	<none:< td=""></none:<>
25	6 J04737	gene, complete cds.	- 0.01			
		Bos taurus clone	1	I		
1	· I	bm1308	ا	1 .	(Y09905) snail like protein	1
1	1	microsatellite and ar	0.61	1922280	[Gallus gallus]	0.51
2:	57 U06756	lp repeat region.				
	1	p15=cyclin D-		1		
	1	dependent kinases 4	.	1	1	
-	l		1	1	1	
1	1	and 6-binding protein/p15 product	1	Ī		1
-	ì	protein pro product		l	hypothetical protein 253 -	İ
1	1	(exon/intron 1) (human, brain tumo	-c	,	Streptomyces griseus plasmid	2.2
- 1	1	1	0.61	484938	pSG1 (fragment)	0.13
2	58 \$75756	Genomic, 753 nt]				
Г	T	Drosophila	.		(Z70750) similar to vanadate	1
1	}	melanogaster tumo	' 	1	resistance protein	
1	ì	supressor (warts)	l l	1	transmembranous domains	~
1	l l	mRNA exons 1-8.	0.61	3875131	[Caenorhabditis elegans]	le-09
	259 L3983	7 complete cds	1 0.01			

Dark St		ou av C	-basio I	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
	Nearest N	leighbor (BlastN vs. Ge	enbank)	Nearest Neighbor (Blasta Vs. Non-Redundant Proteins)			
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
					(AF125443) contains similarity		
		Human fatty acid			to S. pombe phosphatidyl		
		synthase gene, partial			synthase (GB:Z28295)		
260	U52428	cds	0.61	4226073	[Caenorhabditis elegans]	2e-26	
		Plasmodium				1	
}		falciparum gene for				1	
i		heat-shock protein				1	
261	X15292	pPf203	0.60	<none></none>	<none></none>	<none></none>	
						ţ l	
		Homo sapiens mRNA				·	
1		for KIAA0856	l	! -	(U00043) No definition line	1	
262	AB020663	protein, partial cds	0.60	470341	found [Caenorhabditis elegans] GALACTOSE-BINDING	5.7	
					•	i i	
					PROTEIN REGULATOR		
			i		glucose/galactose binding	1	
					protein regulator -	1	
Į					Agrobacterium tumefaciens	l i	
		Human checkpoint			>gi 142228 (L10424)	i i	
ł		suppressor 1 mRNA,			glucose/galactose binding		
263	U68723	complete cds	0.60	544375	protein regulator	5.7	
1						1	
		S.griseus sporulation			(AFO10971) Margle! [Mus	1	
ì		protein genes 1590		0500017	(AF012871) Mergla' [Mus	3.3	
264	M32687	and 1422.	0.60	2582017	musculus]	3.5	
i	İ	Homo sapiens			(AF010496) maltose transport	} I	
1	Ì	NKCC2 gene, exon 4,	The state of the s	2120263	\$ *	1.5	
265	AJ005331	isoform B	0.60	3128353_	inner membrane protein	 	
1	Į.	Mus musculus RGL			(U90533) serine protease		
		protein mRNA,	0.60	4099845	inhibitor [Streptomyces fradiae]	0.098	
266	U14103	complete cds.	0.60	4022647	minutor (Suchomyees nadiae)		
	1	Xenopus laevis XL-			1		
1	1	INCENP (XL-			(AF047897) ankyrin-like protein		
1		INCENP) mRNA,	0.59	3282851	HGE-ANK [Ehrlichia sp. BDS]	5.5	
267	U95094	complete cds Methanobacterium	0.39	3202031	TIGE-ALVE (Englished Sp. DDG)		
	1	thermoautotrophicum					
1		from bases 896604 to					
ŀ	İ	1912784 (section 78 of	ļ		HYPOTHETICAL 24.5 KD]	
1	1	148) of the complete		!	PROTEIN IN NADB-SRMB		
260	4 E000032	1	0.59	401553	INTERGENIC REGION	4.3	
268	AE000872	genome	0.55	701333	1		

, 1 1, 1	Nearest N	Veighbor (BlastN vs. Go	enbank)	Nearest Neigh	bor (BlastX vs. Non-Redundant Pro	oteins)
SEQ						
Ð	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					nypometicai protein - numan	
					herpesvirus 4 reading frame 1	
i					[Human herpesvirus 4] 2	
					[Human herpesvirus 4] >gi 1334838 gnl PID e25079 4	
İ					[Human herpesvirus 4]	
· ·		,			>gi 1334840 gnl PID e25081 6	
					[Human herpesvirus 4]	
		!			>gi 1334842 gnl PID e25067 8	
					[Human herpesvirus 4]	
, i		Gallus gallus achaete-			>gi 1334844 gnl PID e25069 10	
		scute homologue			[Human herpesvirus 4]	
	·	(ASH) mRNA,			>gi 1334846 gnl PID e25071 12	i
269	L11871	complete cds.	0.59	628110	[Human herpesvirus 4]	4.2
					NITROGENASE IRON-IRON	
					PROTEIN ALPHA CHAIN	
					(NITROGENASE	
	}	0			COMPONENT I)	
		Oryctolagus cuniculus glycogen			(DINITROGENASE) capsulatus	
		synthase mRNA,			>gi 312238 (X70033)	
270	AF017114	complete cds	0.59	728856	alternative nitrogenase	2.4
	19-23/11					
ł	,	Homo sapiens beta-			(AF067155) truncated rev.	
		casein (CSN2) gene,		2052022	protein [Human immunodeficiency virus type 1]	1.5
271	AF027807	complete cds	0.59	3252932	immunodericiency virus type 1)	1
	1	Human Wnt10B			(Z67990) similar to cuticle	
272	U81787	mRNA, complete cds	0.59	3875538	collagen	1.4
		Apteryx australis 16S				
1	ł	ribosomal RNA gene,				
1	ł	mitochondrial gene		•	(AFOSSORR) ATR binding	
1		for mitochondrial]		(AF055088) ATP-binding cassette; PsaB [Streptococcus	
	V:2006	RNA, partial	0.59	4193356	pneumoniae]	0.83
273	U76036	sequence	0.39	4173330	PTB-ASSOCIATED SPLICING	
1	1				FACTOR (PSF) long form -	
l		Homo sapiens mRNA			human >gi 38458 (X70944)	
1		for KIAA0664			PTB-associated splicing factor	
274	AB014564	protein, partial cds	0.59	1709851	[Homo sapiens]	0.17
		Homo sapiens cyclin-				
1		dependent kinase				
	l	inhibitor 2D			(AT 022626) V27D8 A 17	
		(CDKN2D) gene,	0.50	3925213	(AL032626) Y37D8A.17 [Caenorhabditis elegans]	3e-10
275	AF044171	partial cds	0.59	3342713	(Cacionabottis elegans)	

		·		Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
王肇	Nearest N	leighbor (BlastN vs. Ge	nbank)	Nearest Neighb	of (Blasta vs. 14011-Reddingant 1.5		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
276	L19640	Saccharomyces cerevisiae cdc2/cdc28 related protein kinase gene, complete cds.	0.59	3880115	(Z81130) T23G11.9 [Caenorhabditis elegans]	le-21	
270	217040	Human DNA sequence from cosmid E140G5 on chromosome 22,					
277	Z80999	complete sequence [Homo sapiens]	0.58	<none></none>	<none></none>	<none></none>	
278	Y11108	H.sapiens WNT8B gene	0.58	<none></none>	<none></none>	<none></none>	
279	U80001	Sphyraena idiastes lactate dehydrogenase	0.58	<none></none>	<none></none>	<none></none>	
280	Z49637	S.cerevisiae chromosome X reading frame ORF YJR137c	0.58	<none></none>	<none></none>	<none></none>	
281	X64467	H.sapiens ALAD gene for porphobilinogen synthase	0.58	<none></none>	<none></none>	<none></none>	
	1	G.gallus hox B3	0.58	<none></none>	<none></none>	<none></none>	
282		Cochliobolus heterostrophus polyketide synthase	0.58	<none></none>	<none></none>	<none></none>	
284	AF089084	Arabidopsis thaliana putative auxin efflux carrier protein (PIN1 mRNA, complete cds	0.58	<none></none>	<none></none>	<none></none>	
285	U38481	Rattus norvegicus ROK-alpha mRNA, complete cds	0.58	<none></none>	<none></none>	<none></none>	
286	,	Homo sapiens G protein beta 5 subuni		3236249	(AC004684) hypothetical protein [Arabidopsis thaliana]	9.2	
28		Human glutathione transferase class mu number 4	0.58	1280073	(U55366) Similar to cuticle collagen [Caenorhabditis elegans] (U28741) F35D2.1 gene	7.1	
28		Human mRNA for KIAA0341 gene, partial cds	0.58	861293	product [Caenorhabditis elegans]	7.1	

500	Nearest N	leighbor (BlastN vs. Ge	enbank)	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEQ							
B	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
		NV to a series					
		Neisseria gonorrhoeae			1		
1		carbamoyl phosphate			1 ·		
1 1		synthetase			1	l	
1 1		(glutamine) small			1		
		subunit (carA) and			(AF020283) DG2044 gene		
		large subunit (carB)			product [Dictyostelium		
289	U11295	genes, complete cds.	0.58	2425135	discoideum]	5.3	
		Human mRNA for			(U49836) gamma-glutamyl		
	1	KIAA0179 gene.			transpeptidase precursor [Brugia		
290	D80001	partial cds	0.58	4097223	malayi]	4.1	
		Postoviakia sali	ļ				
1	l	Escherichia coli genes faeG, faeH.]			1	
		fael, fael and IS629-	1			İ	
	1	like insertion					
1	i	sequence. > ::				}	
		emb Z11710 ECFAE				Ì	
i		HIJ E.coli faeH. faeI			İ		
1	ł	and faeJ genes			1		
ì	į	encoding FaeH, FaeI	}		(AC002338) laccase isolog		
291	Z11700	and FaeJ proteins	0.58	2347188	[Arabidopsis thaliana] thaliana]	3.2	
		Mouse hair keratin			HYPOTHETICAL 8.3 KD	}	
1	j	A1 (MHKA1) gene,		141166	PROTEIN >gi 62179	3.2	
292	M77350	complete cds.	0.58	141165	(AB004461) DNA polymerase	3.2	
	Ì	Tal	ł		alpha catalytic subunit [Oryza		
1		T.thermophila gene	0.58	2826900	satival	3.1	
293	X63787	for snRNA U3-2 Human mRNA for	00	1020700			
		KIAA0160 gene.			(U95036) germin-like protein]	
294	D63881	partial cds	0.58	1934730	[Arabidopsis thaliana]	3.1	
1274	1 203801	Gymnocarena			1	•	
		mexicana 16S]		ì	}	
1	i	ribosomal RNA gene.					
1	1	mitochondrial gene	1	j	1	1	
	i	encoding		1	(AC002062) Similar to	}	
	ł	mitochondrial RNA.	1	2104121		3.1	
295	U39378	partial sequence	0.58	2194131	Synechocystis antiviral protein	 	
i		P.pastoris PRC1 gene	.]		1	1	
		>::		`	OCCLUDIN >gi 1276983		
1	1	dbj E12103 E12103	1	1	(U49221) occludin [Canis	1	
Į	Į	DNA encoding	ļ		familiaris]		
			1	1	>gi 1589181 prf 2210347D	1	
	1	precursor of protease	I	l .	occludin [Canis familiaris]	3.1	

Nearest Neighbor (BlastX vs. Non-Redundant Proteins)				. 1 ber (BlaceN us Gent	Nearest Neighbor (BlastN vs. Genbank)				
	ļ į		/	ighbor (Blastiv vs. Gent	Nearest Ne	<i>-</i>			
ALUE	DESCRIPTION P	ACCESSION				EQ			
		ACCESSION	VALUE	DESCRIPTION F	CESSION				
						-			
	1		1	A.thaliana (L.Heynh.)	1				
	(D38529) DRPLA protein		1	hloroplast mRNA	c	- 1			
2.4	[Homo sapiens]	1732444		or recombinant APS-	\f				
	(Mono 3-pro-s)	1/32444	0.58	cinase	X75782	297			
	1		i	Mouse platelet-		-			
	1		1	derived growth factor	į	- 1			
				B chain musculus		- 1			
	1		1	platelet-derived	į,	1			
	(AF055985) pyrrolidone-rich		t	growth factor beta-		1			
1.4	antigen [Onchocerca volvulus]	3025832	0.58	chain (sis) gene, exon		- 1			
			0.56	5.	M64848	298			
	1		. 1	Helicobacter pylori,					
	(AF037454) ubiquitin protein		į.	strain J99 section 21		1			
1.1	ligase [Mus musculus]	2827198	0.58	of 132 of the		1			
	CHDI PROTEIN		0.50	complete genome	AE001460	299			
	>gi 320737 pir S30818					1			
	hypothetical protein YER164w -			1		l			
	yeast (Saccharomyces			1		j			
	cerevisiae) >gi 603404			M.musculus gene for	•	1			
	(U18917) Chdlp: transcriptional			protein kinase C-		I			
1.1	regulator [Saccharomyces			gamma (exon1 and					
	cerevisiae] SEX-DETERMINING	418395	0.58	exon 2)	X65720	300			
	REGION Y PROTEIN			CKON S7	A03720	300			
0.62	determining protein [Mus			Arabidopsis thaliana					
	determining protein (1720)	3024637	0.58	lactate dehydrogenase	AF043130	301			
				Human genes for	AI 043130	301			
	(U64835) T09D3.3			collagen type IV					
0.36	[Caenorhabditis elegans]	1450050		alpha 5 and 6, exon 1					
	Cachonassans	1458250	0.58	and exon 1'	D28116	302			
	1	,		Archaeoglobus		<u> </u>			
•	(Z97991) hypothetical protein			fulgidus section 32 of	ł	1			
0.36	Rv0336	2276333	0.50	172 of the complete	ļ ·	ļ.			
		2210333	0.58	genome	AE001075	303			
	ļ		ľ						
		{			1				
		1	!	Rhodococcus opacus	1	1			
		1	1	chloromuconate	1	1			
0.20	mucin 7 precursor, salivary -	1		cycloisomerase transposase homolog	1	1			
0.28	human	477072	0.58			1			
İ			- 0.55	Human MAGE-7	AF003948	304			
i	The second state of the se	1		antigen (MAGE7)	1	1			
0.05	HOMEOBOX PROTEIN HOX-	}		pseudogene, complet	l	1			
	C11	3287858	0.58	ואספעעטפַבווב, בטווואוכנין		1			

				Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
447	Nearest N	leighbor (BlastN vs. Ge	nbank)	Mentest Meighbor (Dimon 19.			
SEQ		DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
Ð	ACCESSION	DESCRIPTION	1				
		Rhodococcus opacus	1				
			1		İ		
		chloromuconate			1		
ļ		cycloisomerase			(AF058803) mucin 4 [Homo		
		transposase homolog	0.58	3551821	sapiens]	0.041	
306	AF003948	genes, complete cds	0.58	,	VAV PROTO-ONCOGENE		
	1	H.sapiens HFH4			>gi 55221 (X64361) proto-	ł	
	1	gene, exon 1 and	0.58	137483	oncogene [Mus musculus]	0.024	
307	X99350	joined CDS	0.36	137.103		Į.	
	1	Homo sapiens mRNA			1 .	'	
	\ ·	for Ig heavy chain			(AC003682) R27945_2 [Homo	ł	
	1	variable region, clone	0.50	3264846	sapiens]	0.018	
308	AJ234282	lc	0.58	3204040		1	
	1	Mus musculus histone		1		1	
	1	deacetylase 3	1			1	
	1	(Hdac3) gene, exons			(U66220) unknown	}	
	1	4 through 15 and	0.50	1657601	[Nannocystis exedens]	0.014	
309	AF079310	complete cds	0.58	1037001	(: \university		
		Human thiopurine	l		(AF063020) lens epithelium-		
l	i	methyltransferase	ļ		derived growth factor [Homo		
ŀ	İ	(TPMT) gene, exons	0.50	3283352	sapiens	0.011	
310	AF019367	6 and 7	0.58	3203332	Saprons;	1	
		M.musculus gene for		Ì	(U38291) microtubule-	1	
}	}	protein kinase C-	1		associated protein la [Homo		
1	1	gamma (exon1 and	0.50	1790878	sapiens]	0.008	
311	X65720	exon 2)	0.58	1790876	Saprone		
			.		į.	ł	
1	1	Homo sapiens mRNA	`	l	SYNAPSINS IA AND IB		
1	1	for KIAA0583		1251166	>gi 163713	0.006	
31	2 AB011155	protein, partial cds	0.58	1351166	541007.0		
			ţ	1	(D84307) phosphoethanolamin	e	
1	1			1 .	cytidylyltransferase [Homo	1	
1	1	H.sapiens mRNA for		1017540	sapiens]	0.001	
31	3 X63692	DNA	0.58	1817548	[24bicus]		
1	1	Feline	1	1		1	
1		immunodeficiency	l	ł		i	
1	1	virus isolate FIV-	I	i		1	
1	1	Pco336-8 pol	1	1	(U93872) ORF 73, contains	İ	
1	1	polyprotein (pol)			large complex repeat CR 73	2e-05	
31	4 U53746	gene, partial cds	0.58	2246532	large complex repeat CR 15	1	
1		Rattus norvegicus		1	(M64793) salivary proline-ricl	. l	
1	1	(clone rt1-1) pseudo	-		protein [Rattus norvegicus]	le-05	
			0.58	206712	IMMORALM I MALLINE HIM ACKINGO		

四级	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEQ						}	
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
i							
		HSF2=heat shock					
	,	factor 2 {alternatively					
1 1		spliced, splice					
}		junction region}	1				
1		[mice, CBA/J, testis,					
		Genomic, 120 nt.			(AJ222798) tDET1 protein		
316	S79632	segment 2 of 3]	0.58	4038594	[Lycopersicon esculentum] (U55376) coded for by C.	3e-06	
			}		elegans cDNA cm21e6; coded		
ļ			1		for by C. elegans cDNA		
					cm01e2; similar to melibiose		
		•		•	carrier protein	1	
	·	Rat liver mRNA for			(thiomethylgalactoside permease		
317	D43964	Kan-1, complete cds	0.58	1280135	II)	1e-08	
 	D-7.750-4	Isair-1, complete cus			EPIDERMAL GROWTH		
					FACTOR RECEPTOR		
					KINASE SUBSTRATE EPS8		
1		Homo sapiens mRNA			>gi 530823 (U12535) epidermal		
1		for KIAA0449			growth factor receptor kinase	i i	
318	AB007918	protein, partial cds	0.58	2833239	substrate [Homo sapiens]	3e-13	
		Homo sapiens mRNA					
1 !		for Efs1, complete	0.50	2042716	(D45027) 25 kDa trypsin	2e-14	
319	AB001466	cds	0.58	2943716	inhibitor [Homo sapiens]	26-14	
		Saccharomyces cerevisiae IRE1 gene	1		ì		
1 1		for putative protein			(Z81130) T23G11.9		
320	Z11701	kinase.	0.58	3880115	[Caenorhabditis elegans]	9e-21	
1	211701	S.cerevisiae	0.50		(Z83819) dJ146H21.2 (similar		
1		chromosome X			to CYTOCHROME B-245]	
1 1		reading frame ORF			HEAVY CHAIN) [Homo		
321	Z49535	YJR035w	0.58	4106562	sapiens]	3e-33	
		S.cerevisiae DBF20				,,,,,,,,,,	
- 322	M62506	gene, complete cds.	0.57	<none></none>	<none></none>	<none></none>	
		Yeast PSS gene for	ĺ				
]	3705011	phosphatidylserine	0.57	<none></none>	<none></none>	<none></none>	
323	X05944	synthetase Snail gene for ADP-	0.57	CHUNES	CHOILE	31.01.02	
]		ribosyl cyclase,			1]	
324	D38536	complete cds	0.57	<none></none>	<none></none>	<none></none>	
	230330	S.cerevisiae	5.57				
		chromosome XV					
		reading frame ORF	Ī			ļ. I	
325	275004	YOR096w	0.57	<none></none>	<none></none>	<none></none>	
		Homo sapiens		•		ļ l	
		(subclone 10_e10				ļ ļ	
		from P1 H16) DNA				ANONT.	
326	L77034	sequence.	0.57	<none></none>	<none></none>	<none></none>	

173

		· · · · · · · · · · · · · · · · · · ·	mbonk\ I	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
34 T	Nearest N	leighbor (BlastN vs. G	noank)	Memest Meight			
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
		Cyprinus carpio c-					
		myc gene for c-Myc,		•			
327	D37887	complete cds	0.57	<none></none>	<none></none>	<none></none>	
327		Homo sapiens mRNA			Lair Dán		
1	1	for KIAA0662			(M57576) Ig kappa chain [Mus	8.9	
328	AB014562	protein, partial cds	0.57	197406	musculus]	8.9	
		Human DNA sequence from					
		cosmid L75B9,			chaperonin containing TCP-1	1	
`		Huntington's Disease			complex gamma chain - African	·	
		Region, chromosome			clawed frog >gi 793886		
329	Z69651	4p16.3	0.57	1079280	(X84990) Cctg	8.9	
1325	200031	4510.5					
1	ł	Mesocricetus auratus	}			İ	
1	ł	mRNA for inter-alpha	{		1		
1	1	trypsin inhibitor				1	
ł	1	heavy chain 1,			RYANODINE RECEPTOR.		
330	D89285	complete cds	0.57	134132	SKELETAL MUSCLE	6.9	
1		S.cerevisiae			1		
}	1	chromosome XVI	j		(AJ130783) APC2 protein [Mus	5.3	
331	Z48951	cosmid 9723	0.57	4210432	musculus]	3.3	
]		DECARBOXYLASE 2		
1	i		1		4.1.1.25) - parsley >gi 169671	1	
1	1	A.thaliana mRNA for			(M96070) tyrosine		
1	1	salt-tolerance zinc			decarboxylase [Petroselinum	5.2	
332	X95573	finger protein	0.57	1174828	PROBABLE ABC	 	
			} ,		TRANSPORTER ATP-	1	
	t	1	1	1	BINDING PROTEIN IN		
	}			ļ	NTRA/RPON 5'REGION	}	
ļ	ł	Xenopus laevis XL-	ļ		(ORFI) Azorhizobium		
1	1 .	INCENP (XL-	1	1	caulinodans >gi 311388	1	
	1	INCENP) mRNA,	0.57	465646	(X69959) ORF1	4.0	
333	U95094	complete cds	0.57	403040	(20737) 010 1	1	
1	1	Danilla hundarfari	1	1	(AE000653) Na+/H+ antiporter	1	
	1	Borrelia burgdorferi	1		(nhaA) [Helicobacter pylori		
	A 7500000	(section 2 of 70) of	0.57	2314735	266951	4.0	
334	AE001116	the complete genome	1	2317.33	DNA-DIRECTED RNA		
	i		1	l	POLYMERASE I SECOND	1	
	l		1	1	LARGEST SUBUNIT (RNA		
1	1		1	1	POLYMERASE I SUBUNIT 2		
	!	R.norvegicus mRNA	1	į	chain RPA2 - Euplotes		
1	1	for putative chloride	-		octocarinatus (SGC9)	1	
225	Z34291	channel.	0.57	1350832	>gi 578407 octocarinatus]	3.0	
335	234291	Jenanner.	1 0.57				

to manual C	Nearest N	leighbor (BlastN vs. Ge	enbank)	Nearest Neight	oor (BlastX vs. Non-Redundant Pro	oteins)
SEQ	1.04.05(.)	.c.g.noo.				
ID ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
—					(Z81063) similar to Actinin-type	
		Homo sapiens A30			actin-binding domain containing	
} '		Vk germline gene,			proteins [Caenorhabditis	
336	D88255	partial cds	0.57	3875983	elegans]	3.0
1330					(U61933) Similar to kinesin-like	
<u> </u>				•	protein; coded for by C. elegans cDNA yk184h5.3; coded for by	
					C. elegans cDNA yk184h5.5;	
					coded for by C. elegans cDNA	
1					yk13d7.3; coded for by C.	
i					elegans cDNA yk13d7.5; coded	
1	•				for by C. elegans cDNA	
1				• .	yk31e1.5; co >gi 3493541	
1	1	Homo sapiens SH3-	_		(AF057567) kinesin-like protein	
1	Ţ	containing adaptor			ZEN-4a [Caenorhabditis	
	. 500504	molecule-1 mRNA,	0.57	1397341	elegans	2.3
337	AF037261	complete cds	0.57	1377341	0.02-0.0	
1	}	Rattus norvegicus			1	}
1	Ì	prostaglandin F2a			1	ì
		receptor regulatory			(AF039656) neuronal tissue-	j
1	ļ	protein precursor,			enriched acidic protein [Homo	
338	U26595	mRNA, complete cds	0.57	2773160	sapiens]	2.3
					(AE001009) quinone-reactive	
1	i	R.norvegicus mRNA			Ni/Fe-hydrogenase B-type	
1	1	for interleukin 4		24,0100	cytochrome subunit (hydC) [Archaeoglobus fulgidus]	1.8
339	X69903	receptor	0.57	2649193	Archaeoglobus fulgidus)	1.0
-	l	S.cerevisiae			(U64846) F47D2.5 gene	1
ł	1	chromosome XV reading frame ORF			product [Caenorhabditis	
1 240	274925	YOL083w	0.57	1458319	elegans	1.4
340	Z74825	Foot-and-mouth	5.5,			
1	l	disease virus O vp1			proline-rich protein - mouse	
341	AJ131469	gene, strain O/A/58	0.57	91206	(fragment) musculus]	1.4
	1				•	
1		Mus musculus	[
ł	J	regulator of G-protein				1
1		signaling 7 (RGS7)			I I' A sussiana labores	0.80
342	AF011360	mRNA, complete cds	0.57	542514	gelsolin - American lobster	0.80
	1	Maria managarilas	,			
1	1	Mus musculus regulator of G-protein	1		gelsolin - American lobster	
- [}	signaling 7 (RGS7)		ł	>gi 452313 gelsolin [Homarus	
343	AF011360	mRNA. complete cds	0.57	1078946	americanus]	0.80
343	VI.011200	macra, complete cus				

		Di Nin Co	abank) T	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
-2 1 -	Nearest N	leighbor (BlastN vs. Ge	noank)	Troub est Trongs.			
SEQ			DVALUE	ACCESSION	DESCRIPTION	P VALUE	
D	ACCESSION	DESCRIPTION	P VALUE	ACCESSION			
					·		
i		Homo sapiens inosine	1		(X77466) 98.8kD polyprotein		
		monophosphate	1		Strawberry latent ringspot		
		dehydrogenase type II	0.57	559526	virus	0.79	
344	L39210	gene, complete cds	0.37	339320	(1.100)		
	ł	Human endometrial	i		1	İ	
	}	bleeding associated			(K01702) HMW/LMW collagen		
	{	factor mRNA,	0.57	211499	subunit precursor [Gallus gallus]	0.79	
345	U81523	complete cds	0.57	211433	Substitution of the substi		
	1	T				1	
	1	Tetrahymena			HYPOTHETICAL 100.5 KD		
	1	thermophila polyubiquitin (TTU3)			PROTEIN IN IAP-CYSH		
	l .				INTERGENIC REGION		
	l	gene, complete cds.	,		>gi 882654 (U29579) alternate		
	l .	and RNA polymerase		ĺ	gene name ygcB; ORF_f888		
		II subunit 2 (RPB2)	0.57	2506493	[Fscherichia coli] >gi[1789119	0.60	
346	U46561	gene, partial cds	0.57	2000.50	NEUROFILAMENT TRIPLET		
			1		M PROTEIN (160 KD	1	
	ì		1		NEUROFILAMENT	1	
	1		i	İ	PROTEIN) (NF-M)	Į.	
		C.japonica mRNA for		İ	>gi 1083164 pir S55395	1	
İ	1	legumin (clone	1	1	neurofilament protein M - rabbit		
	V05542	CjLeg31)	0.57	1709261	(fragment) >gi 854353	0.46	
347	X95543	CILEGIII				1	
1	ì	Homo sapiens mRNA	ł	}	(AF055904) unknown		
348	Y17282	for cytokeratin type I		3044086	[Myxococcus xanthus]	0.45	
340	117202	Frog mRNA fragmen			(AF079369) transcriptional		
1		for alpha-A2-	ŀ]	repressor TUP1 [Dictyostelium	0.00	
349	X00716	crystallin _	0.57	3406654	discoideum]	0.20	
343	700710	Klebsiella sp.				j	
1	i	bacteriophage K11	}	ţ		1	
1.	1.	gene 1 for RNA		, '		0.16	
350	X53238	polymerase	0.57	1228093	(Z46913) polyketide synthase	0.10	
 	100000		T	1	(S78897) GOR=antigenic	1	
	1	H.sapiens FUS gene,	ļ	1	epitope [chimpanzees, Peptide,	0.090	
35	X99012	exon 12	0.57	# 243898	427 aa] [Pan]	0.090	
1-1-		Human DNA				1	
1	1	sequence from PAC	1	1	area social Standards area chemos		
	1 .	390N22 on	1	1	(U53585) fibronectin attachmen	0.053	
35	2 AL008711		0.57	1469545	protein [Mycobacterium avium	0.055	
1 22					(U58748) similar to potential	[
1	1	SOX9 [human, fetal	1	I	transmembrane domains in S.	1	
1	1	brain, Genomic, 149	4	ł	cerevisiae nulcear division	0.017	
35	3 S74506_	nt, segment 3 of 3]	0.57	1326350	RFT1 protein (SP:P38206)	1 0.017	

SEQ ID ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION	oteins)	oor (BlastX vs. Non-Redundant Pro	Nearest Neighb	enhank)	Nearest Neighbor (BlastN vs. Genbank)		
D ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION				ciioank)	leignoor (Blasti Vs. Co	Nearest	
D25542 golgi antigen gcp372, complete cds D.57 4063399 discoideum dis	P VALUE	DESCRIPTION	ACCESSION	P VALUE	DESCRIPTION	ACCESSION	- 1
D25542 golgi antigen gcp372, complete cds Mus musculus mRNA for alpha1,3- fucosyltransferase IX, complete cds Xenopus mRNA for APEG protein, containing a highly repetitive amino acid sequence 0.57 1929056 [Xenopus laevis] EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8 Segi 530823 (U12535) epidems growth factor receptor kinase substrate [Homo sapiens] AB007918 protein, partial cds 0.57 2833239 substrate [Homo sapiens] AB001466 cds 0.57 2943716 inhibitor [Homo sapiens] (AC002400) Glutamyl rRNA synthetical protein ybk4; similar to P38164 (PID:g586461) [Homo sapiens] (AC004982) similar to past hygorhetical protein ybk4; similar to P38164 (PID:g586461) [Homo sapiens] (ANONE)		(AFLO2575) call surface protein			`		
D25542 Complete cds D.57 4063399 discoideum							
Mus musculus mRNA for alphal , 3- fucosyltransferase IX, fucosyltr	0.005		10.0000				
Sequence	0.003	discoideum	4063399	0.57	complete cds	D25542	354
Sequence Section Sequence Section Sequence Section Sequence Section Sequence Section Sequence Section Sequence Sequ		į					
AB015426 Complete cds Complete cds Complete cds Xenopus mRNA for APEG protein. Containing a highly repetitive amino acid sequence Clycopersion esculentum FIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8 Sejl530823 (U12535) epidermal growth factor receptor kinase substrate [Homo sapiens mRNA for KIAA0449 Complete cds Clycopersion esculentum FACTOR RECEPTOR KINASE SUBSTRATE EPS8 Sejl530823 (U12535) epidermal growth factor receptor kinase substrate [Homo sapiens] CD45027) 25 kDa trypsin inhibitor [Homo sapiens] CD45027) 25 kDa trypsin inhibitor [Homo sapiens] CD45027) 25 kDa trypsin inhibitor [Homo sapiens] CD45027) 25 kDa trypsin inhibitor [Homo sapiens] CD45027) 25 kDa trypsin inhibitor [Homo sapiens] CAC002400) Glutamyl tRNA synthetase [Homo sapiens] CAC004982) similar to yeast hypothetical protein ybk4; similar to P38164 Sequence 19 from Patent WO9719110 D.57 3419847 CPID:g586461) [Homo sapiens] CAC004982) similar to past hypothetical protein ybk4; similar to P38164 CPID:g586461) [Homo sapiens] CAC004982 CAC0		(V15732) DNA polymerase beta			for alpha 1,3-		
Xenopus mRNA for APEG protein. (Y12090) putative 3,4- dihydroxy-2-butanone kinase (Lycopersicon esculentum)	7e-11		2661842	0.57			
APEG protein. containing a highly repetitive amino acid sequence 0.57 1929056 1929056 (Y12090) putative 3,4- dihydroxy-2-butanone kinase (Lycopersicon esculentum) EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8 >gif530823 (U12535) epidermal growth factor receptor kinase substrate [Homo sapiens] AB007918 Homo sapiens mRNA for KIAA0449 protein, partial cds for Efs1, complete cds AB001466 AB001466 Rabbit mRNA for adult fast skeletal troponin-C H.sapiens brca2 gene exon 3 > :: emb A62778 A62778 Sequence 19 from Patent W09719110 B.vulgaris mRNA for betavulgin Patent W09719110 B.vulgaris mRNA for betavulgin Mycoplasma genitalium DNA gyrase subunit B complete cds, DNA polymerase III beta subunit (dnaN) and seryl-uRNA		(Achopus lacvis)	2001042	0.37	Complete cds	AB015426	355_
containing a highly repetitive amino acid sequence 0.57 1929056 (Lycopersicon esculentum) EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8 Sejl530823 (U12535) epidermal growth factor receptor kinase substrate [Homo sapiens] Homo sapiens mRNA for Efs1, complete cds 0.57 2943716 (D45027) 25 kDa trypsin inhibitor [Homo sapiens] Rabbit mRNA for adult fast skeletal troponin-C 0.57 2576348 (AC002400) Glutamyl tRNA synthetase [Homo sapiens] (AC004982) similar to yeast hypothetical protein ybk4; similar to P38164 (PID:g586461) [Homo sapiens] B.vulgaris mRNA for betavulgin Mycoplasma genitalium DNA gyrase subunit B complete cds, DNA polymerase III beta subunit (dnaN) and seryl-tRNA	İ	1					
Tepetitive amino acid sequence 0.57 1929056 CLycopersicon esculentum							
356 X51394 sequence 0.57 1929056 (Lycopersicon esculentum)		dihydroxy-2-butanone kinase		l			
Homo sapiens mRNA FACTOR RECEPTOR FACTOR RECEPTOR KINASE SUBSTRATE EPS8 Sgi 530823 (U12535) epidermal growth factor receptor kinase Substrate [Homo sapiens] Factor receptor kinase Substrate [Homo sapiens] Factor receptor kinase Substrate [Homo sapiens] Factor receptor kinase Substrate [Homo sapiens] Factor receptor kinase Substrate [Homo sapiens] Factor receptor kinase Substrate [Homo sapiens] Factor receptor kinase Substrate [Homo sapiens] Factor receptor kinase Substrate [Homo sapiens] Factor receptor kinase Substrate [Homo sapiens] Factor receptor kinase Substrate [Homo sapiens] Factor receptor kinase Factor receptor kinase Substrate [Homo sapiens] Factor receptor kinase Factor receptor kinase Substrate [Homo sapiens] Factor receptor kinase Factor receptor kinase Substrate [Homo sapiens] Factor receptor kinase Factor receptor kinase Factor receptor kinase Substrate [Homo sapiens] Factor receptor kinase Factor receptor kinase Factor receptor kinase Factor receptor kinase Substrate [Homo sapiens] Factor receptor kinase	9e-12	[Lycopersicon esculentum]	1929056	0.57	l •	Y51304	256
Homo sapiens mRNA for KIAA0449 357 AB007918 protein, partial cds Homo sapiens mRNA for KIAA0449 Barbore Efs1, complete cds Cds Rabbit mRNA for adult fast skeletal troponin-C H.sapiens brca2 gene exon 3 > :: emb A62778 A62778 Sequence 19 from B.vulgaris mRNA for betavulgin B.vulgaris mRNA for betavulgin Mycoplasma genitalium DNA gyrase subunit B complete cds, DNA polymerase III beta subunit (dnaN) and seryl-tRNA KINASE SUBSTRATE EPS8 >gi 530823 (U12535) epidermal growth factor receptor kinase subunit cash spide and protein kinase subunit agrowth factor receptor kinase subunit agrowth factor receptor kinase substrate [Homo sapiens] (D45027) 25 kDa trypsin inhibitor [Homo sapiens] (AC002400) Glutamyl tRNA synthetase [Homo sapiens] (AC002400) Glutamyl tRNA synthetase [Homo sapiens] (AC004982) similar to yeast hypothetical protein ybk4; similar to P38164 (PID:g586461) (Homo sapiens) NONE>	1	EPIDERMAL GROWTH			Sequence	AJ1354	330
Homo sapiens mRNA for KIAA0449	,					[
for KIAA0449 protein, partial cds Homo sapiens mRNA for Efs1, complete cds Rabbit mRNA for adult fast skeletal troponin-C H.sapiens brca2 gene exon 3 > :: emb A62778 A62778 Sequence 19 from A859 Y 285967 B. vulgaris mRNA for betavulgin B. vulgaris mRNA for betavulgin Mycoplasma genitalium DNA gyrase subunit B complete cds, DNA polymerase III beta subunit (dnaN) and seryl-tRNA 2833239 2833239 2833239 2833239 2833239 2833239 2833239 2833239 2833239 2833239 2833239 2833239 2833239 2833239 2833239 2833239 2833239 2843716 (D45027) 25 kDa trypsin inhibitor [Homo sapiens] (AC002400) Glutamyl tRNA synthetase [Homo sapiens] (AC002400) Glutamyl tRNA synthetase [Homo sapiens] (AC004982) similar to yeast hypothetical protein ybk4; similar to P38164 (PID:g586461) [Homo sapiens] NONE>	į]	ĺ	
for KIAA0449 protein, partial cds Homo sapiens mRNA for Efs1, complete cds Rabbit mRNA for adult fast skeletal troponin-C H.sapiens brca2 gene exon 3 > :: emb A62778 A62778 Sequence 19 from 361 X85967 B.vulgaris mRNA for betavulgin Mycoplasma genitalium DNA gyrase subunit B complete cds, DNA polymerase III beta subunit (dnaN) and seryl-tRNA 2833239 growth factor receptor kinase substrate [Homo sapiens] (D45027) 25 kDa trypsin inhibitor [Homo sapiens] (AC002400) Glutamyl tRNA synthetase [Homo sapiens] (AC004982) similar to yeast hypothetical protein ybk4; similar to P38164 (PID:g586461) [Homo sapiens]	1 .	>gi 530823 (U12535) epidermal		•	Homo sapiens mRNA	ţ	
Homo sapiens mRNA for Efs1, complete cds 0.57 2943716 inhibitor [Homo sapiens]		growth factor receptor kinase				i	
Sample	3e-13	substrate [Homo sapiens]	2833239		protein, partial cds	AB007918	357
AB001466 cds 0.57 2943716 inhibitor [Homo sapiens] Rabbit mRNA for adult fast skeletal troponin-C 0.57 2576348 synthetase [Homo sapiens] H.sapiens brca2 gene exon 3 > :: emb A62778 A62778 Sequence 19 from Sequence 19 from B.vulgaris mRNA for betavulgin Mycoplasma genitalium DNA gyrase subunit B complete cds, DNA polymerase III beta subunit (dnaN) and seryl-tRNA O.57	ł				Homo sapiens mRNA		
Rabbit mRNA for adult fast skeletal troponin-C 0.57 2576348 synthetase [Homo sapiens] H.sapiens brca2 gene exon 3 > :: emb A62778 A62778 Sequence 19 from B.vulgaris mRNA for betavulgin 0.57 3419847 (PID:g586461) [Homo sapiens] B.vulgaris mRNA for betavulgin 0.56 NONE> NONE> Mycoplasma genitalium DNA gyrase subunit B complete cds, DNA polymerase III beta subunit (dnaN) and seryl-tRNA	2e-14			}	for Efs1, complete	į .	
adult fast skeletal troponin-C	26-14	inhibitor [Homo sapiens]	2943716	0.57		AB001466	358
359 Y00760 troponin-C H.sapiens brca2 gene exon 3 > :: emb A62778 A62778 Sequence 19 from 360 X95153 Patent WO9719110 B.vulgaris mRNA for betavulgin Mycoplasma genitalium DNA gyrase subunit B complete cds, DNA polymerase III beta subunit (dnaN) and seryl-tRNA Synthetase [Homo sapiens] (AC004982) similar to yeast hypothetical protein ybk4; similar to P38164 (PID:g586461) [Homo sapiens] ANONE> NONE>		(ACOORAGO) Gluramyl (RNA		I			
H.sapiens brca2 gene exon 3 > :: emb A62778 A62778 Sequence 19 from 360 X95153 Patent WO9719110 0.57 3419847 (PID:g586461) [Homo sapiens] B.vulgaris mRNA for betavulgin 0.56 <none> <none> Mycoplasma genitalium DNA gyrase subunit B complete cds, DNA polymerase III beta subunit (dnaN) and seryl-tRNA</none></none>	2e-28		2676240	0.67		l	t
exon 3 > :: emb A62778 A62778 Sequence 19 from 360 X95153 Patent WO9719110 0.57 3419847 (PID:g586461) [Homo sapiens] B.vulgaris mRNA for betavulgin 0.56 <none> <none> Mycoplasma genitalium DNA gyrase subunit B complete cds, DNA polymerase III beta subunit (dnaN) and seryl-tRNA</none></none>	<u> </u>	Syllthetase (Home suprems)	2370348	0.57	troponin-C	Y00760	359
emb A62778 A62778 Sequence 19 from 360 X95153 Patent WO9719110 0.57 3419847 (PID:g586461) [Homo sapiens] B.vulgaris mRNA for betavulgin 0.56 <none> <none> Mycoplasma genitalium DNA gyrase subunit B complete cds, DNA polymerase III beta subunit (dnaN) and seryl-tRNA</none></none>	1	(AC004982) similar to yeast		1		ł	1
Sequence 19 from Sequence 19 from Sequence 19 from Patent WO9719110 0.57 3419847 (PID:g586461) [Homo sapiens] B.vulgaris mRNA for betavulgin 0.56 <none> <none> Mycoplasma genitalium DNA gyrase subunit B complete cds, DNA polymerase III beta subunit (dnaN) and seryl-tRNA</none></none>						1	l
360 X95153 Patent WO9719110 0.57 3419847 (PID:g586461) [Homo sapiens] B.vulgaris mRNA for B.vulgin 0.56 NONE> <none> Mycoplasma genitalium DNA gyrase subunit B complete cds, DNA polymerase III beta subunit (dnaN) and seryl-tRNA</none>	ł]	1
B.vulgaris mRNA for B.vulgaris mRNA for betavulgin Mycoplasma genitalium DNA gyrase subunit B complete cds, DNA polymerase III beta subunit (dnaN) and seryl-tRNA	2e-55		3419847	0.57		V05152	360
361 X85967 betavulgin 0.56 <none> <none> Mycoplasma genitalium DNA gyrase subunit B complete cds, DNA polymerase III beta subunit (dnaN) and seryl-tRNA</none></none>	Γ					X93133	300
Mycoplasma genitalium DNA gyrase subunit B complete cds, DNA polymerase III beta subunit (dnaN) and seryl-tRNA	<none></none>	<none></none>	<none></none>		1 -	X85967	361
gyrase subunit B complete cds, DNA polymerase III beta subunit (dnaN) and seryl-tRNA	1.				Mycoplasma	1	
complete cds, DNA polymerase III beta subunit (dnaN) and seryl-tRNA		,	·			ł	
polymerase III beta subunit (dnaN) and seryl-tRNA							1
subunit (dnaN) and seryl-tRNA		1				ł	1
seryl-tRNA						I	1
1 I I I		,		1		· ·	
1			·	1	1 -	1 .	1
synthetase (serS) 100351 cores partial cds 0.56 SNONES SNONES	<none></none>	NONE	ALONT.	0.54			1
362 U09251 genes, partial cds. 0.56 <none> <none></none></none>	+	\.\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	<none></none>	0.36	genes, partial cds.	U09251	362
Chloroplast Euglena	1		j	1	Chloroplast Euglena	1	1
gracilis genes coding	1		}	1		1	ŀ
for transfer RNAs			ĺ	1	, -	1	1
specific for threonine,	1			.]	•		
glycine, methionine,	1.		1	Ί			1
363 V00158 serine and glutamine. 0.56 <none></none>	<none></none>	NONE	<none></none>	0.56		V00158	362

	Nearest N	leighbor (BlastN vs. G	enbank)	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
	1,02,0311	TEIGHOOF (DIESE TO O					
SEQ ID	ACCESSION		P VALUE	ACCESSION	DESCRIPTION	P VALUE	
		Clostridium					
		perfringens DNA for				l I	
		D-alanine:D-alanine		,	1	1 1	
		ligase, cortical			1	1	
		fragment-lytic					
364	D88151	enzyme	0.56	<none></none>	<none></none>	<none></none>	
	ı	Methanococcus			ļ	1 1	
		jannaschii section 20		•		1	
		of 150 of the	256	NONTE	NONE	<none></none>	
365	U67478	complete genome	0.56	<none></none>	<none></none>	CHOINES	
		Tachyglossus			ļ		
		aculeatus beta-globin				ļ i	
		homolog (HBB)			į.	1 1	
366	L23800	gene, complete cds	0.56	<none></none>	<none></none>	<none></none>	
300	L23800	gene, complete cus	0.50	4101122			
		Homo sapiens mRNA				1 1	
1 1		for KIAA0557			1		
367	AB011129	protein, partial cds	0.56	<none></none>	<none></none>	<none></none>	
		Homo sapiens					
	!	(subclone 10_e10]	
		from P1 H16) DNA			1		
368	L77034	sequence.	0.56	<none></none>	<none></none>	<none></none>	
		C.albicans gene for			1	1	
1		TFIIIB (BRF1)				,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	
369	Z47202	subunit.	0.56	<none></none>	<none></none>	<none></none>	
		Clostridium				!	
i		acetobutylicum			1	1 1	
		mannitol-specific phosphotransferase					
					İ]	
	:	system (PTS) system, mtlA, mtlR, mtlF, and			1	1	
}				,			
370	U53868	mtlD genes, complete cds	0.56	' <none></none>	<none></none>	<none></none>	
3/0	908550	cus	0.,0	310110			
		Homo sapiens breast			1	1	
1 1		cancer putative					
1 1		transcription factor					
		(ZABCI) mRNA.] 	1		
371	AF041259	complete cds	0.56	<none></none>	<none></none>	<none></none>	
					<u>}</u>		
		Plasmodium		!	1		
]]	·	falciparum variant-			1		
}]		specific surface]	
		protein (var-7)			(707050) 1	, ,	
372	_L42636	mRNA, complete cds.	0.56	2213557	(Z97052) hypothetical protein	8.8	

1000	Name I	T : 11 (DlaceNive C	ble\	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
	ivearest i	Neighbor (BlastN vs. G	enbank)	Troubest treiginor (Blasec vs. From Reddingalit Florent			
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
		Human protein					
1 1		tyrosine phosphatase	i		THIOREDOXIN REDUCTASE		
1 1		(TEP1) mRNA,			thioredoxin reductase (NADPH)		
373	U96180	complete cds	0.56	731016	[Coxiella burnetii]	8.7	
		Homo sapiens PTS			(Y12225) Spi-1/PU.1		
374	L76259	gene, completé cds	0.56	2369863	transcription factor	6.7	
		Mus musculus					
		D16Jhu17 YAC			hypothetical protein - common		
1 1		98B3 acentric end,	1		sunflower protein [Helianthus	}	
375	AF045946	partial sequence	0.56	2130017	annuus]	5.1	
] [M.musculus mRNA		•			
1 1		for desmocollin type	}		(AC005936) hypothetical		
376	X97986	1	0.56	4038031	protein [Arabidopsis thaliana] SPINDLE POLE BODY	3.9	
1			1		•		
1 1					COMPONENT SPC42 yeast		
1 1			į.		(Saccharomyces cerevisiae)		
1 1					>gi 486054 (Z28042) ORF		
					YKL042w [Saccharomyces		
			ł		cerevisiae] >gi 666098		
		M.musculus whey	1		(X71621) hypothetical 42.3 kD		
777	¥70427	acidic protein (WAP)	0.56	540670	protein [Saccharomyces	3.9	
377	X79437	gene, exon 1	0.56	549670	cerevisiae]	3.9	
		Rat cardiac specific	1		ENDOGLUCANASE G		
l i		sodium channel alpha-	4		PRECURSOR 3.2.1) CelCCG		
1 1		subunit mRNA.	1		precursor - Clostridium		
378	M27902	complete cds.	0.56	585234	cellulolyticum cellulolyticum]	3.9	
	1127702	Jonipiete eds.	- 5.55	303234	gp70=envelope protein		
i 1		Caenorhabditis	ł		{endogenous provirus} host=cat		
1		elegans cosmid	j		lymphoid tissues, Peptide, 445	I	
379	AF036696	F15B10	0.56	546071	[22]	3.6	
					(U14101) putative reverse		
}. I		ļ	1	•	transcriptase; ORF2; encodes aa	į	
		1	j		motifs conserved in reverse	ſ	
) i	_	Caenorhabditis	[transcriptases; most closely	j	
<u> </u>		elegans cosmid	- 1		related reverse transcriptases are	l	
		B0331, complete			those of non-LTR	<u>}</u>	
[i		sequence			retrotransposons. The 3' 901 bp		
{ i	ı	[Caenorhabditis	\$		of this CDS are identical to the	- 1	
380	Z99102	elegans]	0.56	603664	3' 901 bp	3.0	
			į			ĺ	
		Equus caballus (clone	ł			ŀ	
		T131) T-cell receptor	1				
381	L27850	DNA, V-region.	0.56	1079150	transcription factor shn - fruit fly	1.7	

24.5.3	Nearest N	Neighbor (BlastN vs. Go	nbank)	Nearest Neigh	bor (BlastX vs. Non-Redundant Pro	oteins)
	i realest l	TOTELLOCI (DIESET 13. OF				
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					HYPOTHETICAL 113.1 KD	
		M.musculus mRNA			PROTEIN IN PRE5-FET4	
		for desmocollin type			INTERGENIC REGION	
382	X97986	1	0.56	2497227	>gi 1072409 (Z54141) unknown	1.7
		Didelphis virginiana			(U12964) contains ankyrin-like	
		G protein receptor			repeats; similar to human	
]		kinase 2 mRNA.	1		desmoplakin repeat region	1
383	AF087455	complete cds	0.56	1213453	[Caenorhabditis elegans]	1.3
		Human mRNA for]
	i	KIAA0189 gene,				
384	D80011	complete cds	0.56	226535	protease [Hepatitis B virus]	1.1
		Mus musculus mRNA		•		
	1	for HAP1-A protein,			(AB014572) KIAA0672 protein	,,
385	AJ002272	3' region	0.56	3327158	[Homo sapiens]	1.0
1	ļ		ł		1	{
1						i I
		Homo sapiens inosine			1	
l		monophosphate	[coat protein - strawberry latent	1
		dehydrogenase type II	0.56	628431	ringspot virus	0.77
386	L39210	gene, complete cds Mouse Thy-1.2 gene	0.36	020431	Illigspot virus	****
Į	į .	5' untranslated region			(AB014516) KIAA0616 protein	1
387	X02770	and exon 1	0.56	3327046	[Homo sapiens]	0.59
307	A02770	and exon 1				
i	}	Schizosaccharomyces	1			
ł	j	pombe Wiskott-			1	1
ł	İ	Aldrich Syndrome			salivary proline-rich	
1	ļ .	protein homolog			phosphoprotein precursor PRH1]
}	•	(wspl+) genc,			(allele PIF) - human >gi 190484]
1		complete cds, and			(K03203) prepro salivary	j
Ì	1	BTF3/beta-NAC	1		proline-rich protein [Homo	
388	AF038575	gene, partial sequence	0.56	88466	sapiens] >gi 190512	0.35
		Rat mRNA for fetal			1	j !
] .	1	intestinal lactase-		•	magan line and hamatana	j
1		phlorizin hydrolase			(Z48674) chitinase homologue	0.23
389	X56747	precursor, partial	0.56	2072742	[Sesbania rostrata]	U.23
1	1	G.arboreum mRNA			1	1
]	1	for farnesyl			(X07882) Po protein [Homo]
]		pyrophosphate	0.54	206670	•	0.20_
390	Y12072	synthase	0.56	296670	sapiens	
	ł	p15=cyclin D-			1	
		dependent kinases 4			1	
		and 6-binding				1 !
1	1	protein/p15 product			protein kinase (EC 2.7.1.37)	1
i	i .	{exon/intron 1}			SPRK - human sapiens]	[]
	l	(human, brain tumors,	Į.		>gi 1090771 prf 2019437A	[]
391	S75756	Genomic, 753 nt]	0.56	1082743	protein Tyr kinase I	0.15 [.]
727	3/3/30	rectionine, 755 inj	<u> </u>	1000.10		

- Lâi-	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEQ			1	cmeat retgi	1001 (Diasot vs. 1401)-Reduitant F	iciciis)	
D	ACCESSION	DESCRIPTION	PVALUE	ACCESSION	DESCRIPTION	 	
ا	I		FVALUE	ACCESSION	DESCRIPTION	P VALUE	
	 	Equus caballus type	ļ		10	<u> </u>	
392	U62528	II collagen mRNA.	0.54	461671	[Segment 1 of 2] COLLAGEN		
1776	002328	complete cds C.reinhardtii mRNA	0.56	461671	ALPHA 1(I) CHAIN	0.030	
[ł	for unknown lumenal		1	(AC003672)	_[
393	X96877	polypeptide	0.56	3341678	(AC003672) putative zinc finger protein [Arabidopsis thaliana]	9	
	12,0077	рогурсравс	0.50	3341078	protein [Alabidopsis thanana]	5e-09	
[]		1]	
	Ī			1			
	ł				(AL009196) 1-		
	l				evidence=predicted by content;		
					1-method=genefinder;084; 1-]	
					method_score=59.41; 1-]	
					evidence_end; 2-	1	
					evidence=predicted by match; 2-		
		<u>- </u>			match_accession=AA950019; 2-		
		cGATA-3 [chickens,			match_description=LD29959.5p		
704	626266	liver, Genomic, 979			rime LD Drosophila		
394	S78788	nt, segment 4 of 4]	0.56	2661590	melanogas	2e-11	
		Drosophila			(U41534) coded for by C.		
		melanogaster Ste20-			elegans cDNA CEESI42F; Similar to helicases of		
		like protein kinase			SNF2/RAD54 family.		
395	AF006640	mRNA, complete cds	0.56	1109830	[Caenorhabditis elegans]	6e-12	
	32 00000		- 3.30	1109030	(U41534) coded for by C.	06-12	
		Drosophila		,	elegans cDNA CEESI42F;		
		melanogaster Ste20-	į		Similar to helicases of		
		like protein kinase	. [SNF2/RAD54 family.		
396	AF006640	mRNA, complete cds	0.56	1109830	[Caenorhabditis elegans]	4e-13	
					(AL030996) dJ1189B24.4		
					(novel PUTATIVE protein		
	l		ĺ	•	similar to hypothetical proteins		
		Aquifex aeolicus	İ	, •	S. pombe C22F3.14C and C.	ł	
397		section 48 of 109 of		260262	elegans C16A3.8) [Homo	`	
39/		the complete genome S.cerevisiae	0.56	3688350	sapiens)	3e-66	
ł	ſ	chromosome II				i	
į		reading frame ORF				}	
398		YBR210w	0.55	<none></none>	<none></none>	NONE	
		Mus musculus mRNA	(CHOILES	<inoine></inoine>	<none></none>	
ı		for ubiquitin				1	
399	1	conjugating enzyme	0.55	<none></none>	NONE	<none></none>	
		Homo sapiens			3.13.12		
1	(subclone 2_g5 from	1		·	1	
- 1		BAC H107) DNA	ł			1	
400	AC001461 s	sequence	0.55	<none></none>	<none></none>	<none></none>	

SEQ D ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION ACCESSION DESCRIPTION ACCESSION ACCESSION DESCRIPTION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION ACCESSION DESCRIPTION ACCESSION	(CRO.	Nearest	Neighbor (BlastN vs. C	enbank)	Nearest Neigh	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE Alouatta seniculus Stream of varian susceptibility (BRCA1) gene, 401 AF019079 partial cds 0.55 <none></none>	SEC		1		- tremest treign	TOOL (Blaster vs. 14011-Reduildain F)	T Cleris)		
Alouatta seniculus Stream	1	1	DESCRIPTION	PVALUE	ACCESSION	DESCRIPTION	P VALUE		
AF019079 AF019079			Alouatta seniculus				 		
AF019079 Partial cds			breast and ovarian						
401 AF019079 partial cds 0.55 NONE> NONE> NONE NONE	1		susceptibility	j	1		ł		
Human serglycin gene, exons 1,2, and 3.	1	<u> </u>	(BRCA1) gene,	[.			j		
Human serglycing gene, exons 1, 2, and 3,	401	AF019079	partial cds	0.55	<none></none>	<none></none>	<none></none>		
Mus musculus CLM2 gene for cytohesin 2, complete and partial cds, alternative splicing	1		Human serglycin						
Mus musculus CLM2 gene for cytchesin 2, complete and partial cds, alternative splicing	i		gene, exons 1,2, and						
gene for cytohesin 2, complete and partial cds, alternative splicing	402	M90058	3.	0.55	<none></none>	<none></none>	<none></none>		
Bacteriophage P1 ban gene			gene for cytohesin 2, complete and partial cds, alternative	·					
PHOSPHOPROTEIN deltoides Sqi 2143326 gn PID e319090 (Y13328) 10kDa phosphoprotein [Populus deltoides] Mosphoprotein [Populus deltoides] 6.6	403	AB013469	splicing	0.55	1729760	hirsutum]	8.6		
404 AJ011592 gene						PHOSPHOPROTEIN deltoides] >gi 2143326 gnl PID e319090 (Y13328) 10kDa			
T.brucei kinetoplast maxicircle variable region DNA 0.55 2970432 [Florometra serratissima] 6.5	104	4.701.600							
Maxicircle variable region DNA 0.55 2970432 Florometra serratissima 6.5	404	AJ011592		0.55	2493689		6.6		
A05 Z15118 region DNA 0.55 2970432 [Florometra serratissima] 6.5	i i			j			i		
S.cerevisiae Chromosome XVI Cosmid 9723 O.55 4210432 Chromosome XVI Cosmid 9723 O.55 4210432 Chromosome XVI Cosmid 9723 O.55 A210432 Chromosome XVI	405	715110		0.55	2020.402		1		
AGO01389 Chromosome XVI Cosmid 9723 0.55 4210432 (AJ130783) APC2 protein [Mus musculus] 4.9	103	213116		0.33	2970432	[Florometra serratissima]	6.5		
Homo sapiens mad protein homolog Smad2 gene, promoter, exon 1a and exon 1b 0.55 3319290 [Homo sapiens] 4.9 KRUEPPEL PROTEIN Sgi 72899 pir TWFF Krueppel gap protein - fruit fly (Drosophila sp.) melanogaster] region, clone: Sgi 224875 prf 1202348A Sgi 224875 prf 1202348A Krueppel gene Sgi 224875 prf 1202348A Krueppel gene Sgi 24875 prf 1202348A Krueppel gene Sgi 24875 prf 1202348A Krueppel gene Sgi 24875 prf 1202348A Krueppel gene Sgi 24875 prf 1202348A Krueppel gene Sgi 24875 prf 1202348A Krueppel gene Sgi 24875 prf 1202348A Krueppel gene Sgi 24875 prf 1202348A Krueppel gene Sgi 24875 prf 1202348A Krueppel gene Sgi 25684 Krueppel gene	406	Z48951	chromosome XVI	0.55	4210432	,	49		
KRUEPPEL PROTEIN Sgi 72899 pir TWFF Krueppel gap protein - fruit fly (Drosophila sp.) melanogaster] sgi 224875 prf 1202348A Krueppel gene 3.8 X-LINKED PEST- CONTAINING Plasmodium vivax major blood stage surface antigen gene. AGOO MATCAO MATCAO KRUEPPEL PROTEIN Sgi 72899 pir TWFF Krueppel gap protein - fruit fly (Drosophila sp.) melanogaster] sgi 224875 prf 1202348A Krueppel gene Sgi 224875 prf 1202348A Krueppel gene Sgi 24875 prf 1202348A Sgi 24875 prf 1202348A Sgi 24875 prf 1202348A Sgi 24875 prf 1202348A	407		protein homolog Smad2 gene, promoter, exon 1a	0.55		(AF055994) thyroid hormone receptor-associated protein complex component TRAP220			
Plasmodium vivax Plasmodium vivax Plasmodium vivax Plasmodium vivax TRANSPORTER transporter - human >gi 458255 (U05321) X- linked PEST-containing	408	ļ	genomic DNA, 21q region, clone:	0.55		KRUEPPEL PROTEIN >gi 72899 pir TWFF Krueppel gap protein - fruit fly (Drosophila sp.) melanogaster] >gi 224875 prf 1202348A			
Plasmodium vivax Plasmodium vivax major blood stage surface antigen gene. CONTAINING TRANSPORTER transporter - human >gi 458255 (U05321) X- linked PEST-containing			21111DIII42	0.33	123084		3.8		
400		1	najor blood stage			CONTAINING TRANSPORTER transporter - human >gi 458255 (U05321) X-			
- I Dian Control of the control of t	409		partial cds.	0.55	549453	transporter [Homo sapiens]	3.8		

学是	端 Neares	Neighbor (BlastN vs. C	ienhank)	I Manage N	11 (D) V	
SEC		Torgroot (Brase vs. C	Jenoank)	Nearest Neig	ghbor (BlastX vs. Non-Redundant P	roteins)
B	1		P VALUE	ACCESSION	DESCRIPTION	P VALUE
 		Fugu rubripes mRNA				1. 17.0.01
	1	for sodium channel				
1		alpha subunit, partial			1	l
410	D37977	cds	0.55	1435038	(D38024) ORF [Homo sapiens]	3.7
1		Ostertagia ostertagi			(30000000000000000000000000000000000000	
Į	ļ	cathepsin B-like		j	i	l
411	1400505	cysteine protease	ĺ		(AF000900) p45 [Rattus	
411	M88505	gene, partial cds.	0.55	3941277	norvegicus)	2.9
1	1	Xenopus laevis				
1	1	mitotic		İ	(AB008376) 17-kDa PKC-	
412	U95098	phosphoprotein 44			potentiated inhibitory protein of	
1 712	093098.	mRNA, partial cds Human mibp gene,	0.55	2570154	PP1 [Sus scrofa]	2.8
413	U89241	partial cds	0.55.		(U62253) 16kDa secretory	
 112	009241	Xenopus laevis	0.55	4097465	protein [Sus scrofa]	2.2
1	Ì	survival of motor				
1]	neuron protein			1	
1	l	interacting protein I	i i		(AL034463) putative single-	
l	l	(SIP1) mRNA.	1		strand polynucleotide binding	
414	AF027151	complete cds	0.55	1007700	protein [Schizosaccharomyces	i
		Bufo marinus		4007790	. pombe)	1.7
1]	natriuretic peptide	i		1	
		receptor C mRNA,			(707242) CTD birdi - D 4 D 2 1	
415	AF006821	partial cds	0.55	2245075	(Z97343) GTP-binding RAB2A	
		Lactococcus lactis		2243073	protein	1.7
}		cremoris plasmid	1		1]
		pJW565 DNA.			(AF035120) type I procollagen	i
		llabiiM, llabiiR genes	i		pro-alpha 2 chain [Canis	
416		and orfX	0.55	3386334	familiaris]	1.3
		Mus musculus				
		collagen alpha-1 type	1		1	
		l gene, 5' flanking	1		1	1
417		region, partial	1		gastric mucin - human	1
41/		sequence.	0.55	1362802	(fragment) >gi 547517	1.3
418		Mouse mRNA for			(D83032) nuclear protein,	
710	D13473	Rad51 protein Bungarus fasciatus	0.55	1374698	NP220 [Homo sapiens]	1.3
ŀ		cetylcholinesterase	j			
Ĭ		gene, alternatively				
1		pliced products.	- 1			
419	AF045238	artial cds	0.55	204100	(Z94752) hypothetical protein	j
		Methanobacterium	0.55	3261734	Rv1004c	0.99
	1	hermoautotrophicum	1			
- 1		rom bases 1 to			i	
- 1		0208 (section 1 of	1		i	1
ł	li li	48) of the complete	1	Į	(140.1121)	1
420		enome	0.55		(M94131) mucin [Homo	1
			5.55	186396	sapiens]	0.97

	程 Neare	st Neighbor (BlastN vs.	Genbank)	T Manual V			
SE		Tander (Diabet Vs.	Tomatk)	14cmest 14618	thbor (BlastX vs. Non-Redundant	Proteins)	
п	· .	DN DESCRIPTION	P VALUE	ACCERGION	DESCRIPTION OF	j	
		Y.lipolytica SEC62	1 VALUE	ACCESSION	DESCRIPTION	P VAL	UE
42	1 X99537	gene	0.55	3876397	(Z81068) F25H5.2		
		Aquilegia sp.	- 0.33	3876397	[Caenorhabditis elegans]	0.58	
j		phytochrome			j		
1		(PHYB/D) gene,			(AF005370) ribonucleotide-	1	
42:	U08147	partial cds.	0.55	2338024	reductase, large subunit	0.57	
1	ł				ge decent	0.57	_
- [1	H.sapiens CpG DNA	•	· ·		i i	
423	Z56586	clone 12c8, reverse			(U46007) espin [Rattus		į
172	230386	read cpg12c8.rt1d.	0.55	3320122	norvegicus)	0.44	ı
1.	ł	Mus musculus					
1	į į	glutamine:fructose-6-	.[•		`. .	
1		phosphate				1	ı
ı	1	amidotransferase	1			1	1
1	ı	(GFAT) gene, 5'			hypothetical protein -		- [
424	U39442	region and partial cds	0.55	282600	Mycoplasma hyorhinis	0.42	١
	1	Rat chymotrypsin B			in a second manual myorining	0.43	4
425		(chyB) gene,	1 1		(Y17034) Bassoon [Mus		ı
425	K02298	complete cds.	0.55	3413810	musculus]	0.33	ı
426	X84792	M.musculus clusterin					7
1-0	R04792	gene Capra aegagrus	0.55	1652475	(D90905) hypothetical protein	0.25	1
į.	Į	Saanen and Weisse	j				7
1	l	Edel breeds DR beta-	1				Ĺ
1	1	chain antigen binding					1
1	i	domain, MHC class II			SUBTILIN BIOSYNTHESIS	İ	
427	U00185	DRB	0.55	2507136	PROTEIN SPAB	0.19	ı
ı					THE TELLY OF THE	0.19	┨
]		H.sapiens CpG DNA,			ł		ı
428	Z54946	clone 178a12, reverse			(M17294) unknown protein	1	ı
420	234946	read cpg178a12.rt1a.	0.55	807646	[Human herpesvirus 4]	0.065	L
1 1		Oryctolagus	i		_		1
1 1		cuniculus anion	1		, -		1
1 1		exchanger 3 brain					l
		isoform (AE3)	1		(U68412) fibrillar collagen		
429	AF031650	mRNA. complete cds	0.55	1778210	[Arenicola marina]	0.044	
					(i nemedia maima)	0.044	l
		Bovine adenylyl	l		(AE000997) consérved		
430	1405570	cyclase Type I	ĺ	ļ	hypothetical protein		
430	M25579	mRNA. complete cds.	0.55	2649040	[Archaeoglobus fulgidus]	0.023	
431	Z48796	H.sapiens Ski-W mRNA for helicase	0.55		(M14708) DNA polymerase		
	2.0170	india ioi ilelicase	0.55	330452	Human cytomegalovirus]	0.023	

nSi	Neares	Neighbor (BlastN vs.	Genhank)	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEC		Torgroot (Blase) vs.	Genoank)	inearest ineig	indor (Blastx, vs. Non-Redundant P	roteins)	
D	ACCESSIO	N DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	<u> </u>	
	T		1	1 ACCESSION	DESCRIPTION	P VALUE	
					(Z99709) similar to Elongation	 	
1			İ	1	factor Tu family (contains	ſ	
l	i	İ	ļ		ATP/GTP binding P-loop);		
ļ	i ·			ĺ	cDNA EST EMBL:D76223	1 :	
ł	1	Cow dopamine		!	comes from this gene; cDNA	1 1	
	Ì	transporter mRNA,		· .	EST yk478c5.5 comes from this	i i	
432	M80234	putative cds.	0.55	3874972	gene [Caenorhabditis elegans]	4e-04	
1					(Z68314) similar to G-protein;	1007	
	ł	İ			cDNA EST EMBL:C11959		
	1	1 .	i		comes from this gene; cDNA	! !	
İ					EST EMBL:C10341 comes	[· [
	1	Ī	l j		from this gene; cDNA EST	i 1	
l	l		1 1		yk494e4.3 comes from this		
Ī	Ì]		gene; cDNA EST yk448a8.5		
	1		1 1		comes from this gene comes		
	ł		1 1		from this gene; cDNA EST		
	1]]		EMBL:C10341 comes from this	Í	
			1		gene; cDNA EST yk494e4.3	ı	
					comes from this gene; cDNA		
		ļ	1 1		EST yk448a8.5 comes from this	1	
] [•	gene [Caenorhabditis elegans]	1	
		ļ	1 1		>gi 3880364 gnl PID e1349948		
1			1		(Z83016) similar to G-protein;	ł	
			1		cDNA EST EMBL:C11959	Ī	
			1		comes from this gene; cDNA	- 1	
i]		EST EMBL:C10341 comes	i	
- 1			1		from this gene; cDNA EST	- 1	
					yk494e4.3 comes from this	İ	
I		Human I kappa B	1		gene; cDNA EST yk448a8.5	ľ	
433		epsilon (IkBe)	1	•	comes from this gene	İ	
433	U91616	mRNA, complete cds	0.55	3875577	[Caenorhabditis elegans]	7e-06	
1		Arabidopsis thaliana			·		
- 1		Atpk7 gene for serine/threonine	1		(Z81505) Similarity to		
j		protein kinase.	į į		Metanococcus hypothetical	ı	
434		complete cds	055	307/075	protein 0682 (TR:Q58095)		
		Swinepox virus	0.55	3876072	[Caenorhabditis elegans]	4e-42	
i		complete ORFS			ļ i	1	
		C20L-C1L > ::		i		j	
- 1		gb 158297 158297	- 1			1	
		Sequence 14 from			·	ł	
435		patent US 5651972	0.54	<none></none>	NONE	MONE:	
				411011162	<none></none>	NONE>	
- 1	[1	-Tuman	-				
- 1		mmunodeficiency	i	1	· · · · · · · · · · · · · · · · · · ·		
436	Z92653	rirus type 1 env gene	0.54	<none></none>	<none></none>	NONE>	

548 5	Neares	t Neighbor (BlastN vs.	Genhank)	Negrae Maia	thos (Blast V us N - D 1	<u> </u>
SEC		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Conduit.	TACTICST IAGIS	hbor (BlastX vs. Non-Redundant	Proteins)
Б	ACCESSIO	N DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUI
<u> </u>	 	- dolambacahata				
l		E.coli phosphate- repressible	1			<u> </u>
1	1	periplasmic	1.	i	1	1
1	ł	phosphate-binding	_			
1	I	protein (phoS),				1
1	Í	peripheral membran	_]			[
1	ł	proteins (pstC, pstB	⁼			1
Ĭ.		and phoU) and		1		j
į.	ŀ	integral membrane	İ	į.		l
1	•	protein (pstA) genes	İ	ì	· ·	ĺ
437	K01992	complete cds.	0.54	27027		1
<u> </u>	101772	Plasmodium	0.54	<none></none>	<none></none>	<none></none>
1	1	falciparum			ì]
1		chromosome 2.				1
1	I	section 52 of 73 of			i .	1
1	ł	the complete	1			1
438	AE001415	sequence	0.54	<none></none>	<none></none>	<none></none>
1						CAOIVES
1	j	Helianthus tuberosus	1			1
		lectin 2 mRNA,	1			
439	AF064030	complete cds	0.54	<none></none>	<none></none>	<none></none>
440	Viacoi	E.coli plasmid DNA				
440	X12591	for colicin E9	0.54	<none></none>	<none></none>	<none></none>
ľ		Caenorhabditis	j		}	
1 1		elegans YNKI-a	1 1		1	1 [
441	U73679	mRNA, complete cds	0.54	<none></none>		1
		Unidentified	0.54	ZHONES.	<none></none>	<none></none>
		bacterium DNA for				1 1
442	Z93990	16S ribosomal RNA	0.54	<none></none>	<none></none>	NONT
		B.vulgaris mRNA for		4.025	(Z37980) ORF12 [Escherichia	<none></none>
443	X85967	betavulgin	0.54	757836	coli)	8.3
· 1				· · · · · · · · · · · · · · · · · · ·		
ı		Sambucus nigra	!			} j
l		ribosome inactivating	j			1
444		protein precursor			(M80653) tetraheme	
444	U76524	mRNA. complete cds	0.54 .	151377	[Pseudomonas stutzeri]	6.2
ł	1					
J	Į.	H.sapiens gene for 5S				
1		rRNA (640 bp) > ::	1	i		1
j		emb X71801 HS5SR6	- 1			· }
ŀ		40B H.sapiens gene	Í		() F001016 \ T	j
445		for 5S rRNA (640 bp)	0.54	3222652	(AE001216) T. pallidum	
		Human mibp gene.		3322653	predicted coding region TP0369 (U62253) 16kDa secretory	2.7
446		partial cds	0.54		protein [Sus scrofa]	22
				1027403	protein (Sus scrota)	2.2

-170	Negross	Mainhhan (Dlass) in C				
	ivealest	Neighbor (BlastN vs. C	enoank)	Nearest Neig	hbor (BlastX vs. Non-Redundant I	roteins)
SEQ	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUI
		Rattus norvegicus Q-			(AJ005583) p75 protein	
447	L16013	like gene sequence	0.54	3087760	[Crypthecodinium cohnii]	0.95
448	U60275	Capra hircus skeletal muscle voltage-gated chloride channel gClC-1 mRNA, partial cds	0.54	1781344	(Y10438) FK506 polyketide synthase	0.95
449	U36795	Myxococcus xanthus rfbABC O-antigen biosynthesis operon, rfbA, rfbB, and rfbC genes, complete cds.	0.54	3877232	(Z81540) predicted using Genefinder	0.74
450	AF053091	Drosophila melanogaster eyelid (eld) mRNA, complete cds	0.54	2144110	zinc finger protein RIZ - rat	0.14
451	V00602	Genome of the bacteriophage fd (Inoviridae).	0.54	2661620	(AL009197) hypothetical	0.11
452	ļ	Human semaphorin (CD100) mRNA, complete cds	0.54	126692	KERATIN, ULTRA HIGH- SULFUR MATRIX PROTEIN (UHS KERATIN) >gi 109116 pir A36686 ultra- high-sulfur keratin - sheep >gi 1306 (X55294) ultra high- sulphur keratin protein [Ovis	
7,52		complete cas	0.54	125682	aries	0.003
					(Z99709) similar to Elongation factor Tu family (contains ATP/GTP binding P-loop); cDNA EST EMBL:D76223 comes from this gene; cDNA	
ì		S.coelicolor secD,	ł		EST yk478c5.5 comes from this	
453	X85969 s	ecF & apt genes	0.54	3874972	gene [Caenorhabditis elegans]	7e-06
		H.sapiens mRNA for DAN26 protein,			(Z70750) similar to vanadate resistance protein transmembranous domains	
454	Y08265 p	artial	0.54	3875131	[Caenorhabditis elegans]	5e-12

A.	Nearest	Neighbor (BlastN vs. (Cambra-la)	1		
		Neignbor (Blastin vs. (Jenbank)	Nearest Neig	hbor (BlastX vs. Non-Redundant)	Proteins)
SEQ			1		· ·	1
B	ACCESSION		P VALUE	ACCESSION	DESCRIPTION	P VALUE
<u> </u>	-	Hydromantes				
		platycephalus				
1	ĺ	cytochrome b (cytb)	1			1
1	1	gene, mitochondrial	1		·	1
1		gene encoding	ļ	İ	1 .	1
1,55		mitochondrial	Ì	1	•	ł
455	U89613	protein, partial cds	0.53	<none></none>	<none></none>	<none></none>
1		Habrobracon hebetor	i			
1	İ	cytochrome oxidase	ł	ł	1	
i		II gene, partial cds;	I			1
1		and tRNA-Asp, tRNA	1			
1	i	His, and tRNA-Lys]			ļ.
1	ŀ	genes, complete		i		1 1
1	·	sequence,		İ		1 1
		mitochondrial genes			1	1 1
}		for mitochondrial				1 1
456	AF034597	products	0.53	<none></none>	<none></none>	1
			0.05	- CHOILES	ZNONES	<none></none>
1 1		Yeast (S.cerevisiae)				1 1
1 1		tau repetitive element	į		1	1
457	K02653	and Cys-tRNA.	0.53	<none></none>	<none></none>	<none></none>
		Human mRNA for				CHOINES
450		actin-binding protein			bullous pemphigoid antigen 2 -	1 1
458	X53416	(filamin)	0.53	2134839	human	6.2
i i			1			
		Drosophila	•			
! !	1	subobscura alchohol	l	•	1	
j j		dehydrogenase (Adh)		•		
	The state of the s	gene, and alchohol	[
[dehydrogenase (Adh-	Ì]
! [dup) gene, complete	1	•	Land to the state of	l l
459		eds's.	0.53	2126965	hair keratin cysteine rich protein	1
			0.23	2136865	- sheep	2.1

7	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
	inearest r	veignbor (Blasuv vs. U	cnoank)	ivemest iveight	DOI (BIASIA VS. 14011-REGUNGANT PT	otenis)	
SEQ		DESCRIPTION.	DVALIE	A COTTONION	DESCRIPTION	D 1/41 III	
D	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
-		Methanobacterium				 _	
		thermoautotrophicum					
		methylene-					
1		tetrahydromethanopte			HYPOTHETICAL 91.6 KD		
		rin dehydrogenase			PROTEIN IN HXT8-CRT1		
		(mtd),			INTERGENIC REGION		
		imidazoleglycerol-			>gi 1078261 pir S50773		
		phosphate			probable membrane protein		
]		dehydrogenase			YJL212c - yeast		
		(hisB), and putative			(Saccharomyces cerevisiae)]	
] [ferredoxin (fdxA)			>gi 496950 (Z34098) ORF		
		genes, complete cds.			[Saccharomyces cerevisiae]		
		orf9 gene, partial cds,			>gi 1015596 (Z49487) ORF		
460	U19362	orfs	0.53	731969	YЛL212c	0.54	
					GERM CELL-LESS PROTEIN		
					fruit fly (Drosophila		
		Rattus norvegicus			melanogaster) >gi 157490		
		mRNA for MEGF1.			(M97933) germ cell-less protein	1	
461	AB011527	complete cds	0.53	417037	[Drosophila melanogaster]	3e-06	
1	,	Bacillus firmus MsyB			,		
		gene, 5' upstream					
462	U64313	region and partial cds Caenorhabditis	0.52	<none></none>	<none></none>	<none></none>	
1 1		elegans paraquat			1		
		responsive protein					
1 1		(CePqM132) mRNA,					
463	AF008590	complete cds	0.52	<none></none>	<none></none>	<none></none>	
		Mus saxicola	Í				
		spermidine/spermine			1		
		N1-acetyltransferase		•	·		
l l		(SSAT) gene.			\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	NONT	
464	L10245	complete cds.	0.52	<none></none>	<none></none>	<none></none>	
					FACTOR IB PRECURSOR		
		Arabidopsis thaliana	ļ		(IGF-IB) (SOMATOMEDIN C)	1	
		cellulose synthase			>gi 69361 pir IGHU1B insulin-		
! i		catalytic subunit (Ath-			like growth factor IB precursor -		
] i		A) mRNA, complete	·]		human prepropeptide [Homo		
465	AF027173	cds	0.52	124263	sapiens]	7.7	

WO 01/02568 PCT/US00/18374

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
鐵業	Nearest N	Neighbor (BlastN vs. Ge	nbank)	Nearest Neighbor (Blasca Vs. Non Redundar Florance)			
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
		Caenorhabditis					
		elegans cosmid					
1		H31B20, complete			1		
		sequence			1		
		[Caenorhabditis			(D88451) aldehyde oxidase [Zea		
466	AL021066	elegans]	0.52	2589162	mays]	6.0	
					(U39850) coded for by C.		
					elegans cDNA yk37g1.5; coded		
					for by C. elegans cDNA		
			1		yk5c9.5; coded for by C.		
l		Porphyra linearis 18S			elegans cDNA ykla9.5;		
		ribosomal RNA gene,			alternatively spliced form of		
467	AF038588	3' partial sequence	0.52	1055055	F52C9.8b	4.6	
					1		
		Borrelia burgdorferi	1	•			
1		(section 11 of 70) of	i		(AB021287) polyprotein	ا مما	
468	AE001125	the complete genome	0.52	4115827	[Hepatitis G virus]	2.0	
					(U41534) coded for by C.	1 1	
ł	ì	Drosophila	,		elegans cDNA CEESI42F;		
1		melanogaster Ste20-]		Similar to helicases of	1	
		like protein kinase	ļ		SNF2/RAD54 family.	0.002	
469	AF006640	mRNA, complete cds	0.52	1109830	[Caenorhabditis elegans]	0.002	
		Aplysia californica					
1		ubiquitin carboxyl-			1		
1		terminal hydrolase				1	
		(Ap-uch) mRNA.		NO.	<none></none>	<none></none>	
470	U90177	complete cds	0.51	<none></none>	KNONES	Q.O.L.	
	1	S.cerevisiae				1	
1		chromosome XI			i		
1		reading frame ORF	0.51	<none></none>	<none></none>	<none></none>	
471	Z28304	YKR079c	0.51	<nune></nune>	ZIVOI122		
1	1	Caenorhabditis		•			
1		elegans cosmid	1			!	
1.	1.	R03E1, complete		· '		1	
		sequence	1		HYDROPHOBIC SEED		
1	700007	[Caenorhabditis	0.51	′123506	PROTEIN (HPS)	7.6	
472	Z92837	elegans Mouse mRNA for	0.51	123300	1,0120,0120,		
1		RecA-like protein	1				
1	1	MmRad51, complete	1		(AB014607) KIAA0707 protein		
1,77	D12002	1	0.51	3327228	[Homo sapiens]	4.5	
473	D13803	cds	0.51	332,323	1		
1	1		}		(AE001299) hypothetical	}	
474	X07187	Pea hsp21 mRNA	0.51	3328678	protein [Chlamydia trachomatis]	4.4	
4/4	A0/10/	Ir ca napar matter	1				

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEQ		reighbor (Blasua Vs. G	endank)	Nearest Neigh	bor (BlastX vs. Non-Redundant F	roteins)	
EQ ED	ACCESSION		P VALUE	ACCESSION	DESCRIPTION	P VALUE	
		CCAAT/enhancer-				1	
		binding protein			 		
1	ł	delta=transcription					
!	1	factor CRP3 homolog			İ	I	
l	1	(human, prostate				į.	
1	ŀ	carcinoma cell line			(D90911) apolipoprotein N-	ł	
I		LNCaP, Genomic,			acyltransferase [Synechocystis	I	
475	S63168	1594 nt]	0.51	1653215	sp.]	1.2	
476	V/C7070	Xenopus laevis C2- HC type zinc finger protein X-MyT1			(AF067520) PITSLRE protein kinase beta SV2 isoform [Homo		
476	U67078	mRNA, complete cds	0.51	3850320	sapiens)	0.17	
477	L38933	Homo sapiens GT198 mRNA, complete ORF	0.51	3219965	HYPOTHETICAL 100.6 KD TRP-ASP REPEATS CONTAINING PROTEIN C2C6.04C IN CHROMOSOME		
		Lycopersicon		3217703		0.059	
478	AF001000	esculentum polygalacturonase 1	0.50	<none></none>	<none></none>	<none></none>	
		S.cerevisiae chromosome XI reading frame ORF					
479		YKR079c	0.50	<none></none>	<none></none>	<none></none>	
480	X97225	Oncorhynchus keta IGF-II gene	0.50	<none></none>	<none></none>	<none></none>	
481	. 6	Homo Sapiens, RP58 DNA for complete nRNA	0.50)/O/E			
70.1	73001300	MININ	0.50	<none></none>	<none></none>	<none></none>	

4	Nearest	Neighbor (BlastN vs. (ienhank)	Negros N-:-	hhor (BlessV N. D.	D
SEC		Treighter (Blasa v vs.)	Jenoank)	Memest Meig	hbor (BlastX vs. Non-Redundant	Proteins)
D	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUI
		Homo Sapiens, RP58				T VALUE
		cDNA for complete	1			
481	AJ001388	mRNA	0.50	<none></none>	<none></none>	<none></none>
		P.occultum 23S			1 310112	CNONES
l	•	ribosomal RNA,	1]		
482	M86626	partial cds.	0.50	<none></none>	<none></none>	<none></none>
					CHROMOSOME ASSEMBLY	/ UNDIVE
1	1		1		PROTEIN XCAP-E African	
	1	Sambucus nigra lectin	Í		clawed frog >gi 563814	i
	1	precursor mRNA,	l	j	(U13674) XCAP-E [Xenopus	1
483	U76523	complete cds	0.50	1722856	laevis]	3.2
1	·					
	. ====	Mus musculus striatin		ł	(M63730) BPAG2 [Homo	1
484	AF031663	mRNA, complete cds	0.50	179521	sapiens]	3.2
l		**				
	ł	Haemophilus influenzae Rd section				
	1	44 of 163 of the				1 .
485	U32729		0.50	2055400	(Z92829) F10A3.15	1 .
1	032129	complete genome Dictyostelium	0.50	3875699	[Caenorhabditis elegans]	0.65
	1	discoideum clone			HYPOTHETICAL 28.3 KD	1
İ	ì	9.10 Tdd-3 and RED	i		PROTEIN IN GBD 5 REGION	1 1
		repetitive elements.			(ORF4) >gi 2120954 pir 139562	1
486	AF067198	partial sequence	0.50	2494740	ORF4 - Alcaligenes eutrophus	
	10000	Human interleukin 4		2494740	>gi 695274 (L36817) ORF4	0.008
		(IL-4) gene, complete	1			1 1
487	M23442	cds.	0.49	<none></none>	<none></none>	SNONTE
				410112	KNONES	<none></none>
	ì	Caenorhabditis) <u> </u>
		elegans POU			(AF098499) contains similarity	
		homeobox protein	1		to Saccharomyces cerevisiae	!!
		CEH-18 (ceh-18)	· 1		MAF1 protein (GB:U19492)	
488		mRNA, complete cds.	0.47	3786409	[Caenorhabditis elegans]	8.9
		Lycopersicon	1			
400	1	esculentum	1]	
489		polygalacturonase 1	0.45	<none></none>	<none></none>	<none></none>
	1	Yersinia	1			
490		enterocolitica wbb			1	į
490		gene cluster Human mRNA for	0.41	<none></none>	<none></none>	<none></none>
		KIAA0230 gene,	i	•		
491		cartial cds	0.36	20/7:5	(M64793) salivary proline-rich	1
```	200783	om tial Cus	0.35	206712	protein [Rattus norvegicus]	4e-05
]	,	Helianthus tuberosus	l			i
- 1		ectin 2 mRNA,	j		!	1
492		omplete cds	0.33	NONE		
	=	Cimpieto eus	0.55	<none></none>	<none></none>	<none></none>

	Neares	t Neighbor (BlastN vs. (Tenhank)	Nesses M-:-	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEC	2	1 211001 (Diasut VS. (Jenoank,	ivearest Neig	nbor (BlastX vs. Non-Redundant	Proteins)		
D	ACCESSIO	DESCRIPTION.	l			Ţ		
<u> </u>	TACCESSION		P VALUE	ACCESSION	DESCRIPTION	P VALUE		
-	+	Vitreoscilla sp. outer						
]	i	membrane protein	1			 		
	1	homolog gene,		[
]	I	complete cds; Trp				j		
1	1	repressor binding		1	j	1		
1	Į.	protein gene, partial	l	ł	HYPOTHETICAL 24.5 KD	1		
493	45065000	cds; and unknown	Ì		PROTEIN IN NADB-SRMB	I		
493	AF067083	genes	0.33	401553	INTERGENIC REGION	8.3		
İ	ł	Don't have a	ł					
j	l	Papio hamadryas		1	[
494	Y15520	anubis gene encoding			1	1		
1 474	.113320	fertilin alpha-II	0.29	2408049	(Z99164) hypothetical protein	3.1		
1					ARYL HYDROCARBON			
1		·			RECEPTOR NUCLEAR	1		
1					TRANSLOCATOR	1		
		Alaman			HOMOLOG (DARNT)	1		
1	1	Alestes sp.	i		(TANGO PROTEIN)	1 1		
495	U33475	ependymin mRNA,			transcription factor [Drosophila	1 1		
475	033473	partial cds Mouse DNA for 8-	0.28	3913078	melanogaster]	1.4		
Į,		oxodGTPase.						
496	D88356	complete cds	0.00					
1,50	200330	Methanococcus	0.22	<none></none>	<none></none>	<none></none>		
1		jannaschii section 145	į					
1 1		of 150 of the	l			i 1		
497	U67603	complete genome	0.22	22222	(U51222) p40 [Streptomyces	1		
	007005	complete genome	0.22	2209261	halstedii]	8.3		
		Malurus cyaneus	i		droots .			
498		microsatellite McyU2	0.22	992631	(U29131) Mg-chelatase subunit			
		S.cerevisiae	0.22	392031	[Synechocystis sp.]	0.56		
j i	1	chromosome X	į					
ļ [reading frame ORF	į					
499	_	YJR125c	0.21	<none></none>	310377			
		Dictyostelium		VIONES	<none></none>	<none></none>		
	į.	discoideum AX2	1			1		
ł	l _i	protein tyrosine	ł			i		
j		kinase gene, complete	- 1			ł		
500		ds.	0.21	<none></none>	NONE			
				ZITOITES	<none></none>	<none></none>		
ļ	1	Human prostate-	İ		1			
- 1		pecific antigen (PA)	1		(Y07018) gaza 12 I	1		
501		ene, complete cds.	0.21		(X97918) gene 12.1 [Bacteriophage SPP1]			
				2,07033	Dacteriophage SPP1]	6.0		

11	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEQ		1		remest reignoof (Diasta vs. Non-Redundant Proteins)			
Ð	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
<u> </u>					u0002b protein -		
ĺ	•				Mycobacterium tuberculosis	1	
1	Į		į.		tuberculosis]	ł	
	1]	>gi 1694863 gnl PID e283373	l	
١.	ł	B.taurus mRNA for		1	(Z83018) hypothetical protein	J	
	W07410	thrombospondin	i .	•	Rv2968c [Mycobacterium	ľ	
502	X87618	(partial) 2162 bp	0.21	2146000	tuberculosis]	3.5	
	Į.	B.taurus microsatellite	1	ł			
503	X71591		1 000		1		
303	X/1391	sequence INRA048 Human germline	0.21	1354453	(U52830) orf [Homo sapiens]	2.7	
		immunoglobulin	j	1	ì	1	
		lambda light chain			propollogos bee Welste 2	1	
504	X57808	gene	0.21	2119158	procollagen type V alpha 2 -		
		B	0.21	2113120	mouse >gi 309181 HYPOTHETICAL 78.8 KD	2.7	
			1		PROTEIN IN ABF2-CHL12		
			Ì		INTERGENIC REGION	!	
1					>gi 1078003 pir \$52835]	
					hypothetical protein YMR075w]	
		Xenopus laevis	1 1		yeast (Saccharomyces		
		mitotic	i		cerevisiae) >gi 763022		
		phosphoprotein 44			(Z48952) unknown		
505	U95098	mRNA, partial cds	0.21	2497139	[Saccharomyces cerevisiae]	2.0	
	:		1 1		UDP-		
			1 1		GLUCOSE:GLYCOPROTEIN		
		Mycobacterium	1 1		GLUCOSYLTRANSFERASE		
		fortuitum plasmid	1 1		PRECURSOR (DUGT)	1	
		pJAZ38 replication	1 1		glucosyltransferase - fruit fly		
- 1		protein Rep (rep)	•		(Drosophila sp.)	1	
506	T I	gene, complete cds	0.21	2499087	glucosyltransferase precursor [Drosophila melanogaster]	0.000	
					n Diosophila mejanogasterj	0.003	
Ì		Rattus norvegicus	·			Ì	
- 1	. [nonmuscle myosin		•		j	
ľ		heavy chain-A	. 1		(Z81130) predicted using	j	
507	U31463	mRNA, complete cds.	0.21	3880111	Genefinder	0.002	
1	į,				LRR47 protein - fruit fly		
1	i i	Rabbit mRNA for	- 1		(Drosophila melanogaster)	1	
50P		aminopeptidase N	1		>gi 415947 (X75760) LRR47	. 1	
508		(partial)	0.21	630864	[Drosophila melanogaster]	le-06	
		Homo sapiens full ength insert cDNA	ł				
509		clone ZD88F12	0.20	-NO.			
		Helicobacter pylori	0.20	<none></none>	<none></none>	<none></none>	
- 1		plasmid pHPM186.	1	·			
510		complete sequence	0.20	<none></none>	<none></none>	ANONT:	
511		gunnii CAD gene.	0.20	<none></none>		<none></none>	
			0.20	CITOINES	CNONES (<none></none>	

12.0	Nearest	Neighbor (BlastN vs. G	enhank)	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEQ		T Signoor (Diable) vs. C	ichowik,	14641621 14618	indor (Blasta vs. Non-Redundant F	roteins)	
E	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
	T T	T.aestivum		i necession	J DESCRIPTION	PVALUE	
		mitochondrial nad7				 -	
	l	gene for NADH	l	ì	i		
ı	ľ	dehydrogenase		į.	j		
512	X75036	subunit 7	0.20	<none></none>	<none></none>	1	
		E.coli genomic DNA,		310112	CNONES	<none></none>	
1		Kohara clone			1.		
513	D90875	#422(55.5-55.8 min.)	0.20	<none></none>	<none></none>	NONTO	
		Caenorhabditis		3.02	- Grones	<none></none>	
1		elegans cosmid				J	
1		F59B8, complete				İ	
		sequence			}	1 :	
1		[Caenorhabditis			1	1	
514	Z68343	elegans]	0.20	<none></none>	<none></none>	<none></none>	
1		M.musculus V alpha				4.07.02	
515	X62486	11.1 gene 5'-region	0.20	<none></none>	<none></none>	<none></none>	
]		1			PHOSPHORYLASE B		
1			Ì		KINASE ALPHA	i i	
1 1			•		REGULATORY CHAIN.	1	
			i		SKELETAL MUSCLE	1	
	<u> </u>		ĵ		ISOFORM	i 1	
1	į	ļ	J		(PHOSPHORYLASE KINASE		
		Caenorhabditis	j		ALPHA M SUBUNIT)	1	
		elegans cosmid	i		>gi 2135923 pir 138111	1	
516	AF040651	W04H10	0.20	1150/00	phosphorylase kinase (EC		
" 	711 040031	WU4HIU	0.20	1170683	2.7.1.38) - human >gi 791043	7.4	
1 1		Pseudomonas		•	}		
		fluorescens PHA	4		1	1	
!]		depolymerase (phaZ)	1		(AB016024) Pfj2 [Plasmodium		
517		gene, complete cds.	0.20	3721862	falciparum)	1.9	
		Human mRNA for			LAMININ ALPHA-I CHAIN	1.7	
	j	KIAA0194 gene,	1		PRECURSOR precursor -	j	
518	D83778	partial cds	0.20	126363	human	0.65	
					(AC004908) similar to	- 0.05	
		c-scr=pp60c-src,	j		ribosomal protein L23a; similar		
		sdr=src downstream	1		to P29316 (PID:g132848)	İ	
519		egion	0.20	4159887	[Homo sapiens]	0.52	
- 1	l l	Vius musculus Balb/c					
- 1		prain-specific kinase	j]]	
570		Bsk) mRNA.			(M64793) salivary proline-rich		
520	U07357 c	omplete cds.	0.20	206712	protein [Rattus norvegicus]	0.51	

11112	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
	14carest 1	reignoor (Blasur vs. C	Circaik)	The sale religious (Diaste vs. 14011-Reduited in Fiolettis)			
SEQ	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
		Penicillium thomii					
}		internal transcribed	l i			İ	
1 1		spacer 1, 5.8S				1	
1 1		ribosomal RNA gene			İ		
(i		and internal			AMINO-ACID		
	,	transcribed spacer 2,			ACETYLTRANSFERASE	1	
		complete sequence;			Pseudomonas aeruginosa	Ì	
		and 28S ribosomal			>gi 151036 (M38358) N-	ł	
		RNA gene, partial			acetylglutamate synthase	<u>†</u>	
521	AF034460	sequence	0.20	114136	[Pseudomonas aeruginosa]	0.39	
				• .	ASSOCIATING FACTOR 1 (B	<u> </u>	
j 1					CELL-SPECIFIC	1	
					COACTIVATOR OBF-1) (OCT		
					BINDING FACTOR 1) (BOB-	l	
				•	1) (OCA-B) Bobl, B-cell-	ļ	
					specific - mouse	İ	
			•		>gi 1881818 bbs 179852		
} }					mBobl=B-cell specific	1	
1		Xenopus laevis			transcriptional coactivator line	ł	
1		mitotic	İ		J558L, Peptide, 256 aa]	İ	
1		phosphoprotein 44	ł		>gi 1353792 (U43788) Oct	i	
522	U95098	mRNA, partial cds	0.20	2842674	binding factor 1 [Mus musculus]	0.073	
					(AL032643) similar to		
					Uncharacterized protein family		
		'			UPF0034, Double-stranded		
					RNA binding motif; cDNA EST		
	Į		1		yk489b3.5 comes from this		
		e tinidana antica	[gene; cDNA EST yk439g7.5		
523		S.lividans groEL2	0.20	202527	comes from this gene	ا م ر	
323	X95971	gene Ovis aries	0.20	3925277	[Caenorhabditis elegans]	4e-19	
		vasopressin VI	j	<i>.</i> *.			
· [T I	receptor (VIR) gene,	•		·		
524		complete cds	0.19	<none></none>	<none></none>	<none></none>	
		K.pneumoniae		3.01122	31.0112	2.01.22	
·	i,	oxalacetate	1				
ŀ	[·	decarboxylase alpha					
į	J:	subunit gene.	1			Į	
525		complete cds.	0.19	<none></none>	<none></none>	<none></none>	
	1	Helicobacter pylori,				•	
		strain J99 section 12			!	1	
]		of 132 of the	i		.	1	
526	AE001451	complete genome	0.19	<none></none>	<none></none>	<none></none>	

24608	Naarra	Maiabhas (BlassNI C		Manus Mainhar (Diany) as Non Dada and Dada			
12.72.34		Neighbor (BlastN vs. G	enbank)	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
<u> </u>						T	
		Pedicularis verticillata chloroplast DNA, intergenic region between trnT(UGU)					
527	D88084	and trnL(UAA)5'exon	0.19	<none></none>	<none></none>	<none></none>	
528	U67599	Methanococcus jannaschii section 141 of 150 of the complete genome	0.19	<none></none>	<none></none>	<none></none>	
		Human beta-spectrin (SPTB) mRNA,			,		
529	J05500	complete cds.	0.19	<none></none>	<none></none>	<none></none>	
620	V10127	M.mycoides ftsY gene homologue and gene encoding	0.5	\\a\=			
530	Y10137	hypothetical protein	0.19	<none></none>	<none></none>	<none></none>	
531	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.19	<none></none>	<none></none>	<none></none>	
532		Mouse thymic stromal cell mRNA for TLSF-beta, complete cds	0.19	<none></none>	<none></none>	<none></none>	
533	AJ012585	Tetrahymena thermophila macronuclear gene encoding ribosomal protein L3, exons 1-2	0.19	<none></none>	<none></none>	<none></none>	
534	V51475	Brassica napus 5- enolpyruvylshikimate- 3-phosphate synthase gene	0.19	<none></none>			
	1	Sambucus nigra			<none></none>	<none></none>	
535		nRNA. complete cds	0.19	<none></none>	<none></none>	<none></none>	
536	1	Scerevisiae chromosome X reading frame ORF YJR125c	0.19	<none></none>	ANONT:	NOTE	
			U.17	THOINES	<none></none>	<none></none>	

建	Nearest	Neighbor (BlastN vs. (Genbank)	Negret Naighbor (Blast Vive Non Bedander Brasin)			
SEQ		TALIBOT (DIASET VS. C	Jenouik)	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
		H.sapiens pilot				T-11202	
537	X63741	mRNA	0.19	<none></none>	<none></none>	<none></none>	
538	Y11255	O.latipes mRNA for annexin max4	0.10			1410112	
1000	111233	annexiti max4	0.19	<none></none>	<none></none>	<none></none>	
539	L63537	Oncorhynchus mykiss (clone Jb-10) beta-2 microglobulin (B2m) mRNA. complete cds.		<none></none>	<none></none>	Nove	
		N.tobacum T92 gene		4.02	CHONES	<none></none>	
540	X70903	for auxin-binding protein	0.19	<none></none>	<none></none>	<none></none>	
	-	Caenorhabditis				TATORES	
	l	elegans cosmid	·			1	
541	U61958	C25A8	0.19	<none></none>	<none></none>	<none></none>	
5.00		Macaca fascicularis fertilin beta mRNA,					
542	U33959	complete cds	0.19	<none></none>	<none></none>	<none></none>	
543	Z49835	H.sapiens mRNA for protein disulfide			(Z95556) hypothetical protein		
1 343	249633	isomerase	0.19	2113940	Rv2507	9.4	
544	A 5025 450	Spinacia oleracea heat shock 70 protein			PROBABLE E4 PROTEIN papillomavirus (type 1) >gi 61015 (X62844) E4 gene product [Pygmy chimpanzee		
344	AF035458	protein, complete cds	0.19	267293	papillomavirus type 1]	9.4	
545	U23441	Tetrahymena thermophila B internal deletion sequence.	0.19	3877185	(Z66563) F46C3.2		
		Pneumocystis carinii		3677163	[Caenorhabditis elegans]	9.3	
546	i	major surface glycoprotein	0.19	3548901	(AF052502) DA26 homolog [Epiphyas postvittana nucleopolyhedrovirus]	9.3	
547		Rat ankyrin binding glycoprotein-1 related mRNA sequence.	0.19	3337352	(AC004481) putative chromatin structural protein Supt5hp		
		Methanococcus jannaschii section 102 of 150 of the			(Y13585) serotonin receptor 4	9.1	
548		complete genome	0.19	3183689	[Cavia porcellus]	.,	
549	l R R	Mus musculus pacteria binding macrophage receptor MARCO mRNA.			(AF089083) complement	8.7	
	210724	complete cds.	0.19	3659853	component ClqB like protein	7.1	

	Negross	Maiathas (Blass)		Name Victor (D)			
		Neighbor (BlastN vs. C	Jenbank)	Nearest Neig	hbor (BlastX vs. Non-Redundant Pr	oteins)	
SEQ				1		Î	
ID	ACCESSION	DESCRIPTION	PVALUE	ACCESSION	DESCRIPTION	P VALUE	
<u> </u>					(U58751) C07G1.7 gene		
1					product [Caenorhabditis	 	
550	X66467	C.albicans sec 18 gene	0.19	1326385	elegans]	6.9	
1	l		ł		DIHYDROPYRIMIDINASE		
1		Syngaster lepidus 16S			(DHPASE) dihydropyrimidinase	1	
l		ribosomal RNA gene,	1		- rat		
551	AF003487	partial sequence	0.19	3122039	>gi 1378019 gnl PID d1010479	6.9	
1		Rat calmodulin-	}				
1	[sensitive plasma			1.		
ì		membrane Ca2+-		i			
1	ĺ	transporting ATPase			hypothetical protein - fruit fly		
1				1	(Drosophila melanogaster)		
552	J05087	(PMCA3) mRNA,	0.10		>gi 296434 (X68408) ORF		
1332	103087	complete cds. Homo sapiens	0.19	422462	[Drosophila melanogaster]	5.3	
1	1	glutamate					
1	Ĭ.	oxaloacetate		ľ	PROBABLE E4 PROTEIN	ı	
553	AF080464	transaminase	0.19	2024024	>gi 790898 position 32863288	j	
1 335	71 000404	Human MEK kinase	0.19	3024834	is first start codon; putative	5.3	
		3 mRNA, complete			(7)700000	1	
554	U78876	cds	0.19	1710445	(U78083) unknown [Emericella		
	073070	Vigna radiata mRNA	0.19	1710445	nidulans]	5.3	
ļ i		for proton			(AP000002) 256aa long	Į.	
1 1		pyrophosphatase.			hypothetical protein		
555	AB009077	complete cds	0.19	3256922	[Pyrococcus horikoshii]	5.1	
				3230722	[1 viococcus norikosnii]	3.1	
i					(AF125463) contains similarity	1	
		Xenopus laevis	ı		to BTB (also known as BR-	1	
		mitotic	ı		C/Ttk) domains (Pfam:PF00651.	- 1	
		phosphoprotein 44	ì		Score=62.8, E=7.6e-15, N=1)	1	
556	U95098	mRNA, partial cds	0.19	4226159	[Caenorhabditis elegans]	4.1	
ı					(cacho nacaris cicaris)		
' I			ı	•	(AL031583) I-	1	
. 1	1		j		evidence=predicted by content;	I	
			ľ		1-method=genefinder;084; 1-	Į.	
I	ŀ	ĺ	- 1		method_score=47.46; 1-		
į		}	l l		evidence_end; 2-	- 1	
1]		ł		evidence=predicted by match; 2-	}	
· [ı	Escherichia coli K-12	ł		match_accession=SWISS-	1	
		MG1655 section 282	į		PROT:P23792; 2-		
ا ۔۔۔ ا	1	of 400 of the	1		match_description=DISCONNE	1	
557	AE000392	complete genome	0.19	3645960	CTED PROTEIN.; 2-matc	4.0	

	Nearest	Neighbor (BlastN vs. C	ienbank)	Nearest Neighbor (Blast X vs. Non-Redundant Proteins)			
SEC		The grider (Diagram of the Control o	T T	Memest Meik	nbor (Blast.) vs. Non-Redundant Pi	roteins)	
B	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
-	 	 				<u> </u>	
	·				(AL031583) 1- evidence=predicted by content; 1-method=genefinder;084; 1- method_score=47.46; 1- evidence_end; 2-		
558	AE000392	Escherichia coli K-12 MG1655 section 282 of 400 of the complete genome	0.19	3645960	evidence=predicted by match; 2-match_accession=SWISS-PROT:P23792; 2-match_description=DISCONNECTED PROTEIN.; 2-matc		
	,	Homo sapiens	<u>,</u>	3043300	CIED PROTEIN.; 2-maic	4.0	
559	L81774	(subclone 3_d1 from P1 H25) DNA sequence	0.19	4001725	(AB015981) MnhA [Staphylococcus aureus]	3.0	
560	AL021108	Drosophila melanogaster cosmid clone 137E7	0.19	4001688	(AB015718) protein kinase [Homo sapiens]	3.0	
561	AB001510	Carabus leptoplesioides mitochondrial DNA for NADH dehydrogenase subunit 5, partial cds	0.19	3758855	(Z98551) MAL3P6.11 [Plasmodium falciparum]	2.4	
562	AF069696	Egernia stokesii clone EST1 microsatellite	0.19	3328994	(AE001326) Amino Acid (Branched) Transport [Chlamydia trachomatis]	2.4	
563	X64144	F.pringlei ppcA1 gene for phosphoenolpyruvate carboxylase Human	0.19	3242974	(AF069555) G protein-coupled receptor p2y3 [Meleagris gallopavo]	2.3	
564		immunodeficiency virus type 1 gag polyprotein (gag) gene. partial cds	0.19	2257710	(U73041) resolvase-like protein [Thiobacillus ferrooxidans]	2.3	
		Danio rerio Notch		·	dependant epimerase/dehydratase family; cDNA EST EMBL:C10103 comes from this gene; cDNA EST EMBL:D66400 comes from this gene; cDNA EST EMBL:D70143 comes from this gene; cDNA EST	2.3	
565		complete cds	0.19		comes from	1.8	

WO 01/02568 PCT/US00/18374

22	選 Neares	t Neighbor (BlastN vs.	Genbank)	Nearest Neio	hbor (BlastX vs. Non-Redundant P	roteins\
SE				THE TOTAL PROPERTY.	1001 (Diastre vs. 14011-Redundant F	Totems)
п	- 1	N DESCRIPTION	PVALUE	ACCESSION	DESCRIPTION	
 	1		I VALUE	ACCESSION	DESCRIPTION	P VALUE
				 	masquerade precursor - fruit fly	ļ
İ		{			(Drosophila melanogaster)	1
	Ĭ		1		>gi 665545 (U18130)	
ł		}	i	Ì	masquerade [Drosophila	1
	4	R.norvegicus mRNA	1	ĺ	melanogaster]	!
56	6 Y12502	for factor XIIIa	0.19	2122602	>gi 1095942 prf 2110286A	
<u> </u>	1	Tor factor zerra	0.19	2133693	masquerade gene	1.8
	1		l		1	1
i	•	BB1=malignant cell	i .		1	1
1	1	expression-enhanced			1	}
1	. 1	gene/tumor	1		j .	
	1	progression-enhanced	1		· 1	
•		gene (human, UM-				İ
ļ	1	UC-9 bladder			(U77783) N-methyl-D-aspartate	
1	1	carcinoma cell line,			receptor 2D subunit precursor	
56	7 S82470	mRNA, 1897 nt]	0.19	2444026	[Homo sapiens]	1.8
ļ		Caenorhabditis				 -
	. [elegans cosmid]		225K protein - Babesia bovis	
568	U97408	F48A9	0.19	542433	(fragment)	1.8
1	i	Daniel and an an an] [
1		Pseudomonas fluorescens PHA	1 1		1	Ī
1	1	depolymerase (phaZ)				İ
569	U10470	gene, complete cds.	0.19	2701070	(AB016024) Pfj2 [Plasmodium	ŀ
1	0.0470	Ovis aries MAF214	0.19	3721862	falciparum]	1.7
1		locus polymorphic			(U56963) T13A10.5 gene	- 1
570	M88160	dinucleotide repeat .	0.19	1293816	product [Caenorhabditis	
			0.17	1293610	elegans	1.4
	1	mRNA for pollen			1	
ł	1	allergen (Hol I 2,	1		1	ł
1	1	group II) > ::	- 1		1	
		emb AJ131339 LIT13	1		1	
	1.	1339 Lolium italicum	. j	•	1 . 1	1
ļ	J.	mRNA for pollen			1	
	1	allergen (Lol i 2,	i		1	1
		group II) > allergen			1	Ē
		(Poa p 2, group II) >				
l		::	j			- (
		emb AJ131338 TAE1	1			i
		31338 Triticum	j		1	j
		aestivum mRNA for	İ]
571	AJ131336	pollen allergen (Tri a 2. group II)	0.0	3000	(AL032675) predicted using	1
		S.cerevisiae ARG8	0.19	3880447	Genefinder	0.82
572		and CDC33 genes	0.19	3882041	(1010105) hamadada	
		and CDC33 Selles	U.17	3882041	(AJ010405) hypothetical protein	0.62

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
	Nearest P	vergnoor (Blasus vs. C	CIIDAIIK)				
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
		Human WD protein			mucin - human >gi 501033		
		IR10 pre-mRNA.			(U14383) mucin [Homo		
573	U57058	partial cds	0.19	631302	sapiens	0.60	
		Penicillium thomii internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2,		•	AMINO-ACID ACETYLTRANSFERASE		
		complete sequence;			Pseudomonas aeruginosa	1	
	_	and 28S ribosomal			>gi 151036 (M38358) N-		
	•	RNA gene, partial			acetylglutamate synthase		
574	AF034460	sequence	0.19	114136	[Pseudomonas aeruginosa]	0.35	
		Xenopus laevis mitotic phosphoprotein 44			alpha-2-adrenergic receptor - human name 'ADRA2R' [Homo		
575	U95098	mRNA, partial cds	0.19	105270	sapiens	0.27	
576	AG001475	Homo sapiens genomic DNA, 21q region, clone: 125H6N2	0.19	94977	hypothetical protein 3 - Pseudomonas sp. (DSM 6898) plasmid pKB740 >gi 45867 (X66604) ORF3	0.16	
577	M63284	Mouse IgG receptor (beta-Fc-gamma-RII) gene, exons 9 and 10, clones lambda-Fc(3.2.93).	0.19	3024681	TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) of RNA polymerase II transcription factor TFIID [Homo sapiens]		
		Pseudomonas aeruginosa orotate phophoribosyl transferase (pyrE). catabolite repression control protein (crc) and RNasePH (rph)			(AF055904) unknown		
578	U38241	genes, complete cds	0.19	3044086	[Myxococcus xanthus]	0.052	
		Lontra longicaudis transthyretin intron 1.			pistil extensin-like protein (clone pMG14) - common tobacco (fragment) >gi 19927 (Z14015) pistil extensin like	0.020	
579	AF039734	partial sequence	0.19	322759	protein [Nicotiana tabacum]	0.030	
		Xenopus laevis XL- INCENP (XL- INCENP) mRNA,					
580	U95094	complete cds	0.19	2147194	collagen - Paralvinella grasslei	0.002	

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEC				inearest Meig	HUDE (Blasta vs. Non-Redundant P	roteins)	
ID		DESCRIPTION	D.V				
۳	ACCESSION	VI DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
-	 	Drosophila	ļ	 			
1		melanogaster mRNA					
	ł	for DAD polypeptide.				ł	
581	AB004232	complete cds	0.19	2400765	PEROXISOMAL MEMBRANE	1	
1 30.	12004232	Gallus gallus alpha-	0.19	2498765	PROTEIN PEX16 lipolytica	0.002	
j	1	globin gene domain 5'	1		(U41272) T03G11.6 gene	į į	
582	AF098919	region	0.19	1086863	product [Caenorhabditis elegans]		
	1	i cg.on	0.15	100000	eregans	4e-05	
		}	[į	•		
1	ł	<u> </u>					
	1						
	ł		İ	' '	(AL022018) 1-		
1	1				evidence=predicted by content;		
1					I-method=genefinder;084; 1-		
	J	1			method_score=165.48; 1-		
1	I	[i		evidence_end; 2-		
•	ł	Helicobacter pylori,			evidence=predicted by match; 2-		
1	İ	strain J99 section 18	÷		match_accession=AA264666; 2-	j	
1		of 132 of the			match_description=LD08351.5p	•	
583	AE001457	complete genome	0.19	2924552	rime LD Drosophila melanoga	3e-05	
i	[Plasmid RP4 traE	j				
1		gene, 3' end; traD			•		
584	L10329	gene, complete cds;	0.0		(Z49068) mitochondrial carrier		
364	L10329	traF gene, 5' end.	0.19	3878117	protein	8e-07	
1		Borrelia burgdorferi	ļ		(H28720) -iil TDD		
		(section 41 of 70) of	ŀ		(U28739) similar to TPR domains in e.g. yeast STI1	- 1	
585	AE001155	the complete genome	0.19	861276	protein [Caenorhabditis elegans]	2.12	
		Orf virus E10R		001270	protein [Caenornabditis elegans]	2e-12	
	' [homolog gene, partial	ł		1		
		cds, and DNA	j		(AL033385) dna-directed rna		
		polymerase gene.	[polymerase iii subunit	j	
586		complete cds	0.19	3850072	[Schizosaccharomyces pombe]	le-15	
ĺ		Xenopus laevis					
	· .	RanGTPase	}		(X91258) pid:e198503		
587	U88155	activating protein	0.19	995714	[Saccharomyces cerevisiae]	4e-16	
l	ł	. 1		 			
- 1	İ		i		(AC005164) match to ESTs	j	
ı	}	1	1		AA731149 (NID:g2140138),		
İ		Sahinaanahaan	ł		AA731908 (NID:g2752719),	1	
j		Schizosaccharomyces	į.		AA287837 (NID:g1933519),		
588	_ 1	combe Clr4p (clr4)	0,0 1	724277	AA262811 (NID:g1898382),	I	
300		gene, complete cds Scerevisiae CHS2	0.19	3242750	and AA825820 (NID:g2899132)	5e-19	
ł		gene encoding chitin	i				
589		ynthase.	0.18	NONE.	NONE	NONE	
		Jimust.	0.10	<none></none>	<none></none>	<none></none>	

	Nearest	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEC		Troughoof (Blastit Vs. C	Jenoank)	Nearest Neig	hbor (BlastX vs. Non-Redundant I	roteins)	
D	ACCESSION		P VALUE	ACCESSION	DESCRIPTION	P VALUE	
<u> </u>		Xenopus laevis XL-					
1	1	INCENP (XL-				+	
1	I	INCENP) mRNA,	1			i	
590	U95094	complete cds	0.18	<none></none>	<none></none>	<none></none>	
i		Caenorhabditis				410112	
1	i	elegans cosmid		1	1	1	
591	AF067610	F41A4	0.18	<none></none>	<none></none>	<none></none>	
1	ĺ	Homo sapiens				1	
ł		gonadotropin-					
	ı	releasing hormone		1	1	1	
1		precursor, second	İ	l			
	ł	form (GnRH-II) gene.		· .		1	
592	AF036329	complete cds	0.18	<none></none>	<none></none>	<none></none>	
ı	ł	H.sapiens					
1		mitoxantrone-		1	1		
		resistance associated		i .		1	
593	Z49216	mRNA	81.0	<none></none>	<none></none>	<none></none>	
l		T					
		Torulopsis glabrata			1	i i	
		mitochondrial DNA				1 1	
		for tRNA-Thr,-His			1	! !	
594	. 202167	and Glu upstream of				1 1	
1394	X02167	cytochrome b gene R.communis	0.18	<none></none>	<none></none>	<none></none>	
		(Carmencita) Scr1	i			1 1	
		mRNA for sucrose	-			1 1	
595	Z31561	carrier	A 10	11015		ŀ	
2/3		Homo sapiens	0.18	<none></none>	<none></none>	<none></none>	
		(subclone 2_c9 from	ł			l f	
ı		P1 H56) DNA	1	•	SE VE EDVEVE OCIONE]	
596		sequence	81.0	1246575	55 KD ERYTHROCYTE	.	
		Joque 1100	- 0.10	1346575	MEMBRANE PROTEIN	8.4	
	1:	Nocardia	i				
	į.	lactamdurans pcbAB	j	•		i i	
I		and pcbC genes for	1			l l	
- 1		alpha-aminoadipyl-L-	j				
1		ysteinyl-D-valine	!	·			
- 1		ynthetase and	j		SEED LIPOXYGENASE-2 (L-	•	
		sopenicillin N	- 1		2) soybean >gi 170014 (J03211)	1	
597		ynthase	0.18	126404	lipoxygenase (EC 1.13.11.12)	6.5	
\Box	5	Sus scrofa			1100xygetiase (DC 1.13.11.12)	0.3	
1	l:	parathyroid receptor	- 1	ŀ		}	
- 1	lċ	PTH) mRNA,	į		(X04647) collagen alpha-2(IV)	i	
598		omplete cds	0.18		chain [Mus musculus]	3.8	
-					[trius muscutus]	٥.د	

-	型 Nearest	Neighbor (BlastN vs. (Genbank)	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEC		1	1	racment IACI	inor (biastic vs. Hon-Redundant Pr	roteins)
B	-	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
	 	<u> </u>	<u> </u>			
	1		1		VERSICAN CORE PROTEIN	
				Į	PRECURSOR	
1	j	Plasmodium	1		PROTEOGLYCAN CORE	
1	ł	falciparum DNA ***	1		PROTEIN 2) (GLIAL	İ
	1	SEQUENCING IN	1	Ì	HYALURONATE-BINDING	
į.	1	PROGRESS ***	İ	ĺ	PROTEIN) (GHAP) >gi 608515	l
1	1	from contig 3-85,	1		(U16306) chondroitin sulfate	i
599	AL010158	complete sequence	0.18	2506916	proteoglycan versican V0 splice-	1
	1 2000	complete sequence	0.18	2506816	variant precursor peptide u0002b protein -	3.7
1					Mycobacterium tuberculosis	
1	ĺ	1	j	·	tuberculosis]	
1			1		>gi 1694863 gn1 PID e283373	
1	ł	Bos taurus mRNA for]		(Z83018) hypothetical protein	
1	1	thrombospondin 1,	i l		Rv2968c [Mycobacterium	
600	AB005287	complete cds	0.18	2146000	tuberculosis]	2.9
1	l	Drosophila			(AL031371) hypothetical	
1		melanogaster cosmid			protein SC4G2.06	
601	AL021108	clone 137E7	0.18	3483032	[Streptomyces coelicolor]	2.9
l	ł	Danio rerio Notch	l į			
l .		homologue 3 mRNA,	ľ		l	1
602	U57975	complete cds	0.18	85719	collagen alpha l'(II) chain	
	3373	complete eas	0.18	63719	precursor - African clawed frog (AL021387) similar to Zinc	1.7
					tinger, C4 type (two domains);	
		j	j		cDNA EST yk452f4.5 comes	1
		j			from this gene; cDNA EST	ł
! !		P.aeruginosa			EMBL:T00774 comes from this	
		autonomously	j		gene receptor NHR-3	
603	M30124	replicating sequence.	0.18	3878017	[Caenorhabditis elegans]	1.3
		.]			STEM CELL PROTEIN	
1			1		chicken >gi 62845 (X63371)	į
604	V54065	c II am by			transforming capacity [Gallus	
-004		G.sp alpha 5HR DNA Xenopus laevis	0.18	134304	gallus	1.3
ı		nitotic			(VOSDOS) ETATISS ST	- 1
j	4	hosphoprotein 44	ŧ		(X98893) hTAFII68 [Homo	1
605		nRNA, partial cds	0.18	1628403	sapiens] splicing [Homo	,,
				1028403	sapiens]	1.3
ŀ		Oryctolagus	1		92 KD TYPE IV	
1	1	uniculus renal	1		COLLAGENASE	
J		odium-dependent	1		PRECURSOR IV, 92K,	j
ł	1.	hosphate transporter	I		precursor - rat >gi 1022784	
,,,		ype II mRNA.	i		(U36476) 92-kDa type IV	1
606	U20793 c	omplete cds.	0.18	1705984	collagenase (Rattus norvegicus)	1.2

	₩ Neares	Neighbor (BlastN vs. (ienbank)	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SE		, , , , , , , , , , , , , , , , , , ,	Juliank)	i veal est iveig	nuor (BlastX vs. Non-Redundant P	roteins)	
B	_	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
<u> </u>						 	
1		Human				 	
1		cholecystokinin type		Ì	ł	1	
		A receptor (CCK-A)		İ	(Z94752) hypothetical protein		
607	U23427	gene, exons 1 and 2.	0.18	3261734	Rv1004c	0.97	
	1	Rattus norvegicus	1				
1	1	protein kinase MUK2		1			
608	U49953	mRNA, complete cds	0.0		(X81847) pectate lyase 1	į į	
1 000	043333	Human alpha globin	0.18	551238	[Erwinia carotovora]	0.43	
		gene cluster on					
	1	chromosome 16: zeta				1 1	
609	J00182	gene.	0.18	1585259	tral gene [Amycolatopsis	1	
			V.16	1303239	methanolica] HYPOTHETICAL 28.3 KD	0.41	
1	1				PROTEIN IN GBD 5 REGION		
1]			(ORF4) >gi 2120954 pir I39562		
1.		M.gallopavo gene for			ORF4 - Alcaligenes eutrophus		
610	X62513	metallothionein	81.0	2494740	>gi 695274 (L36817) ORF4	0.21	
1		Goat embryonic alpha			251023274 (E30817) ORF4	0.31	
1	l	globin gene zeta					
611	X04862	exons 2-3	0.18	86837	androgen receptor B - human	0.082	
1	ł	Rat vitamin D			The second secon	0.002	
ł		binding protein	1		ì		
612	1 1010100	(DBP) mRNA,	į į		(AJ130783) APC2 protein [Mus	1	
612	M12450	complete cds.	0.18	4210432	musculus)	0.038	
į .		Mus musculus muscle					
		NSP-like 1 (Nspl1)	- 1			- 1	
613	AF038539	mRNA, complete cds	0.13	2007077	(AJ224868) GNAS1 [Homo]	
	12 00 00 00	inda (71, complete cus	0.13	3297877	sapiens]	0.029	
		Bacteriophage P22			l	1	
		right operon, orf 48.	J	ı	i	- 1	
		replication genes 18	į.			ľ	
		and 12, nin region	1				
ĺ		genes, ninG					
į		phosphatase, late	ŀ	i	ľ	ł	
1		control gene 23, orf	- 1	[1	
į		60, complete cds, late	ł		(U42436) C49H3.3 gene	ŀ	
٠.,		control region, start	1	l l	product (Caenorhabditis	ŀ	
614	X78401	of lysis gene 13	81.0		elegans]	0.009	
]	,	ig mRNA for inter-	1				
ŀ		Ipha-trypsin	İ	1	_	j	
- 1	1	nhibitor heavy-chain	1		(U61947) C06G3.8 gene	Į.	
615		II. complete cds	0.18		product [Caenorhabditis	į	
	1	complete cus	0.10	1397275	elegans	7e-06	

ALC: 100	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEO		Torginoor (Diaga viole)	T		inoor (Blases Vs. Non-Redundant Pr	oteins)
B	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
<u> </u>					LRR47 protein - fruit fly	
l		Rabbit mRNA for	1		(Drosophila melanogaster)	
		aminopeptidase N	1	1	>gi 415947 (X75760) LRR47	1
616	X51508	(partial)	81.0	630864	[Drosophila melanogaster] HYPOTHETICAL IT.3 KD	6e-07
l						
ì	•				PROTEIN C2C6.07 IN	
1	į.				CHROMOSOME I	Í
	ł	Í			>gi 2370504 gnl PID e339194	j
	i		1		pombe]	
i	1.	S.kluyveri linear	1		>gi 3451305 gnl PID e1316730	
1	1	plasmid pSKL DNA			(AL031324) very hypothetical	
617		for open reading		٠.	protein [Schizosaccharomyces	,
617	X54850	frames 1-10	0.18	3183405	pombe]	2e-08
		'			(ALU32626) CDNA EST	
					EMBL:D70654 comes from this	
					gene; cDNA EST	•
					EMBL:Z14359 comes from this	
	i				gene: cDNA EST	
					EMBL:D33409 comes from this	
			1		gene; cDNA EST	
		Human peripheral	·		EMBL:D36239 comes from this	
		benzodiazepine	•		gene; cDNA EST	
618	L21954	receptor gene, exon 4.	0.18	3005011	EMBL:Z14766 comes from this	
	L21934	Oryctolagus	0.18	3925211	gene	4e-09
l		cuniculus protein			1	
ł		phosphatase 2A1 B				1
i	ı ı	gamma subunit			(11.07.1392)	
	<u>.</u>	(skeletal muscle			(AL034382) putative mitosis and maintenance of ploidy	
	1	isolate) mRNA.	i			j
619	f	complete cds.	0.18	3947877	protein [Schizosaccharomyces pombel	8e-11
一					MYOSIN LIGHT CHAIN	0C-11
ł	ł		1		KINASE, SMOOTH MUSCLE	·
. [Į.	Γ.cruzi hsp70 mRNA	ł		AND NON-MUSCLE	ı
- 1		for 70 kDa heat shock	ľ	•	ISOZYMES (MLCK)	į
620	_	protein, partial cds	0.18	3024081	(CONTAINS: TELOKIN)	9e-12
					(CONTAINS, TELORIN)	96-12
	1	Mus musculus	ŀ			
J	l:	proteasome regulator			(U28739) similar to TPR	ì
	ļī	PA28 beta subunit			domains in e.g. yeast STI1	I
621	AF060195 g	gene, complete cds	0.18	861276	protein [Caenorhabditis elegans]	le-14
		Methylobacterium			, control of the cont	
- 1	ļe	xtorquens serine	į		(AF027208) AC133 antigen	į
622	L27235 c	ycle proteins	0.18	2688949	i	

		Neares	t Neighbor (BlastN vs. C	ienhank)	No.		
	SE			I I	Nearest Neig	hbor (BlastX vs. Non-Redundant F	roteins)
	B	•	N DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
	623	AF006573	Drosophila virilis maltase 1 (Mav1) and maltase 2 (Mav2) genes, complete cds	0.18	2500558	PUTATIVE RIBONUCLEASE III (RNASE III) >gi 3876420 gnl PID e1346063 (Z81070) similar to ribonuclease	
	624		Staphylococcus aureus strain SA502A AgrB	0.17	<none></none>	[Caenorhabditis elegans]	2e-23
	625	AJ223364	Homo sapiens germ- line DNA upstream of Jkappa locus Human	0.17	<none></none>	<none></none>	<none></none>
	626	J03059	glucocerebrosidase (GCB) gene, complete cds	0.17	<none></none>	<none></none>	
	627	AB008860	Fugu rubripes Ca12 gene for pheromone receptor, complete cds	0.17	2198849	(AF004900) E3KARP [Homo sapiens] >gi 2665826 (AF035771) Na+/H+ exchanger regulatory factor 2 [Homo sapiens] factor 2 [Homo sapiens] >gi 3618353 gnl PID d1034182 exchanger isoform A3 [Homo sapiens]	<none></none>
	628		Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete	0.17	539355	SCD25 protein (version 1) -	
é	529		Homo sapiens histone deacetylase 3 (HDAC3) gene, complete cds	0.17		hypothetical protein C15H7.1 - Caenorhabditis elegans	4.5

	版 Near	est Neighbor (BlastN vs.	Genbank)	Negrest Mai	abbas (Blass V vs. No. D. 1	
SE	Q			emest idel	ghbor (BlastX vs. Non-Redundant	Proteins)
	- 1	ON DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
<u> </u>	- 			 	HYPOTHETICAL 83.2 KD	
					PROTEIN F58A4.11 IN CHROMOSOME III >gi 3874287 gn PID e1344088	
1	· I			1	EST EMBL:C12577 comes	[
	1		1	i	from this gene; cDNA EST	ı
	l	}			yk227e7.5 comes from this	
	ł		1		gene; cDNA EST yk303d1.5	1
	ı	j	ł	1	comes from this gene; cDNA	1.
	i		}	ĺ	EST yk314c12.5 comes from]
1			1	٠,	this gene; cDNA	1
İ	I				EMBL:C11886 comes from this	1
1					gene; cDNA EST	1 1
1	1	1			EMBL:C12577 comes from this	1 1
1	1	Homo sapiens histone	.]		gene; cDNA EST yk227e7.5	! I
	j	deacetylase 3	'		comes from this gene; cDNA	1 1
1		(HDAC3) gene,			EST yk303d1.5 comes from this	1
630	AF059650		0.17	465932	gene; cDNA EST yk314c12.5	1 1
		Chinese harmster		403932	comes from this gene; cDNA	4.4
1	1	metallothionein II			(AC005169) putative Cys3His	1 1
631	X55065	gene	0.17	3687237	zinc-finger protein	
l					cyclin E type II - fruit fly	1.5
1	ł	Rattus norvegicus	i		(Drosophila melanogaster)	ı
l	1 .	oxytocin receptor	l j		>gi 429168 (X75027)	
632	771.7000	(OTR) gene, exon 3			Drosophila cyclin E type II	
032	U15280	and complete cds	0.17	542565	[Drosophila melanogaster]	0.45
	l	Goat embryonic alpha	i i			- 3.13
633	X04862	globin gene zeta				j
- 333	704002	exons 2-3 Plasmodium	0.17	86837	androgen receptor B - human	0.080
	ĺ	falciparum DNA ***	- 1			
		SEQUENCING IN			(X95466) CPG2 protein [Rattus	1
		PROGRESS ***	į		norvegicus]	1
		from contig 4-09,	ł		>gi 1588593 prf 2208498A	ł
634	AL010222	complete sequence	0.17	1177322	plasticity-related gene [Rattus	
			<u> </u>	1177322	norvegicus)	7e-07
		H.sapiens mRNA for	1		(1102715) haven	I
635	X60111	MRP-1	0.17	3237306	(U92715) breast cancer antiestrogen resistance 3 protein	3.00
		Orf virus E10R			anticstrogen resistance 3 protein	3e-09
ł	ł	homolog gene, partial	1		·	j
ŀ		cds, and DNA	1		(AL033385) dna-directed rna	
		polymerase gene,	1		polymerase iii subunit	
636	U49979	complete cds	0.17		[Schizosaccharomyces pombe]	7e-15
					onnoe	10-17

WO 01/02568 PCT/US00/18374

	Nearest	Neighbor (BlastN vs. C	enbank)	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEO		The second of th	T T	TVCalest IVeign	ibbi (Blasta vs. Non-Redundant Pi	oteins)
D	ACCESSION	DESCRIPTION	PVALUE	ACCESSION	DESCRIPTION	
				T ACCESSION	DESCRIPTION	P VALUE
		†			PUTATIVE RIBONUCLEASE	
1		Drosophila virilis	1	1	III (RNASE III)	
1	j	maltase I (Mav I) and	ĺ	1	>gi 3876420 gnl PID e1346063	
ı	į.	maltase 2 (Mav2)	}		(Z81070) similar to ribonuclease	
637	AF006573	genes, complete cds	0.17	2500558	[Caenorhabditis elegans]	2e-29
l i						
		Borrelia burgdorferi				
630		(section 27 of 70) of			(U52370) fertilin beta [Homo	
638	AE001141	the complete genome	0.16	1850327	sapiens]	. 2.3
				}	(AC005164)	
				• •	(AC005164) match to ESTs	
					AA731149 (NID:g2140138),	
		Anthonomus grandis			AA731908 (NID:g2752719),	
		vitellogenin gene			AA287837 (NID:g1933519),	
639	M72980	(VTG), complete cds.	0.12	3242750	AA262811 (NID:g1898382), and AA825820 (NID:g2899132)	0.50
		Simulium vittatum		3242/30	and AA823820 (NID:g2899132)	2e-56
1 1		ATPase 6 gene,				
		mitochondrial gene	i			
		encoding			j	
		mitochondrial				
640	AF023532	protein, partial cds	0.11	<none></none>	<none></none>	<none></none>
ŀ		Sambucus nigra lectin	Į			
641	U76523	precursor mRNA,		0.4000.40	1	
- 0-1	070323	complete cds	0.10	3482965	(AL031369) putative protein	0.49
l		Danio rerio mRNA	ļ		LANOSTEROL SYNTHASE	-
- 1	ſ	for opioid receptor]		5.4.99.7) - fission yeast	ł
642		homologue	0.099	1706694	(Schizosaccharomyces pombe)	2.3
		Oryctolagus			(Semilosaccinaroni yees pointoe)	
	ļ	cuniculus Na and Cl	1			Į.
- 1		dependent betaine	j		(AF033381) betaine	i
1		transporter mRNA,	ı		homocysteine methyl transferase	ŀ
643		complete cds.	0.099	2645804	[Mus musculus]	0.59
		Bacteriophage Cp-5				
		(S.pneumoniae) 3	}			j
ا		inverted terminal			(AE000649) type IIS restriction	
644		repeat.	0.082	2314695	enzyme R and M protein	4.3
		Streptomyces sp.		İ		
645		gene for alkaline	0.072		(U54641) 220 kDa silk protein	
040	A/4103 S	serine protease I	0.073	1314734	[Chironomus thummi]	6.3

**	Nearest	Neighbor (BlastN vs. (Genbanki	Negreet Neigh	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEQ		1		1 TOMEST INCID	TOO (DIASEL VS. NOII-REGUNDANT F	TOTEIRS)		
B	ACCESSION		P VALUE	ACCESSION	DESCRIPTION	P VALUI		
<u></u>		Caenorhabditis						
	j	elegans cosmid						
1	1	F32G8. complete		J.	İ			
ı	1	sequence		•				
646	Z72509	[Caenorhabditis	0.072	17017				
1000	2/2309	elegans]	0.072	<none></none>	<none></none>	<none></none>		
647	X70282	X.laevis xanf-1 gene	0.070	3851202	(AC005954) ZO-3 [Homo	0.40		
	11.0202	Human DNA	0.070	3831202	sapiens] [Homo sapiens]	0.40		
		sequence from				i		
l	}	cosmid E141E2, on						
ļ		chromosome 22,						
1		complete sequence		•				
648	Z69906	[Homo sapiens]	0.069	<none></none>	<none></none>	<none></none>		
1						T		
1	ŀ	Drosophila virilis	1					
649	A F056040	retrotransposon Tv1,	0.000		(U93872) ORF 73, contains	1		
049	AF056940	complete sequence Homo sapiens	0.069	2246532	large complex repeat CR 73	5e-12		
650	AJ001151	genomic sequence	0.068	<none></none>	-NONT-	27027		
	12001151	Bacteriophage BF23	0.000		<none></none>	<none></none>		
651	X54455	gene 17 and gene 18	0.067	<none></none>	<none></none>	<none></none>		
		P.pinea internal			1	- CIVOLVE		
		transcribed spacers 1	l		(U95374) aldehyde]		
		& 2 of ribosomal	ľ		dehydrogenase [Haloferax			
652	X87936	DNA	0.067	2459733	volcanii]	4.3		
		Dictyostelium	1					
		discoideum TipD				j i		
653		(tipD) gene, complete	0.067	3600036	(AB018320) KIAA0777 protein			
555	AI 019230	cds	0.067	3882275	[Homo sapiens] METHIONINE	1.1		
	j		j		AMINOPEPTIDASE 2			
į		O.cuniculus mRNA	1		(METAP 2) GLYCOPROTEIN)			
654		for p53 protein	0.067	1703275	(P67)	0.29		
		Mus musculus						
	I I	putative T1/ST2	- 1					
1		receptor binding	j		1			
	1	protein precursor			(U17326) neuronal nitric oxide			
655		mRNA, partial cds	0.067	642518	synthuse [Homo sapiens]	0.29		
j		Homo sapiens KIAA0421 mRNA,						
656		oartial cds	0.066	-NONE:	37037	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		
		Plasmodium	0.000	<none></none>	<none></none>	<none></none>		
J		alciparum DNA ***	į			l		
1		SEQUENCING IN	ł		[ŀ		
- 1		PROGRESS ***	1			į		
- 1	Į f	rom contig 3-109.	!	ļ				
657	AL010213 c	omplete sequence	0.066	<none></none>	<none></none>	<none></none>		

1	Nearest	Neighbor (BlastN vs. C	Senhank)	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEC		Tierenoor (Diasa v vs. C	Jenoank)	Nearest (Neig	nbor (BlastX vs. Non-Redundant P	roteins)	
B	~ J	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
<u> </u>						+	
1	1	Homo sapiens mRNA				 	
1	1	for KIAA0646		[1	
658	AB014546	protein, complete cds	0.066	1082461	homeotic protein HB9 - human	0.38	
1	ľ						
1	1	Rattus exulans isolate		İ	1	1	
1	Į.	huahine30			(U24189) RRM-type RNA	1	
659	15101155	mitochondrial D-			binding protein (Caenorhabditis	1	
623	AF104156	loop, partial sequence	0.066	1002380	elegans]	0.29	
1		M.musculus mRNA					
660	X97581	for spalt transcription	2255		(AL035075) putative myosin	1	
1000	A9/381	factor Human clone H20 N-	0.066	. 4107313	heavy chain	0.28	
ļ	1	acetylglucosaminyltra					
1	1	nsferase III DNA,	· •	•	1	i I	
661	D85378	exon 2	0.066	2114472	(U96963) p140mDia [Mus	1	
-	203378	exon 2	0.066	2114473	musculus]	0.22	
1	j	Human (clone	ł		1	! I	
1	1	LA179) chromosome			1	i I	
662	M97561	21 sequence.	0.065	<none></none>	NONE		
		Plasmodium	0.003	Q10I1E	<none></none>	<none></none>	
	İ	falciparum					
j		chromosome 2.	I				
l		section 10 of 73 of					
		the complete			ł		
663		sequence	0.065	<none></none>	<none></none>	<none></none>	
	l i	growth hormone				CHOILE	
1		receptor, growth	į	•			
[hormone binding	í		1	ł	
		protein {GHR/BP			·	ſ	
	l i	gene) [mice, C57	1				
	ľ	black/6, Genomic,	1]	j	
		179 nt. segment 8 of	1		·		
664		10]	0.065	<none></none>	<none></none>	<none></none>	
ı		Homo sapiens	l				
	•	syntaxin 4 binding	Ī			. [
ļ	j.	protein UNC-18c		İ			
665		UNC-18c) mRNA,	0.055		(AB006074) topoisomerase III	1	
-303		omplete cds vp[40]=svp-related	0.065	3061308	[Mus musculus]	0.82	
ł		uclear	1				
j		eceptor/retinoid	j	į	· [ļ.	
i		ignaling modulator	ł	ŀ	/U5072 ()		
[zebrafishes, mRNA.	I		(U58734) weak similarity to		
666		S76 nt]	0.065		ankyrin G (Caenorhabditis	1	
			3.003	1320200	elegans)	0.12	

温	Neare	est Neighbor (BlastN vs.	Genbank)	Nonena N. :	the course	
SE	Q.	STATE OF TENANCE VS.	Gettbattk)	Nearest Neigh	hbor (BlastX vs. Non-Redundant)	Proteins)
	ACCESSIO	DESCRIPTION		1	1	
<u> </u>	I ACCESSIO	ON DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
-					HYPOTHETICAL 74.2 KD	
į.	ı	1		i	PROTEIN IN AMDI-RAD52	
1	1	Í	1		INTERGENIC REGION	i
	1			1	>gi 1077180 pir S49745	1
	1		1		probable membrane protein	1
I	l l		ļ	1	YML034w - yeast	1 1
1	1	G.domesticus mRNA			(Saccharomyces cerevisiae)	
	ı	for ventricular myosi		1	>gi 575685 (Z46659) unknown orf, len: 656, CAI: 0.13	1 1
66	7 X59552	heavy chain	0.065	2497098	[Saccharomyces cerevisiae]	000
1				2191090	[Saccitatomyces cerevistae]	0.014
	1	1	1		(AC005164) match to ESTs	1 1
	1	j	1	' '	AA731149 (NID:g2140138),	1 ' 1
	1				AA731908 (NID:g2752719),	1 1
		Anthonomus grandis			AA287837 (NID:g1933519),	1 1
668	1 172000	vitellogenin gene	1 _		AA262811 (NID:g1898382),	1
1000	M72980	(VTG), complete cds.	0.065	3242750	and AA825820 (NID:g2899132)	5e-33
	ŀ	Homo sapiens mRNA				
		for KIAA0646				1 1
669	AB014546		0.064	<none></none>		j 1
		protein complete cas	0.004	CNOINES	<none></none>	<none></none>
1		Sheeppox virus strain	! [1
	J	KS-I ORF HMI	i i	i		
1		gene, partial cds;				
1	1	ORF HM2 and ORF]			
	į	HM3 genes, complete				1
670	1420000	cds; and ORF HM4	j	i		- 1
10,0	M30039	gene, partial cds Caenorhabditis	0.064	<none></none>	<none></none>	<none></none>
	ł	elegans cosmid	1			
ł	ł	W02H3, complete				į.
		sequence				1
}		[Caenorhabditis	}	. 1	.1	1
671	Z68013	elegans	0.064	<none></none>		
				CITOITES	<none></none>	<none></none>
		Bodo saltans	ł		ĺ	ł
	' 	unknown mRNA,	j		i	1
		kinetoplast gene	1	1	1	1
672	1501.222	encoding kinetoplast	j	1	·	1
672	AF041332	protein. complete cds	0.064	<none></none>	<none></none>	<none></none>
ľ		Mouse germline IgG-	l			
- 1		3 chain gene, D-J-C	1		1	ł
673		region, and switch	0.061	2101	i	
		region.	0.064	<none></none>	<none></none>	NONE>

	Nearest	Neighbor (BlastN vs. (ienbank)	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEC			T	INCIDES! INCID	indor (BlastX vs. Non-Redundant P	roteins)	
В	-	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
	1	Dictyostelium discoideum K7					
674	U41289	kinesin-like protein mRNA, complete cds	0.064	3482972	(AL031369) putative protein	9.3	
675	M37395	L.lactis (strain SK11) proteinase plasmid pSK111 DNA, complete cds.	0.064	993019	(X87246) alternative start codon		
676	Z15030	H.sapiens gene for ventricular myosin light chain 2 > :: gb L01652 HUMVM LC Human ventricular myosin light chain 2 gene, seven exons.	0.064	730343	PROLACTIN RECEPTOR PRECURSOR (PRL-R) mouse >gi 220576 gnl PID d1001535 (D10214) prolactin receptor precursor [Mus musculus] >gi 293770 (L14811) prolactin receptor [Mus musculus] >gi 347842 (L13593) prolactin receptor [Mus musculus] receptor:ISOTYPE=long form [Mus musculus]	9.1	
6 7 7	Z12021	G.max gene for catalase	0.064	2498711	ORIGIN RECOGNITION COMPLEX PROTEIN, SUBUNIT 2 >gi 1185461 (U38472) essential ORC2- related fission replication factor Orp2 [Schizosaccharomyces pombe]	5.3	
678	s s	protein erine/threonine cinase (pstk1) gene. omplete cds.	0.064	733140	(U22453) carboxypeptidase [Simulium vittatum]	5.3	

連載	Nearest Neighbor (BlastN vs. Genbank)			Negros Nai	abbas (Bluss V vs. No. B. d. 1		
SE				TACTICS! IAS!	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
п	7	DESCRIPTION				l	
F	ACCESSIC	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
	+						
}	ŀ		j		HYGROMYCIN-B KINASE		
	Ì		1	ŀ	(HYGROMYCIN B	1	
j	ı		[1	PHOSPHOTRANSFERASE)	I .	
1	1		ł		(APH(7"))		
j		·	1		>gi 66885 pir WGSMHH	}	
.	1		1		hygromycin B	l 1	
	1	į			phosphotransferase (EC 2.7.1)	ļ	
ì	J		1		Streptomyces hygroscopicus		
	ł		1		>gi 581682 (X03615) pot. hyg		
	ſ				protein [Streptomyces		
		· ·	1	•	hygroscopicus]		
1	1	1			phosphotransferase [synthetic		
1.	j	j			construct] >gi 2739064 cloning		
		1	1		vector] >gi[2739068		
	1	Mus musculus alpha-] [(AF025747) hygromycin B	į.	
1	ł	galactosidase A gene.	1		phosphotransferase [unidentified]	i	
679	U50715	complete cds	0.064	125398	cloning vector]	2.3	
1	1	S.cerevisiae			Om(2D) protein - fruit fly		
	1	chromosome XI	1		(Drosophila ananassae)	ľ	
(00		reading frame ORF	l		>gi 4-13770 gn1 PID d1006095		
680	Z28182	YKL182w	0.064	1079035	(D26553) ORF	1.8	
	1	Human ornithine	1				
681	M29917	aminotransferase	2061	*****	(U97553) unknown [murine	ì	
100.	1/12/9/1/	gene, exon 1.	0.064	2317934	herpesvirus 68]	1.4	
1	Í	Homo sapiens mRNA	j		(7730.54) 505550		
	ł	for KIAA0902			(U29154) T07F12.3 gene		
682	AB020709	protein, complete cds	0.064	861404	product [Caenorhabditis		
			9.504	001404	elegans)	0.47	
1	I	Homo sapiens mRNA]				
	i	for KIAA0646	1		HOMEOBOX PROTEIN HB9		
683	AB014546	protein, complete cds	0.064	1708118	>gi 507425	0.35	
		Homo sapiens mRNA					
40.	4.00.0	for NORI-1, complete	1		(AF015539) precollagen P	1	
684	AB010427	cds	0.064	2388676	[Mytilus edulis]	0.018	
		0-6	1	 -			
		Orf virus ankyrin-like	1				
		repeat protein, F11L homolog, and F12L	i		SSFI PROTEIN	1	
		homolog genes.		•	>gi 626624 pir S46700 SSF1	1	
685	U34774	complete cds.	0.064	731669	protein - yeast (Saccharomyces		
		complete cus.	0.004	731668	cerevisiae)	le-05	
		Mus musculus	1			l	
	· ·	neuropilin-2(a5)	Ī		(AF073359) benzaldehyde	1	
į		mRNA, alternatively	ì		dehydrogenuse [Pseudomonas		
686	AF022861	spliced, complete cds	0.064	4091978	sp. DJ77]	10.05	
					[3p. D377]	1e-05	

36.	Neare:	st Neighbor (BlastN vs.	Genbank)	Nagreet Voi	abbas (Blass V N	
SI	Q	- B	T T	Nearest iven	ghbor (BlastX vs. Non-Redundant P	roteins)
<u></u>	7 1	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
-					(AC004010) similar to Leucine-	
68	7 U14331	Sus scrofa myogenin gene. complete cds	0.064	2781386	rich transmembrane proteins; 44% similarity to U42767 (PID:g1736918) [Homo sapiens]	3e-33
68	8 AF074870	Chironomus pallidivittatus clone 1219 non-telomeric Ssp repeat sequence	0.063			36-33
1	12074870	H.sapiens repeat	0.063	<none></none>	<none></none>	<none></none>
689	Z25523	region DNA.	0.063	∠NONE-		
	1	Plasmodium	0.505	<none></none>	<none></none>	<none></none>
-		falciparum chromosome 2, section 15 of 73 of the complete	٠.			
690	AE001378	sequence	0.063	<none></none>	<none></none>	310375
69 1	Z 72947	S.cerevisiae chromosome VII reading frame ORF YGR 162w	0.063	<none></none>	<none></none>	<none></none>
692	Vilgo	Choanomphalus incertus mitochondrial cytochrome c oxidase				<none></none>
092	Y14723	subunit I gene, partial	0.063	<none></none>	<none></none>	<none></none>
		Streptomyces sp. gene for alkaline			HYPOTHETICAL 108.5 KD PROTEIN IN UME3-PUB1 INTERGENIC REGION >gi 2131866 pir S62935 hypothetical protein YNL023c - yeast (Saccharomyces cerevisiae) >gi 1301855 gnl PID e239870 (Z71299) ORF YNL023c	
693	X74103	serine protease I	0.063	1730713	[Saccharomyces cerevisiae]	47
	E	Homo sapiens Sprouty 2 (SPRY2)			TRANSFERASE GST-6.0 (GST B1-1) >gi 421198 pir S29772 glutathione transferase (EC 2.5.1.18) - Proteus mirabilis >gi 2126142 pir S71882 glutathione transferase (EC	6.7
694		nRNA. complete cds	0.063		2.5.1.18) B - Proteus mirabilis >gi 1053076 (U38482)	
					Eq1033070 (U38482)	5.2

1	Neares	Neighbor (BlastN vs. (Genhanki	Nearan XIII	hhar (Dissay V	
SEC			Jenoank)	Nearest Neig	thbor (BlastX vs. Non-Redundant Pr	oteins)
D	-	N DESCRIPTION	D.///			ļ
-	ACCESSIO	N DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
-	 		 	 		
ł	1		į	1	FRAGILE X MENTAL	
i	1		1	•	RETARDATION SYNDROME	j
1			1	[RELATED PROTEIN 2	
		1			>gi 2135129 pir S60173 fragile	
1	1	1	1		X mental retardation syndrome	
i i	1		ł	l	related protein - human	
1		Mouse M-twist gene			>gi 1098637 (U31501) fragile X	
695	M63650	mRNA. complete cds.	0.067	1500	mental retardation syndrome	
1	14203030	mikiva. complete cus.	0.063	1730141	related protein [Homo sapiens]	1.8
1		Homo sapiens GDP				
1	1	dissociation inhibitor	i i		humathatian lauratia 4 6 1	
696	Y13298	beta pseudogene	0.063	1085930	hypothetical protein 4 - fowl	
		Joean pseudogenie	0.003	1083930	adenovirus 1	1.3
1	I	Rat SOD-2 gene for	į l			
1		manganese-	ì			1
1		containing superoxide			(A BO18351) KIA A0711	ì
697	X56600	dismutase	0.063	3882143	(AB018254) KIAA0711 protein [Homo sapiens]	
			0.005	3002143	HUNTINGTIN	0.60
1	l	M.musculus mRNA	ł		(HUNTINGTON'S DISEASE	1
1		for 5HTx serotonin	•		PROTEIN HOMOLOG) (HD	f
698	Z23107	receptor	0.063	1708162	PROTEIN)	0.45
i		Plasmodium vivax			1.1012111/	0.43
1		circumsporozoite			DNA GYRASE SUBUNIT B	· }
699	M20670	protein gene, 3' end.	0.063	4033395	subunit [Myxococcus xanthus]	0.35
					RETINOIC ACID RECEPTOR	<u> </u>
[]	1		RXR-BETA sapiens]	1
			ł		>gi 3172498 (AF065396)	[
Ì			į.		retinoic X receptor B	1
		j	j		dJ1033B10.11 (Retinoid X	ł
			j		receptor beta (RXRB)) [Homo	
		H.sapiens CpG DNA.	1		sapiens] >gi 4249766	į
700		clone 76g11, reverse	· 1		(AF120161) retinoic X receptor	į
700	Z62997	read cpg76g11.rtla	0.063	1350911	beta	0.16
		Xenopus laevis XL-	1			
ŀ		INCENP (XL-	1			
701	i i	INCENP) mRNA.			(AF048732) cyclin T2b [Homo	1
\O1		complete cds	0.063	2981200	sapiens	0.090
		Xenopus laevis	1			
ł		mitotic	l			į
702	_	phosphoprotein 44	0.000		(Z81555) predicted using	1
-, 52		mRNA, partial cds Xenopus laevis XL-	0.063	3877951	Genefinder	6e-07
ł		NCENP (XL-	1		T	
[NCENP) mRNA.	l			1
703	1	complete cds	0.063		(AL031174) hypothetical	
	- 0,33,4	ompicio cus	0.003	3393018	protein	2e-10

335	斯 Neares	st Neighbor (BlastN vs. C	ienbank)	Nearner Main	11 - (D) - V - N - D	
SE				rientest Mei	ghbor (BlastX vs. Non-Redundant I	Proteins)
II	7	N DESCRIPTION	P VALUE	A CCERCYON	DESCRIPTION	1
	T	E.coli genomic DNA.		ACCESSION	DESCRIPTION	P VALUE
		Kohara clone	1	 	CYTOCIPOLET	
704	D90872	#419(54.7-55.1 min.)	0.063	2498198	CYTOCHROME B561	1
				2430130	(CYTOCHROME B-561)	3e-19
- 1		M.crystallinum		Į		
ĺ	1	ferredoxin-NADP+	1			
705	Massan	reductase (fnrA)	i		-	1
1/03	M25528	mRNA, complete cds.	0.062	<none></none>	<none></none>	<none></none>
1	1	Strongyloides ratti		1		
706	U45256	microsatellite B DNA	0.062	-NO.77		1
		inicrosatemic B DIVA	0.062	<none></none>	<none></none>	<none></none>
ľ	ł	Xenopus laevis				
1	I	mitotic	:			1
	1	phosphoprotein 90				1 1
707	U95102	mRNA, complete cds	0.062	<none></none>	<none></none>	<none></none>
	ł	77.				CATOLILE
	ł	Homo sapiens TEL/AMI.1 fusion				
708	AF044317	gene, partial sequence	0.062		1]
	120-31/	Caenorhabditis	0.062	<none></none>	<none></none>	<none></none>
1	1	elegans cosmid	l			
1	}	T06E8, complete	ľ			1 1
ĺ	· ·	sequence	ı			ŀ
1		[Caenorhabditis	1		(AC004663) Notch 3 [Homo	
709	Z73975	elegans]	0.062	3108187	sapiens]	2.9
					chitinase (EC 3.2.1.14)	- 5.7
		Human mRNA for			precursor - rice precursor - rice	
710	X54232	heparan sulfate			>gi 807955 (X87109) chitinase	
	A34232	proteaglycan	0.062	1076741	[Oryza sativa]	0.59
		Bovine retinal mRNA	ļ		1	
		for transducin beta-	1	•	aialidas Assiss	
711		subunit	0.062	477578	sialidase - Actinomyces viscosus >gi[141852	
		D.melanogaster Jun		41.1376	754141032	0.087
712		and 14-3-3 zeta gene	0.062	3879551	(Z70756) similar to collagen	0.073
1		Bombus terrestris			to conugen	0.073
l	1	mitochondrial	1		(U20600) NADH	
713		cytochrome oxidase I,		. 1	dehydrogenase subunit [Vanda	
	L203/3	partial cds.	0.062		lamellata]	0.039

2	Neares	t Neighbor (BlastN vs. (Genbank)	Nearest Mais	hhor (PlastV vs. No. D.)	
SE	Q			L-Careat IVelg	hbor (BlastX vs. Non-Redundant l	roteins)
II.	-	N DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUI
-	- 				AMINOPERTIDASE B	7
ł	1		ł		(ARGINYL	1
1	1	1	1		AMINOPEPTIDASE)	
1				1	(ARGININE	
ļ	i	1	1	1	AMINOPEPTIDASE)	1
ł	J	1			CYTOSOL	l
ł	1		ŀ	1	AMINOPEPTIDASE IV) (AP-	
ĺ		Human ladinin (LAD)	J	•	B) >gi 2039143 (U61696)	1
714	U58994		3		aminopeptidase B [Rattus	j
	038334	gene, complete cds	0.062	2811078	norvegicus]	9e-06
1	ł	Homo sapiens mRNA			(U58748) similar to potential	
	1	for KIAA0653	1	*	transmembrane domains in S.	
715	AB014553		0.000		cerevisiae nulcear division	
-	7.0014333	protein, partial cds	0.062	1326350	RFT1 protein (SP:P38206) HYPOTHETICAL 38.5 KD	5e-10
1	I				PROTEIN IN ERVI-GLS2	
1		ľ			INTERGENIC REGION	1
i	1				>gi 2132587 pir S64322	1
1	ŀ	1			probable membrane protein	1
1	i	1	1		YGR031w - yeast	l
1	į .		Ì		(Saccharomyces cerevisiae)]
1	i	Mus musculus	- 1		Suil 3230 Iolan Ippola 42077	1 1
1	l	collagen alpha 1 type	j		>gi 1323010 gnl PID e243277 (Z72816) ORF YGR031w	
716	L16898	XVIII mRNA, 5'end.	0.062	1723657		l l
		M.tuberculosis		1723037	[Saccharomyces cerevisiae]	le-14
Į.,		guaA/B & choD	j		(Z49907) B0491.1	!
717	X99343	genes	0.062.	3873807	[Caenorhabditis elegans]	2-10
					[Cachornabultis elegalis]	2e-19
		Homo sapiens MAD-	ľ			
1 1		related gene SMAD7	į.			
		(SMAD7) mRNA,			[- 1
718		complete cds	0.061	<none></none>	<none></none>	<none></none>
719		Myrmeleon sp. 18S	T			
119	L10182	ribosomal RNA.	0.061	<none></none>	<none></none>	<none></none>
	<u>l</u>	Choanomphalus	i			
- 1		incertus		j	ļ	1
J	1	mitochondrial	· 1		1	
ď		1	- 1		1	- 1
720		sytochrome e oxidase	0.00		1	İ
	1 14/23	subunit I gene. partial	0.061	<none></none>	<none></none>	<none></none>
- 1	,	Bovine respiratory	1	ł	·	
- 1		syncytial virus	1	1		į
- 1		nucleoprotein mRNA.	1	[1	1
721		omplete cds.	0.061	512065	I	
		Jpiete eus.	0.001	542955 r	ucleoporin p62 - human	8.6_

200	Neare	st Neighbor (BlastN vs.	Genbank)	Nearest Nain	hbor (BlastX vs. Non-Redundant P	
SE				1.000 036 14618	noor (DiastA vs. Non-Redundant P	roteins)
0	ACCESSIO	N DESCRIPTION	PVALUE	ACCECCANO		1
		Jacob Holy	FVALUE	ACCESSION	DESCRIPTION	P VAL
			 -		Sus scrota	7
1	1	1	ı	ł	>gil494455 pdb TPOS B Sus	
	ł			[scrofa Sus scrofa	į ·
ı	ı				>gi 1421210 pdb 1PCP Porcine	ł
ı		į			Spasmolytic Protein (Psp) (Nmr.	1
ĺ	ı	Xenopus laevis XL-			19 Structures) Spasmolytic	j
	1	INCENP (XL.	1		Polypeptide	ł
1	I	INCENP) mRNA,		•	>gi 1633061 pdb 2PSP B Chain	
722	U95094	complete cds	0.061	****	B, Porcine Pancreatic	l
	1 075074	Xenopus laevis	0.001	494454	Spasmolytic Polypeptide	2.9
1		mitotic	1 1			
1	ł	phosphoprotein 44		• *	(AE001417) hypothetical	
723	U95098	mRNA, partial cds	0.061	. 2046020	protein [Plasmodium	
	1	Sporidiobolus	0.001	3845272	falciparum]	1.3
1	ł	salmonicolor	1 1			
1	1	NADPH-dependent	1 1		į.	
1	1	aldehyde reductase	1		(1/70200 1	
724	U26463	gene, complete cds	0.061	1710288	(U79302) unknown [Homo	
			0.001	1710288	sapiens]	0.44
1			1 1		EMBL:D33048 comes from this	
ł					gene; cDNA EST	
l	ł	1			EMBL:D35780 comes from this	
1			i 1		gene; cDNA EST yk442c6.3	
	ľ		1		comes from this gene; cDNA	
İ	l		1		EST yk442c6.5 comes from this	
•	Í				gene; cDNA EST yk398f6.3	
	i				comes from this gene; cDNA	
					E	
			i		>gi 3979816 gn1 PID e1358315	
		ı	1		EST EMBL:D35780 comes	
			1		from this gene; cDNA EST	
			į		yk442c6.3 comes from this	
	i				gene; cDNA EST yk442c6.5	
		Xenopus laevis weel	1		comes from this gene; cDNA	
70.5		homolog mRNA.	[ł	EST yk398f6.3 comes from this	
725		complete cds	0.061		gene; cDNA E	2e-04
l	l l	Caenorhabditis			HYPOTHETICAL 83.8 KD	20-04
		elegans cosmid	1	ļi	PROTEIN C27F2.7 IN	!
ļ		ZK1321, complete	ı		CHROMOSOME III	į
ŀ	1	sequence	J		gi 1065510 (U40419) C27F2.7	
77.		Caenorhabditis	. }	وا	ene product [Caenorhabditis	ı
726	Z48584 e	legans]	0.061		legans	3e-11

		st Neighbor (BlastN vs.	Genbank)	Nearest Nei	ghbor (BlastX vs. Non-Redundant I	
SE					- Prinser vs. Hon-Redundant I	Toteins)
П	ACCESSIO	N DESCRIPTION	P VALUE	ACCESSION		P VALU
-					HYPOTHETICAL 32.0 KD	
	İ	Zea mays pep gene	1		PROTEIN CO9F5.2 IN	
		for (C3 type)	ł		CHROMOSOME III	1
[1	phosphoenolpyruvate	. [>gi 732538 (U22832) C09F5.2	
72	7 X61489	carboxylase	0.061	2406997	gene product [Caenorhabditis	1
		Drosophila	0.001	2496887	elegans)	le-15
1	1	melanogaster				1
	Ī	Windbeutel (wind)	ı	I	(AC005783) R33083_1 [Homo	1
728	AF025408	gene, complete cds	0.061	3702295	sapiens]	2- 60
1	1	Brassica rapa mRNA			Japieris)	2e-60
		for SRK45, complete	l		1	ļ .
729	AB012106	cds	0.060	<none></none>	<none></none>	<none></none>
1	ı	Archidone:				12.0142
	I	Arabidopsis thaliana cellulose synthase	ł	l		
1	i	catalytic subunit (Ath-		•	·	
	i	B) mRNA, complete]	}
730	AF027174	cds	0.060	ANONIC	/	
		H.sapiens mRNA for	0.000	<none></none>	<none></none>	<none></none>
ļ	J	carnitine			(AF077541) contains similarity	
1	ł	palmitoyltransferase I			to class-I aminoacyl-tRNA synthetases [Caenorhabditis	
731	Y08682	type I	0.060	3319446	elegans]	0.1
l		Xenopus laevis XL-			cicgans	- 8.1
		INCENP (XL-	ł			
732	Tiosoo.	INCENP) mRNA.	Į		(D78016) TRAE [Enterococcus	
/32	U95094	complete cds	0.060	1041119	faecalis]	8.1
	l	Helianthus tuberosus	1			
	1	lectin 2 mRNA.			regulatory protein Rex - primate	
733	AF064030	complete cds	0.060	622200	T-lymphotropic virus PTLV-L	i
		Mus musculus	0.000	632209	(fragment)	3.7
		Pontin52 mRNA,	1		(AF037401) neuropeptide	. 1
734		complete cds	0.060	3098348	Y/peptide YY receptor Yc [Danio rerio]	_ , . I
				3070340	LAR PROTEIN PRECURSOR	2.1
	j		1		(LEUKOCYTE ANTIGEN	i
	1		1		RELATED)	1
	į.	Xenopus laevis	- 1		>gi 70146 pir TDHULK	l
		mitotic	i i		leukocyte antigen-related	
735		phosphoprotein 90			protein precursor - human	f
,,,,	093102	nRNA, complete cds	0.060	125978	>gi 34267 sapiens]	1.2
- 1	,	Sambucus nigra lectin	ļ	i		
1		recursor mRNA.	- 1		(U87306) transmembrane	l
736		omplete cds	0.060	2055201	receptor UNC5H2 [Rattus	1
		luman nuclear pore	<u> </u>	2055394	norvegicus]	0.32
		omplex-associated	1		(VI 1063) CLT1 ::	
737		rotein TPR	0.060		(Y14063) ChT1 thymocyte	
·					antigen [Gallus gallus]	9e-04

	V Nearan	Neighbor (Plank)	7	I N			
SEC		Neighbor (BlastN vs. C	Jenoank)	Nearest Neig	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
B	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
	 				(U58748) similar to potential	1	
1	1 .	Homo sapiens mRNA	· }		transmembrane domains in S.	1	
738	A DO: 4550	for KIAA0653			cerevisiae nulcear division		
138	AB014553	protein, partial cds	0.060	1326350	RFT1 protein (SP:P38206)	le-09	
1	1	Xenopus laevis	1	l			
Ì	j	phosphoprotein 44	l			İ	
739	U95098	mRNA, partial cds	0.060	2622000	(Y15513) Prodos protein		
	0,00,0	macra, partial eds	0.000	2632098	[Drosophila melanogaster]	5e-10	
1	1	H.sapiens telomeric			/	1	
	ľ	DNA sequence, clone		ĺ		i i	
1	į.	12QTEL101, read			1		
740	Z96260	12QTELOO101.seq	0.059	<none></none>	<none></none>	<none></none>	
	j .	Mouse homeobox	—				
	1				· .	[[
741	M93128	protein (EVX2) mRNA, complete cds.	0.059	NONE		1	
	1,1,5120	Brassica rapa mRNA	0.039	<none></none>	<none></none>	<none></none>	
l		for SRK45, complete			(D90904) lysostaphin	1	
742	AB012106	cds	0.059	1652318	[Synechocystis sp.]	4.7	
					[[o]nechooyana ap.]	 / - 	
		Homo sapiens mRNA				i i	
743	4.7007000	for KIAA0451	1		transcription factor brn-3b -	i 1	
/43	AB007920	protein, complete cds	0.059	479491	human	0.71	
		Human histidine	. [1	· 1	
ł		decarboxylase (HDC)	ł		1].	
744	M60445	mRNA, complete cds	0.058	<none></none>	<none></none>	ANONT:	
		and the complete cas	- 0.050	VIIOI1E5	OLIGOPEPTIDE	<none></none>	
					TRANSPORT SYSTEM		
			Í		PERMEASE PROTEIN OPPC		
1 1	į		1		>gi 1075086 pir D64184		
			- 1		oligopeptide transport system		
		**	- 1		permease protein (oppC)C		
		Ustilago maydis	į į		homolog - Haemophilus		
		exodeoxyribonucleas	1		influenzae (strain Rd KW20)		
745	- 1	e (REC1) gene.	0.050	1171000	permease protein (oppC)		
·3	001930	complete cds.	0.058	1171908	[Haemophilus influenzae Rd]	1.5	
	į.	Lycopersicon .	1	•	1		
ŀ		sculentum cytosolic	į		.	1	
j		class II small heat	- 1	•	1	. [
Ì		shock protein HCT2	ļ	•	1		
		(HSP17.4) mRNA.	1		(AF069131) chitinase [Bacillus	j	
746		complete cds	0.058	3193265	subtilis]	0.002	
		Brassica rapa mRNA					
747		or SLG45, complete	0.057		(U03978) dynein heavy chain	ľ	
/-/	AB012105 c	ds	0.057	433385	isotype 7A [Tripneustes gratilla]	3.4	

	Neares	t Neighbor (BlastN vs. (Gunhank)	Norman XI :	Norma Victoria			
SE		THE TOTAL TO	Jenoank)	Nearest Neig	hbor (BlastX vs. Non-Redundant F	roteins)		
П	-	N DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALU		
<u> </u>		Arabidopsis thaliana				IT VALUE		
74	AJ005813	mRNA for neoxanthin cleavage enzyme	0.056	<none></none>	<none></none>	<none></none>		
749	Y16828	Lagopus lagopus genomic microsatellite sequence, LLST4	0.056	3328678	(AE001299) hypothetical protein (Chlamydia trachomatis			
750	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.055	<none></none>				
751	AF074385	Sambucus nigra hevein-like protein mRNA, complete cds	0.055	137339	<none> 69 KD PROTEIN >gi 94375 pir S19150 hypothetical protein, 69K - turnip yellow mosaic virus</none>	<none></none>		
752	U76523	Sambucus nigra lectin precursor mRNA, complete cds	0.035	<none></none>	<none></none>	<none></none>		
753	M92069	Human retrovirus-like sequence-isoleucine c	0.034	<none></none>	<none></none>	<none></none>		
754		GIL=ankyrin-like repeat [orf virus OV. NZ2, Genomic. 1608 nt]	0.033	2804465	(AF043700) contains similarity to human RNA-binding protein FUS/TLS (SW:Q28009) [Caenorhabditis elegans]	0.15		
755		Chicken myosin alkali light chain mRNA, complete cds, clone pF1	0.027	3334221	4- HYDROXYPHENYLPYRUVA TE DIOXYGENASE 4- hydroxyphenylpyruvate dioxygenase [Mycosphaerella graminicola]			
764	c c c	Arabidopsis thaliana rellulose synthase ratalytic subunit (Ath-			(Z96048) predicted using	6e-17		
756	AF027174 c	ds	0.025	000000	Genefinder	5.0		

	Neares	t Neighbor (BlastN vs.	Genhank)	None N.:		
SE		Treignbor (Blastiv vs.	Genbank)	Nearest Neig	thbor (BlastX vs. Non-Redundant F	roteins)
Е	- 8	N DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
-		- 				
757	AJ002291	Streptococcus pneumoniae pbp1b gene, complete	0.025	3880487	(258014) similar to ribose- phosphate pyrophosphokinase; cDNA EST EMBL:D73173 comes from this gene; cDNA EST EMBL:D70909 comes from this gene; cDNA EST EMBL:D73449 comes from this gene; cDNA EST EMBL:D76167 comes from this	
		Benef complete	0.023	3660437	ge	1.7
758	X79104	C.botulinum (NCTC 7272 type A) HA-33 and P-21 genes.	0.024	2648615	(AE000970) tungsten formylmethanofuran dehydrogenase, subunit B (fwdB 2) [Archaeoglobus fulgidus]	6.1
759	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.024	1663698	(D83785) expressed ubiquitously; product similar to D.melanogaster mam protein. [Homo sapiens]	4.7
760	U36197	Chlamydomonas reinhardtii cobalamin- independent methionine synthase mRNA, complete cds	0.024	585723	PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR GAMMA (PPAR-GAMMA) >gi 283818 pir C42214 peroxisome proliferator- activated receptor gamma chain African clawed frog >gi 214668 (M84163) peroxisome proliferator activated receptor gamma [Xenopus laevis]	0.42
761		Macaca mulatta (clone MMVA63) T- cell receptor alpha (TCR A) mRNA,				0.72
101	L38865	partial cds.	0.023	<none></none>	<none></none>	<none></none>
762	AF035948	Mus musculus insulin receptor substrate-3 S.tuberosum mRNA	0.023	2500587	SPLICEOSOME ASSOCIATED PROTEIN 49 spliceosome-associated protein SAP-49 - human >gi 556217	0.40
763	į,	for inorganic phosphate ransporter, StPT1	0.023		proline-rich protein MP4 - mouse >gi 53182	0.18

		est Neighbor (BlastN vs.	Genbank)	Nearest Ne	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
	Q				, S. T. Tou-Redundant	Froteins)		
	D ACCESSI	ON DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	D. 1/47.77		
						P VALUE		
		L.esculentum mRN	1					
76	4 X91212		0.022	<none></none>	<none></none>			
- 1	ł	Homo sapiens			KNONES	<none></none>		
- 1	1	chromosome 5, PI		Ī	i	1.		
-)	1	clone 1209C1 (LBN	L	1	j	- 1		
	i	H104), complete	1			[
	1	sequence [Homo	1	!	1	ł		
76	5 AC00449	8 sapiens]	0.022	<none></none>	100-	1		
1		Human prostatic acid		STORES	<none></none>	<none></none>		
- 1	1	phosphatase (ACPP)	1		•			
76	5 U07083	gene, exon 1	0.022	· <none></none>				
1		S.tuberosum mRNA		KNONES	<none></none>	<none></none>		
.1	j	for inorganic			1	1		
	ł	phosphate						
767	X98890	transporter, StPT1	0.022	<none></none>		1		
		L.esculentum LAT59		CHONES	<none></none>	<none></none>		
ı	1	gene 5'flanking	1 1					
1	i	region. expressed	1			1 1		
1	•	during pollen	1	•		1		
768	X56488	maturation	0.022	-NONE-		1 1		
		Pseudorabies virus	0.0	<none></none>	<none></none>	<none></none>		
1	1	with upstream and	i 1		j			
1	i	downsteam				1 1		
769	M34651	sequences.	0.022	-NONE.		j . j		
		P.taeda gene for	0.022	<none></none>	<none></none>	<none></none>		
I	1	protochlorophyllide			(70000 () ***	1		
770	X66727	reductase	0.022	2070617	(Z92806) K10G4.4	1 1		
		,	0.02_	3878517	[Caenorhabditis elegans]	4.3		
ľ	i	Xenopus laevis	i		1			
l		mitotic	į		L'ESSESSESSESSESSESSESSESSESSESSESSESSESS	1 1		
l		phosphoprotein 90			(D89501) similar to salivary	1 1		
_77i	U95102	mRNA. complete cds	0.022	1854452	proline-rich protein P-B [Homo	!		
· ·		Xenopus laevis	0.022	1034432	sapiens]	4.3		
į į		mitotic			1	1		
		phosphoprotein 44	I		(A POOSOO = (= = ==			
772	U95098	mRNA, partial cds	0.022	3021699	(AB005298) BAI 2 [Homo			
			- 0.022	3021099	sapiens]	0.64		
J		H.sapiens XB gene	- 1		liver stage antigen LSA-1 -	1		
j	;	for tenascin-X, intron	1		Plasmodium falciparum	1		
773	X71932	14	0.022	627050	>gi 9916 (X56203) liver stage	1		
7			0.022	627059	antigen	0.058		
I		C.perfringens nunH	1		(1/79075)	1		
774	X87369	gene & ORF1.2.3 & 4	0.022	2062407	(U78975) poly(ADP-ribose)	1		
			5.522	2002407	glycohydrolase [Bos taurus]	0.056		

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEC		Tiorghoor (Brase, 1 vs.	Genounk)	ivearest (veigi	nbor (BlastX, vs. Non-Redundant I	roteins)	
D	- 1	DESCRIPTION	1	l _	1	1	
<u> </u>	ACCESSIO	DESCRIPTION	PVALUE	ACCESSION	DESCRIPTION	P VALUE	
-		<u> </u>			UI SMALL NUCLEAR		
i	j		1	1	RIBONUCLEOPROTEIN 70		
	İ			Ī	KD (U1 SNRNP 70 KD)		
ı	I		1	i	>gi 85864 pir S02016 U1		
ł			İ	}	snRNP 70K protein - African	1	
i	i	Caller PNA	1	Ì	clawed frog >gi 65179		
775	Y14971	Gallus gallus mRNA for K60 protein	0.022	12400	(X12430) U1 70K [Xenopus	1	
	1	ioi koo protein	0.022	134091	laevis DNA REPAIR PROTEIN	0.032	
1	1	Caenorhabditis				1	
1		elegans cosmid			RAD18 >gi 1150622 protein	1	
776	AF003133	T21E3	0.022	1709997	rad18 (Schizosaccharomyces		
	1	1.0.00	0.022	1703337	pombe) DNA REPAIR PROTEIN	2e-08	
1	ł.	Caenorhabditis			RAD18 >gi 1150622 protein		
1	J	elegans cosmid	1		rad18 [Schizosaccharomyces		
777	AF003133	T21E3	0.022	1709997	pombel	2e-08	
]	Human helix-loop-			pember	2e-08	
1		helix proteins Id-1				1 1	
1		(ID-1) and Id-1' (ID-	1 1			i i	
1		1) genes, complete	1 1			1 1	
778	U57645	cds	0.021	<none></none>	<none></none>	<none></none>	
ł	i	Methanococcus					
1		jannaschii section 112	1		}		
779	1167570	of 150 of the			1] [
1/9	U67570	complete genome	0.021	<none></none>	<none></none>	<none></none>	
		Trypanosoma cruzi calcium-binding]				
		protein (CUB2.8)				1 1	
780	L01584	gene, complete cds.	0.021	NONE		1	
	201504	gene, complete cus.	0.021	<none></none>	<none></none>	<none></none>	
}		Borrelia hermsii outer	ı				
781	L04787	membrane lipoprotein	0.021	<none></none>	-NONTE-	Allow I	
		Xenopus laevis XL-		~10/1E>	<none></none>	<none></none>	
		INCENP (XL-	ł	•	•		
i i		INCENP) mRNA.	Į	į	·		
782	U95094	complete cds	0.021	<none></none>	<none></none>	<none></none>	
i J	7					4	
	1	Saccharomyces	1			· I	
ı	i i	cerevisiae	i	ļ			
	1	mitochondrion	İ	}		ſ	
ľ		ransfer RNA-Thr1	1	ļ	·	l	
1		tRNA-Thr) gene;	1	l		ĺ	
		ransfer RNA-Val tRNA-Val) gene;	1.	ļ	·	<u> </u>	
			1	l		1	
1		oxi2 gene, complete eds; ORF2 and origin	ł	-	1		
783		of replication (ori5).	0.02	,,,,,,,,		i	
	E30090 (C	i replication (0f15).	0.021	<none></none>	<none></none>	<none></none>	

	Neares	t Neighbor (BlastN vs.)	Genbank)	Nearest Neig	hbor (BlastX vs. Non-Redundant	Proteins\
SE	Q				Control Control Control	rio(eins)
E	ACCESSIO	N DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALU
<u> </u>	- 					+
į	1	Homo sapiens biliary	1			
784	M76741	glycoprotein (BGP)	0.00.			1
 /°	W170741	gene, partial cds. Tetrahymena	0.021	<none></none>	<none></none>	<none:< td=""></none:<>
1	ł	thermophila histone		·		
1		H3 (HHT2) gene.			1	
785	M87504	complete cds	0.021	<none></none>	-NONE-	
			3.322	- CONE	<none></none>	<none></none>
	1	Human calpain-like	1			ł
1		protease (htra-3)				
786	U94346	mRNA, complete cds	0.021	<none></none>	<none></none>	<none></none>
[1	Trypanosoma cruzi				
1	1	calcium-binding			1	
787	L01584	protein (CUB2.8)				1 '
 '8'	L01384	gene. complete cds. Pongo pygmaeus CT	0.021	<none></none>	<none></none>	<none></none>
]	microsatellite, clone	į			
	ł	#1, from the tandemly	1			i
l	i	repeated genes			İ	1
		encoding U2 small			1	
1		nuclear RNA (RNU2				ł
788	U36530	locus)	0.021	<none></none>	<none></none>	<none></none>
	,	Human gene for			1	TATOMES
700	*****	interleukin 1 alpha	i		EARLY TRANSCRIPTION	1 1
789	X03833	(IL-1 alpha)	0.021	416974	FACTOR 70 KD SUBUNIT	8.9
		Dictyostelium	1	. —		
		discoideum guanine	į.		}	
		nucleotide-binding	- 1			1
		protein alpha subunit			(IIEEE IO) DATA I II	1 1
		5 (G alpha 5) gene,	1		(U58510) RNA helicase homolog [Chlorarachnion	j i
790		complete cds.	0.021	1401211	CCMP6211	l I
					ACONITATE HYDRATASE	8.8
	ĺ		ŀ	:	(CITRATE HYDRO-LYASE)	
[H.sapiens CpG DNA.			(ACONITASE) >gi 2183256	j
70.		clone 13d2, reverse		·	(AF002133) aconitase	
791	Z59258	read cpg13d2.rt1c . Plasmodium	0.021	3121732	[Mycobacterium avium]	7.0
ł		falciparum strain 7G8			NINE PROTEIN	
		chloroquine	1		>gi 2120251 pir S66581	
- 1	1	esistance candidate	1		hypothetical protein 56 - phage	
J		protein (cg2) gene.	1		82 >gi 1051114 (X92588)	j
792		complete cds	0.021		orf56; related to nin60 (ninE) of bacteriophage lambda	
		lethanococcus	0.021	3024190	oucteriopnage lambda	5.8
- 1		annaschii section 112	1	.		
	o	f 150 of the	1	l.	(AC000104) F19P19.17	
793	U67570 c	omplete genome	0.021		Arabidopsis thaliana]	4.0
						4.0

	Neare	st Neighbor (BlastN vs.	Genbank)	Nanan Mai		
SI	EQ	1	Jenounk)	rearest Nei	thbor (BlastX vs. Non-Redundant P	roteins)
	D ACCESSION	ON DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
-					NUCLEAR FACTOR NF-	1
	į.	1	1		KAPPA-B P100 SUBUNIT	
- 1	Ī			1	(H2TF1) (ONCOGENE LYT-	Į –
- 1	1	l	1	i	10) (LYT10) [CONTAINS:	
-		Human DNA for	1	[NUCLEAR FACTOR NF-	1 1
75	4 D86566		0.021	1708619	KAPPA-B P52 SUBUNIT	3.1
	1	Streptomyces			10200001111	3.1
1	ł	coelicolor sigma		ł	hypothetical 119.5K protein	
	. .	factor (rpoX) gene,	1		(uvrA region) - Micrococcus	
79	5 L11648	complete cds.	0.021	79833	luteus	1.8
1	1				NEUROENDOCRINE	1.3
		ł			CONVERTASE I	·
ł	1	İ	j .		PRECURSOR (NEC 1) (PC1)	} .
	ŀ	Xenopus laevis XI			(PROHORMONE	1 1
1	1	INCENP (XL-	1		CONVERTASE 1) propeptide	1 . 1
1	. 1	INCENP) mRNA.			processing protease [Mus	l f
790	5 U95094	complete cds	0.021	128000	cookii	1.0
l	į.	Rattus norvegicus				1.0
		microtubule-	•		(X74416) beta-3 integrin	
797	U30938	associated protein 2	0.021	468600	[Takifugu rubripes]	1.0
1	ł	Chicken mRNA for			[Tame and Table 1963]	1.0
1		TSC-22 variant,	ı		.[ł
	. _	complete cds, clone	1		27 kda amelogenin	į.
798	D82364	SLFEST52	0.021	693723	(alternatively spliced)	0.61
i	ł				55.564	0.01
700		Gallus gallus eHAND			(AB011541) MEGF8 [Homo	ľ
799	U40041	mRNA, complete cds	0.021	3449308	sapiens]	0.21
i	ł				liver stage antigen LSA-1 -	<u> </u>
ł	Ī	H.sapiens XB gene			Plasmodium falciparum	i i
	l	for tenascin-X, intron	1		>gi 9916 (X56203) liver stage	İ
800	X71932	14	0.021	627059	antigen	0.054
	ł	Oryza sativa 24-		•		0.054
1	ļ ·	methylene lophenol			J	ł
		C24(1)methyltransfer	- 1		1	·
801		ase mRNA, complete	1		(X83413) U88 [Human	
801	AF042333	cds	0.021	854065	herpesvirus 6]	0.014
	ł					0.0.1
	ĺ		i			ì
		Rat apical endosomal	- 1		1	ŀ
902	7.3222	glycoprotein mRNA.	1	j.	TRANSMEMBRANE	1
802	L37380	complete cds.	0.021		PROTEASE, SERINE 2	le-05
					ONA REPAIR PROTEIN	
		Caenorhabditis	j		RAD18 >gi 1150622 protein	· 1
902	4.5000105	elegans cosmid	1	1	ad18 (Schizosaccharomyces	1
803	AF003133	T21E3	0.021		pombe]	3e-08

T	Nearest	Neighbor (BlastN vs. C	nhank)	Non N		
SEQ		Treighbor (Diastra Vs. (Jenbank)	Nearest Neigh	hbor (BlastX vs. Non-Redundant F	roteins)
ID ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DECCO PROMON	
	1	Rabbit mRNA for	1 VALUE	ACCESSION	DESCRIPTION	P VALUE
 	 	calcium channel BI-2	 	 		
1	ļ	(lambda CBP109 and			(41 00011701	İ
804	X57689	(B101)	0.021	2959370	(AL022117) hypothetical	1
	137507	CDIOII	0.021	2939370	protein (U41534) coded for by C.	le-10
1		Xenopus laevis	l	l	elegans cDNA CEESI42F;	1
j	1	mitotic	ľ	j	Similar to helicases of	1
1	ł	phosphoprotein 90	1	}	SNF2/RAD54 family.	1
805	U95102	mRNA, complete cds	0.021	1109830		5e-11
					[Caenorhabditis elegans] HYPOTHETICAL 38.5 KD	Je-11
		.,	ł		PROTEIN IN ERV1-GLS2	į.
1	i			"	INTERGENIC REGION	
i				ł	>gi 2132587 pir S64322	1
1	1	[1	probable membrane protein	
1	1]			YGR031w - yeast	
l .					(Saccharomyces cerevisiae)	1
					>gi 1323010 gnl PID e243277	1
806	V77752	H.sapiens TROP-2			(Z72816) ORF YGR031w]
800	X77753	gene S.tuberosum mRNA	0.021	1723657	[Saccharomyces cerevisiae]	5e-11
ŀ		for inorganic				l
1 1		phosphate				
807	X98890	transporter, StPT1	0.021	2137872	zinc finger protein PZF - mouse >gi 453376	
			0.021	2137672		2e-19
		Arabidopsis thaliana	1	•		·
i I		cellulose synthase	i		}	1 1
		catalytic subunit (Ath-]]
		A) mRNA, complete	i		1	i 6
808		cds	0.020	<none></none>	<none></none>	<none></none>
		Homo sapiens	i			
000		Promotor Region and]	
809	AJ224935	PCK2 gene	0.020	<none></none>	<none></none>	<none></none>
Ī		Sambucus nigra		•		
1		ribosome inactivating	İ			
- 1		protein precursor	1			J
810		mRNA, complete cds	0.020	<none></none>	NONE	
		A.thaliana GBF1	0.020	<140NE>	<none></none>	<none></none>
811		gene	0.020	<none></none>	<none></none>	<none></none>
					110112	2101162
- 1	F	M.musculus mRNA	[i	J
- 1		or tyrosine kinase >	1			- 1
J		: gb S57168 S57168	1			1
		Sek=Eph-related	}			
1		eceptor protein	1	}	ļ	1
		yrosine kinase [mice.			· .	l
812	X65138 r	nRNA, 4242 nt]	0.020	<none></none>	<none></none>	<none></none>

S. 15%:	Nearest	Neighbor (BlastN vs. C	ienbank)	Nanage Main	hbor (BlastX vs. Non-Redundant P	
SEQ		Trenghoor (Diase : vs. e	l l	I demest lasig	Hoof (Blastic Vs. Non-Redundant P	roteins)
B	ACCESSION	DESCRIPTION	PVALUE	ACCESSION	DESCRIPTION	P VALUE
	ļ.,					
1		Borrelia hermsii outer	1			
813	L04787	membrane lipoprotein		<none></none>	<none></none>	<none></none>
1	1	Enterococcus faecium				
1	L	genes encoding	ĺ			
1	i	enterocin L50A and			‡	}
1	ľ	enterocin L50B plus		•	1	į
814	AJ223633	5' and 3' flanking	0.020	2107		
014	AJ223033	regions Brassica rapa mRNA	0.020	<none></none>	<none></none>	<none></none>
i	į	for SRK45, complete		i		1
815	AB012106	cds	0 .020	<none></none>	1	l
10.0	12012100	Helicobacter pylori,	0.020	KNONES	<none></none>	<none></none>
1	}	strain J99 section 100	٠.		(L11895) transmembrane	1
ļ		of 132 of the			protein [Saccharomyces	
816	AE001539	complete genome	0.020	172292	cerevisiael	
			0.020	11-272	CELEVISIAE	8.4
ĺ		Sambucus nigra			pol polyprotein - Chinese	
		hevein-like protein	-		hamster intracisternal A-particle	
817	AF074386	mRNA, complete cds	0.020	94173	CHIAP34	8.0
1 1						0.0
		Herpesvirus saimiri				
		dihydrofolate	ł			
1 1		reductase (DHFR)	ı		1	
ا ا		and snRNA (HSUR)			(Z98745) dJ29K1.2 [Homo	I
818	M55264	genes, complete cds.	0.020	2924250	sapiens]	6.5
					D(4) DOPAMINE RECEPTOR	
			ŀ		(D(2C) DOPAMINE RECEPTOR)	ĺ
]			ł		1	
	i		1		>gi 2119482 pir I49246 D4	1
	j		Ī		dopamine receptor - mouse >gi 758427 (U19880) D4	
	Ì	1	l		dopamine receptor [Mus	Ī
l	j		·]		musculus]	
ł	· • • • • • • • • • • • • • • • • • • •	Homo sapiens clone	1		>gi 1095539 prf 2109259A	
		24456 mRNA	1		dopamine D4 receptor [Mus	İ
819		sequence	0.020	1706288	musculus]	4.9
						
- 1		Sambucus nigra	ŀ		1	Ì
	ŀ	nevein-like protein	ł		(Z83259) AmphiBrf38	1
820	AF074387 r	nRNA, complete eds	0.020	2113798	[Branchiostoma floridae]	4.7
	1		T		(Z67754) cDNA EST	
	l				EMBL:T02354 comes from this	•
	į		ı		gene; cDNA EST	į
	l.				EMBL:D32698 comes from this	
J		Homo sapiens clone	ŀ	í	gene; cDNA EST	į
821		4456 mRNA	0000		EMBL:D35411 comes from this	1
921	AF052163 s	equence	0.020	3874733	gene	4.7

1	Nearest	Neighbor (BlastN vs. G	enbank)	Nearest Neigh	nbor (BlastX vs. Non-Redundant P	roteins)
SEQ					To the state of th	Totellis,
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	L
-	11.002.00101	T DODGRAM HOW	TVALUE	ACCESSION	DESCRIPTION	P VALU
-	 	Rat ankyrin binding				<u> </u>
1	! .	glycoprotein-1 related			7701660 71	1
822	L11002	mRNA sequence.	0.020	553133	(K01664) Bkm-like protein	1
1022	L11002	Helicobacter pylori,	0.020	552132	[Drosophila melanogaster]	3.8
i	ł	strain J99 section 100			(7.11805)	•
1	ľ	of 132 of the		ł	(L11895) transmembrane	ļ
823	AE001539	complete genome	0.020	172292	protein [Saccharomyces	2.0
1 333	1.0001555	complete genome	0.020	172292	cerevisiae	3.8
1	i	<u> </u>			Domain (2 domains); cDNA	ľ
					EST yk390b10.3 comes from	
	ł	• •			this gene; cDNA EST	
Į.					EMBL:D71652 comes from this	
I			٠.		gene; cDNA EST yk275f8.3	
l		1			comes from this gene; cDNA	
1				•	EST yk393b9.3 comes from this	
1					gene; cDNA EST yk37	
					>gi 3880220 gni PID e1349842	
					yk390b10.3 comes from this	}
i		.	Į.		gene; cDNA EST	j
j j		.	1		EMBL:D71652 comes from this	!
1 1		S.tuberosum mRNA			gene: cDNA EST yk275f8.3	
i i		for inorganic			comes from this gene; cDNA	
		phosphate	ı		EST yk393b9.3 comes from this	
824	X98890	transporter, StPT1	0.020	3879798	gene; cDNA EST yk37	1.3
					C-T-TETRAHYDROFOLATE	
					SYNTHASE, CYTOPLASMIC	
			1		(CI-THF SYNTHASE)	
il			1	•	(METHYLENETETRAHYDR	
1			l		OFOLATE	
)	ĺ		DEHYDROGENASE/	
	•	Homo sapiens	- 1	i	METHENYLTETRAHYDROF	j
į	1	podocalyxin-like	. 1		OLATE CYCLOHYDROLASE	
	1	protein mRNA,			C1-tetrahydrofolate synthase	:
825	U97519	complete cds	0.020	1345633	[Rattus norvegicus]	0.066
ſ	ļ	_			DNA REPAIR PROTEIN	
- 1	1	Caenorhabditis	- 1		RAD18 >gi 1150622 protein	
l	1	elegans cosmid	1		rad18 [Schizosaccharomyces	
826	AF003133	Γ21Ε3	0.020	1709997	pombe!	2e-07
1	1.	Saashaaa	· 1			
- 1		Saccharomyces	i		J	1
- 1	1	cerevisiae VARI	j		Į	ł
- 1	1-	gene, mitochondrial	J	ļ	1	
- 1		gene encoding	- !		ľ	
1	1	nitochondrial	j	1	1	}
		protein, 3' processing		,	1	ŀ
827	U32857 s	ite, partial sequence	0.019	<none></none>	<none></none>	<none></none>

1,3	Neares	Neighbor (BlastN vs.	Genbank)	Negrost Mais	ghbor (BlastX vs. Non-Redundant F	
SE		1		THE TIEST THEIR	and (Blasca vs. 1900-Redundant F	Toteins)
ID		DESCRIPTION	PVALUE	ACCESSION	DESCRIPTION	
	+		1 VALUE	ACCESSION	DESCRIPTION	P VALUE
			 	 	NEUROGENIC LOCUS NOTCH HOMOLOG	
1	1	Arabidopsis thaliana	ı			1
1	4	cellulose synthase	{		PROTEIN 4 PRECURSOR	.
1	1	catalytic subunit (Ath]		(TRANSFORMING PROTEIN	
	1	B) mRNA, complete	1		INT-3) mammary gene mRNA,	
828	AF027174	cds	0.019	2506381	complete cds.], gene product	
		1	0.019	2300381	[Mus musculus] (ALU21481) similar to	3.3
ł	1			ł	Phosphoglucomutase and	1
1	1		-		phosphomannomutase	1
	ł		ł		phosphoserine; cDNA EST]
1	1		1		EMBL:D36168 comes from this	
1				1	gene; cDNA EST	` ·
1	1	Laccaria bicolor	1 . 1		EMBL:D70697 comes from this	
1	1	glyoxal malate] i		gene; cDNA EST yk373h9.5]
1	1	synthase protein		, i	comes from this gene; cDNA	1
829	AF034099	mRNA, complete cds	0.019	3880930	EST EMBL:T008	6.16
		Mus musculus	5.5.5	3000730	EST EMBL. 1008	6e-15
ł	i .	Pontin52 mRNA,				1
830	AF100694	complete cds	0.018	<none></none>	<none></none>	<none></none>
		Human RP1 and			4101112	CHOINES
	i .	complement C4B				1
	,	precursor (C4B)			proline-rich protein precursor -	1
831	U24578	genes, partial cds.	0.013	478673	kidney bean vulgaris]	3.1
	1		Į.			
ŀ		Sambucus nigra lectin			•	1
832	1176522	precursor mRNA,				
032	U76523	complete cds Dibenzoluran-	110.0	<none></none>	<none></none>	<none></none>
		degrading bacterium	1			
		DPO360 2.3-	[
	l	dihydroxybiphenyl]	
		1,2-dioxygenase	1]	1
		(bphC) gene.	· 1		[· .	. [
		complete cds and 2-	Į.		1	į
		hydroxy-6-oxo-6-			1	1
		phenylhexa-2.4-	1		'	j
	1	dienoic acid	1			i
833		hydrolase	0.011	<nonf~< td=""><td>NONES</td><td>ATOM TO</td></nonf~<>	NONES	ATOM TO
		Z.mays gene for		<none></none>	<none></none>	<none></none>
l		phosphoenolpyruvate	1	ı	. 1	
834		carboxylase	0.011	<none></none>	<none></none>	<none></none>
T					1101122	ZITOITES
		Celegans collagen		i	(D83706) pyruvate carboxylase	1
835		gene col-13	0.010	1695686	[Bacillus stearothermophilus]	3.1
		Cattus norvegicus NF-				
		CB gene, promotor	- 1		(AB020660) KIAA0853 protein	, 1
836	U83656 r	egion	0.008		[Homo sapiens]	10.0

PCT/US00/18374

<u> </u>	Neare	st Neighbor (BlastN vs.	Genbank)	Nuneaut Mais	hh (D) V N D	
SE			Jenounk,	Nemest Mei	phbor (BlastX vs. Non-Redundant I	Proteins)
П	`	DESCRIPTION		1		1
	ACCESSIC	NA DESCRIPTION	PVALUE	ACCESSION	DESCRIPTION	P VALUE
-		Homo sapiens gene	 	·	POL POLYPROTEIN	T
ł	Į	encoding retina-	i	ł	(ORFIA/IB) [CONTAINS:	
- 1	ď	specific guanylyl	1	[RNA-DIRECTED RNA	ı
83	7 AJ222657	cyclase	0.000		POLYMERASE : HELICASE;	1
		Cyclase	0.008	417704	PROTEASE]	7.4
- 1	1			ĺ	CHLORIDE CHANNEL	
1	ı		1	ł	PROTEIN, SKELETAL	1
ì	İ		ł	ł	MUSCLE (CHLORIDE	I
	į.		!		CHANNEL PROTEIN I) (CLC	'
1	j	1		ł	1) human >gi 397143 (Z25587)	1
	1	1	1		human ClC-1 muscle chloride	j
1	1	Brassica rapa mRNA		<i>'</i> .	channel [Homo sapiens]	
ł		for SRK45, complete		,	>gi 398161 (Z25884) human	
838	AB012106		0.008	544024	CIC-1 muscle chloride channel	j
			0.000	344024	[Homo sapiens]	4.6
1	1	Sambucus nigra			(U13643) similar to reverse	1
1		ribosome inactivating			transcriptase; possible	1 1
1	l	protein precursor	1		pseudogene [Caenorhabditis	i l
839	U76524	mRNA, complete cds	0.008	532468	elegans]	
]					olegans)	3.8
j	l	Sambucus nigra	j			İ
	l	ribosome inactivating			(AF002589) cytochrome	l
1	. 50	protein precursor	- 1		oxidase I [Austrofundulus	
840	AF012899	mRNA, complete cds	0.008	4101160	limnaeus]	2.7
ł	l		j			
1		Sambucus nigra	- 1		1	
841	AF074385	hevein-like protein			SRB-8/9 PROTEIN	ł
1041	ALF074383	mRNA, complete cds	0.008	1711520	>gi 1334996	1.6
		Human non-muscle	1			
		alpha-actinin mRNA.	- 1			
842	U48734	complete cds	0.000		(AC002291) extensin	I
	0 10/34	Homo sapiens 3-	0.008	2829922	[Arabidopsis thaliana]	0.11
l		hydroxyisobutyryl-	j	İ	·	
		coenzyme A	ľ		Į.	j
	I	hydrolase mRNA,	1		i	
843		complete cds	0.007	<none></none>	NO.	
				CHOMES	<none></none>	<none></none>
ĺ		Mouse mRNA for	1	Ī		- 1
- 1	ļ:	P100 serine protease	ſ	İ	. 1	- 1
		of Ra-reactive factor	1	ŀ	1	
844		RaRF), complete cds	0.007	<none></none>	<none></none>	NIONE
					- CHOISES	NONE>

1.30	Neares	t Neighbor (BlastN vs. (Genhanki	Name No.	(D) - V	
SE		1		ivenest (veig	hbor (BlastX vs. Non-Redundant	Proteins)
П		N DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	
	T	Human	1	ACCESSION	DESCRIPTION	P VALUE
		immunodeficiency				
- [ł	virus type 1 proviral		i		1
- 1	1	DNA for envelope	1	[
- 1		glycoprotein, partial	I			1
. 84	5 D90923	cds, isolate 03S	0.007	<none></none>		1
		120, 180,1210 030	0.007	CHONES	<none></none>	<none></none>
	1	Homo sapiens mRNA	.]			1
-	ł	for KIAA0515	j			- (
840	6 AB011087	protein, partial cds	0.007	<none></none>	<none></none>	NONE
1					GIONES	<none></none>
1		Aquifex aeolicus		, ·	İ	1
1	ŧ	section 20 of 109 of	1		1	1 1
847	AE000688	the complete genome	0.007	<none></none>	<none></none>	NONE
1		B.bovis WC1.1			CHOILES	<none></none>
848	X63723	mRNA	0.007	<none></none>	. <none></none>	<none></none>
1						1310112
		Sambucus nigra		•		1
1		hevein-like protein				1 1
849	AF074386	mRNA, complete cds	0.007	<none></none>	<none></none>	<none></none>
	1		- i			
1	i	Human beta globin	1		1] [
850	700007	region Alu repetitive	. 1		1 .	1 1
630	J00097	sequence type T. Human	0.007	<none></none>	<none></none>	<none></none>
1	1	1	j			
		immunodeficiency	ŀ			1 1
1	i	virus type 1 proviral DNA for envelope	l			1 1
i		glycoprotein, partial	1			1 1
851	D90923	cds, isolate 03S	0.007			1
-	270723	Xenopus laevis XL-	0.007	<none></none>	<none></none>	<none></none>
1]	INCENP (XL-	- 1			1 7
	1	INCENP) mRNA,	1] [
852	U95094	complete cds	0.007	· NICONTE		J
		T.castaneum	0.007	<none></none>	<none></none>	<none></none>
853	I	hunchback gene	0.007	<none></none>	NOTE	<u>.</u>
		Rat nontranscribed	0.007	ZIAOIAE>	<none></none>	<none></none>
		spacer (NTS)	ł	j	ļ	ľ
		downstream of 28S				J
854		RNA gene	0.007	<none></none>	<none></none>	NIONIE
					CHONES	<none></none>
	נן	Rattus norwegicus	1	ļ	· j	1
	ļ i	nterleukin-2 receptor	1	ļ		1
		Ipha chain (CD25)	[1
855	M55049 r	nRNA, complete cds.	0.007	<none></none>	<none></none>	<none></none>
				 		~

		Neare	st Neighbor (BlastN vs.	Genbank)	Nearest Neig	hbor (BlastX vs. Non-Redundant	
	SEQ					(Diasta Vs. 140n-Redundani	Proteins)
Ļ	D	ACCESSIO	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
-		 					I VALUE
- 1		}	H.sapiens CpG DNA clone 9e2, reverse	·			
	856	Z64318	read cpg9e2.rt1a.	0.007	NONE	1	1
			read epgsez.itia .	0.007	<none></none>	<none></none>	<none></none>
			Arabidopsis thaliana			ŀ	
-			cellulose synthase				
			catalytic subunit (Ath	1			1 1
ı	857	AF027173	A) mRNA, complete cds	0.007	ANONE:		
Γ				0.007	<none></none>	<none></none>	<none></none>
			Arabidopsis thaliana	ŀ	••		
	I		cellulose synthase				1 1
	- 1		catalytic subunit (Ath- B) mRNA, complete				1 1
1 8	358	AF027174		0.007	-NONTE-		1 1
Γ			- 000	0.007	<none></none>	<none></none>	<none></none>
	- 1	Ť	Sambucus nigra			·]
1	- [ribosome inactivating	j			1 1
8	59	AF012899	protein precursor mRNA, complete cds	0.007			1 1
广	-	10 012099	P.falciparum	0.007	<none></none>	<none></none>	<none></none>
i			complete gene map of	1			i i
-8	60	X95276	plastid-like DNA	0.007	<none></none>	<none></none>	<none></none>
			Lycopersicon	- 1			1
	- 1	·	esculentum class II	- 1		ĺ	1 1
1			small heat shock	1		i	
			protein Le-HSP17.6	1			1
80	51	U72396	mRNA, complete cds	0.007	<none></none>	<none></none>	<none></none>
	i		Mus musculus Pontin52 mRNA.				
86	i2 ·	AF100694	complete cds	0.007	-NONE:		i l
	$\neg \vdash$			-0.007	<none></none>	<none></none>	<none></none>
1			Leucania seperata				
			nuclear polyhedrosis	1			1
	-		virus DNA for p13.	j	1		i 1
86	3 / /		xe, envelope protein.	0.007	NONE		1 1
			John Prote Cas	0.007	<none></none>	<none></none>	<none></none>
۰.			Human DNA for				
86	⁴╂	D86566	NOTCH4, partial cds	0.007	<none></none>	<none></none>	<none></none>
	1		Sambucus nigra	1			
			ribosome inactivating		1		
_	. 1	į,	protein precursor		Ĭ		
865		U76524 I	nRNA, complete cds	0.007	<none></none>	<none></none>	<none></none>
							

ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION DESCRIPTION DESCRIPTION DESCRIPTION DESCRIPTION DESCRIPTION DESCRIPTION DESCRIPTION DESCRIPTION DESCRIPTION DESCRIPTION DESCRIPTION DESCRIPTION DESCRIPTION	/ de	Neare	st Neighbor (BlastN vs.	Genbank)	Nearest Nain	hhor (Blact Y vs. Non Dadinatana	
D ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION R S.9	SI			1	T.C.D.C.St IVEIG	inoi (Biasex vs. 140n-Redundant Pi	roteins)
Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA. complete cds 0.007 3047072 (AF058825) No definition line found [Arabidopsis thaliana] 8.9		_ 1	DESCRIPTION	PVALUE	ACCESSION	DESCRIPTION	
Cellulose synthase catalytic subunit (Ath-A) mRNA. complete O.007 3047072 (AF058825) No definition line found [Arabidopsis thaliana] 8.9				1	I TICCESSION	DESCRIPTION	P VALUE
Caralytic subunit (Ath-A) mRNA, complete des			Arabidopsis thaliana		 		
A mRNA. complete cds			cellulose synthase	ļ	1		ŀ
AF027173 des	ı	i	catalytic subunit (Ath	ı -	İ	i	1
Articologosis thaliana cellulose synthase catalytic subunit (Ath B) mRNA, complete cds		1	A) mRNA, complete			(AF058825) No definition line	1
Arabidopsis thaliana cellulose synthase catalytic subunit (Ath B) mRNA, complete eds AF027174 eds	86	6 AF02717	cds	0.007	3047072		89
Cellulose synthase catalytic subunit (Ath B) mRNA, complete eds	1		A				- 0.5
Catalytic subunit (Ath-B) mRNA, complete cds	1	Í	-	1			i i
B	-	Į.				1	
Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds D.007 1213557 Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds D.007 1213557 Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds D.007 D.00	- 1	į.		1			
Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds D.007 1213557 Entercal Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds D.007 1213557 Entercal Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds D.007 1213557 Entercal Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds D.007 1213557 Entercal Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds D.007 1213557 Entercal Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds D.007 D.0	86	7 AF027174	•	0.007	,, одеже		
Sambucus nigra ribosome inactivating protein precursor mRNA. complete cds 0.007 1213557	"	74.02/1/4	cus	0.007.	9/5754	enterica]	8.6
Sambucus nigra ribosome inactivating protein precursor mRNA. complete cds 0.007 1213557						(U50199) coded for by C	
Sambucus nigra ribosome inactivating protein precursor mRNA. complete cds 0.007 1213557				i !			
Sambucus nigra ribosome inactivating protein precursor mRNA. complete cds 0.007 1213557 121355						for by C. elegans cDNA cm7g5:	İ
Sambucus nigra ribosome inactivating protein precursor mRNA. complete cds 0.007 1213557	1	.		!			
ribosome inactivating protein precursor mRNA. complete cds	1	i		i			i
176524 1	1			1			ı
Brassica rapa mRNA	1			1			
Brassica rapa mRNA for SRK45, complete cds 869 AB012106 cds Rattus norvegicus homer-1c mRNA. complete cds 870 AF093268 cmale described mRNA, complete cds 871 AF074386 mRNA, complete cds 871 AF074386 mRNA, complete cds 872 Brassica rapa mRNA for SRK45, complete cds 874 AF074386 mRNA, complete cds 875 AF074386 mRNA, complete cds 876 AF074386 mRNA, complete cds 877 AF074386 mRNA, complete cds 878 AF074386 mRNA, complete cds 879 AF074386 mRNA, complete cds 870 AF074386 mRNA, complete cds 870 AF074386 mRNA, complete cds 870 AF074386 mRNA, complete cds 870 AF074386 mRNA, complete cds 870 AF074386 mRNA, complete cds 870 AF074386 mRNA, complete cds 870 AF074386 mRNA, complete cds 870 AF074386 mRNA, complete cds 870 AF074386 mRNA, complete cds 870 AF074386 mRNA, complete cds 870 AF074386 mRNA, complete cds 870 AF074386 mRNA, complete cds 870 AF074386 mRNA, complete cds 870 AF074386 mRNA, complete cds 870 AF074386 mRNA, complete cds 870 AF074386 mRNA, complete cds 870 AF074386 mRNA, complete cds 870 AF074386 mRNA, complete cds 871 AF074386 mRNA, complete cds 872 AF074386 mRNA, complete cds 873 AF074386 mRNA, complete cds 874 AF074386 mRNA, complete cds 875 AF075TENTL. 88.4 PR071ENTL. SAPARTATE (D-ASPARTATE (D-ASPARTATE) METHYLTRANSFERASE (PROTEIN-L-ASPARTYL/D-A	000			ŀ			ŧ
ISOASPARTATE(D- ASPARTATE O- METHYLTRANSFERASE (PROTEIN-BETA- ASPARTATE METHYLTRANSFERASE (PROTEIN-BETA- ASPARTATE METHYLTRANSFERASE (PIMT) (PROTEIN L- ISOASPARTYL/D- ASPARTYL METHYLTRANSFERASE METHYLTRA	800	076524	mRNA, complete cds	0.007	1213557	elegans cDNA ykl31f11.5; c	8.4
ASPARTATE) O- METHYLTRANSFERASE (PROTEIN-BETA- ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L- ISOASPARTYL/D- ASPARTYL/D- ASPARTYL/D- ASPARTYL METHYLTRANSFERASE) methyltransferase [Drosophila melanogaster] > gill171337 melanogaster] > gill171337 melanogaster] > 8.3 Rattus norvegicus homer- lc mRNA. Complete cds O.007 AF093268 Sambucus nigra hevein-like protein mRNA, complete cds O.007 AF074386 MRNA, complete cds O.007 AF074386 AF074386	1	i		1		1	
METHYLTRANSFERASE (PROTEIN-BETA- ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L- ISOASPARTYL/D- ASPARTYL METHYLTRANSFERASE) methyltransferase [Drosophila melanogaster] >gi 1171337 melanogaster] >gi 1171337 melanogaster] > 8.3 Rattus norvegicus homer- lc mRNA. Rattus norvegicus homer- lc mRNA. Sambucus nigra hevein-like protein mRNA, complete cds O.007 AF093268 METHYLTRANSFERASE (PROTEIN-BETA- ASPARTYL METHYLTRANSFERASE) methyltransferase [Drosophila melanogaster] >gi 1171337 melanogaster] 6.2 M8095353) toll-like receptor 4 mutant [Mus musculus] 6.2 TRANSCRIPTION Bos taurus (clone TRANSCRIPTION TERMINATION FACTOR	1			1			1
Complete cds Comp	1	1	ļ	1			- 1
ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L- ISOASPARTYL/D- ASPARTYL METHYLTRANSFERASE) methyltransferase [Drosophila melanogaster] > gi 1171337 melanogaster] > gi 1171337 melanogaster] > 8.3 Rattus norvegicus homer-1c mRNA, complete cds 0.007 4092077 METHYLTRANSFERASE) methyltransferase [Drosophila melanogaster] > 8.3 Rattus norvegicus homer-1c mRNA, complete cds 0.007 4092077 Mutant [Mus musculus] 6.2 Sambucus nigra hevein-like protein mRNA, complete cds 0.007 151377 [Pseudomonas stutzeri] 6.2 TRANSCRIPTION TERMINATION FACTOR	1	1					
Brassica rapa mRNA for SRK45, complete eds 0.007 2499568 metanogaster >gi 1171337 metanogaster >gi 1171337 metanogaster >gi 1171337 metanogaster >gi 1171337 metanogaster >gi 1171337 metanogaster >gi 1171337 metanogaster >gi 1171337 metanogaster >gi 1171337 metanogaster <	1	1	j	ŀ		1'	1
Brassica rapa mRNA for SRK45, complete eds 0.007 2499568 metanogaster >gi 1171337 metanogaster >gi 1171337 metanogaster >gi 1171337 metanogaster >gi 1171337 metanogaster >gi 1171337 metanogaster >gi 1171337 metanogaster >gi 1171337 metanogaster >gi 1171337 metanogaster <	1	i		ı		METHYLTRANSFERASE)	i
Brassica rapa mRNA for SRK45, complete cds 869 AB012106 cds Rattus norvegicus homer-1c mRNA, complete cds 970 AF093268 Sambucus nigra hevein-like protein mRNA, complete cds 871 AF074386 mRNA, complete cds 872 AF074386 mRNA, complete cds 873 AF074386 mRNA, complete cds 874 AF074386 mRNA, complete cds 875 AF074386 mRNA, complete cds 876 AF074386 mRNA, complete cds 877 AF074386 mRNA, complete cds 878 AF074386 mRNA, complete cds 879 AF074386 mRNA, complete cds 870 AF074386 mRNA, complete cds 870 AF074386 mRNA, complete cds 870 AF074386 mRNA, complete cds 870 AF074386 mRNA, complete cds 870 AF074386 mRNA, complete cds 871 AF074386 mRNA, complete cds 872 AF074386 mRNA, complete cds 973 AF074386 mRNA, complete cds 974 AF074386 mRNA, complete cds 975 AF074386 mRNA, complete cds 975 AF074386 mRNA, complete cds 975 AF074386 mRNA, complete cds 975 AF074386 mRNA, complete cds 975 AF074386 mRNA, complete cds 975 AF074386 mRNA, complete cds 975 AF074386 mRNA, complete cds 975 AF074386 mRNA, complete cds 975 AF074386 mRNA, complete cds 975 AF074386 mRNA, complete cds 975 AF074386 mRNA, complete cds 975 AF074386 mRNA, complete cds 975 AF074386 mRNA, complete cds 975 AF074386 mRNA, complete cds 975 AF074386 methyltransferase [Drosophila methyltransferase [D	1	1		ı			1
Brassica rapa mRNA for SRK45, complete cds 869 AB012106 Cds Rattus norvegicus homer-1c mRNA, complete cds 870 AF093268 Sambucus nigra hevein-like protein mRNA, complete cds 871 AF074386 MRNA, complete cds 872 AF074386 MRNA, complete cds 873 AF074386 MRNA, complete cds 874 AF074386 MRNA, complete cds 875 AF074386 MRNA, complete cds 876 AF074386 MRNA, complete cds 877 AF074386 MRNA, complete cds 878 AF074386 MRNA, complete cds 879 AF074386 MRNA, complete cds 870 AF074386 MRNA, complete cds 870 AF074386 MRNA, complete cds 870 AF074386 MRNA, complete cds 870 AF074386 MRNA, complete cds 871 AF074386 MRNA, complete cds 872 AF074386 MRNA, complete cds 873 AF074386 MRNA, complete cds 874 AF074386 MRNA, complete cds 875 AF074386 MRNA, complete cds 876 AF074386 MRNA, complete cds 877 AF074386 MRNA, complete cds 878 AF074386 MRNA, complete cds 879 AF074386 MRNA, complete cds 870 AF074386 MRNA, co		i	1				1
Brassica rapa mRNA for SRK45, complete cds 0.007 2499568 melanogaster] >gi]1171337 melanogaster] >gi]1171337 melanogaster] 8.3 Rattus norvegicus homer- 1c mRNA. complete cds 0.007 4092077 mutant [Mus musculus] 6.2 Sambucus nigra hevein-like protein mRNA, complete cds 0.007 151377 [Pseudomonas stutzeri] 6.2 TRANSCRIPTION TERMINATION FACTOR	j	I		1			
for SRK45, complete cds	ľ	ł	<u> </u>	i			
Rattus norvegicus				1	!	methyltransferase [Drosophila	j
Rattus norvegicus homer-1c mRNA, (AF095353) toll-like receptor 4 mutant [Mus musculus] 6.2	860	ABOLDIO				melanogaster] >gi 1171337	
870 AF093268 homer-1c mRNA, complete cds 0.007 4092077 (AF095353) toll-like receptor 4 mutant [Mus musculus] 6.2 Sambucus nigra hevein-like protein mRNA, complete cds 0.007 151377 [Pseudomonas stutzeri] 6.2 TRANSCRIPTION TERMINATION FACTOR	1009	AB012106		0.007	2499568	melanogaster]	8.3
870 AF093268 complete cds 0.007 4092077 [AT 093333] toll-like receptor 4 mutant [Mus musculus] 6.2 Sambucus nigra hevein-like protein mRNA, complete cds 0.007 151377 [Pseudomonas stutzeri] 6.2 TRANSCRIPTION TERMINATION FACTOR	[1		ł		(A F00 53 53)	
Sambucus nigra hevein-like protein mRNA, complete cds 0.007 151377 [Pseudomonas stutzeri] 6.2 TRANSCRIPTION TERMINATION FACTOR	870	AF093268		0.007	4002077		
hevein-like protein (M80653) tetraheme (M80653) tetraheme (Pseudomonas stutzeri) 6.2 Bos taurus (clone TRANSCRIPTION TERMINATION FACTOR			- piece cus	0.007	4092077	mutant [Mus musculus]	6.2
hevein-like protein (M80653) tetraheme (M80653) tetraheme (Pseudomonas stutzeri) 6.2 Bos taurus (clone TRANSCRIPTION TERMINATION FACTOR		I	Sambucus nigra	1		ļ	J
871 AF074386 mRNA, complete cds 0.007 151377 [Pseudomonas stutzeri] 6.2 TRANSCRIPTION TERMINATION FACTOR				1		(M80653) tetraheme	1
Bos taurus (clone TRANSCRIPTION TERMINATION FACTOR	871	AF074386		0.007			62
Bos taurus (clone TERMINATION FACTOR							0.2
	25.		` '	I		TERMINATION FACTOR	j
872 L42319 Sal3.8) tristetraprolin 0.007 2507337 RHO 5.5	872	L42319	Sal3.8) tristetraprolin	0.007			5.5

5.3 5.3 5.1
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PCT/US00/18374

	Neare	st Neighbor (BlastN vs.	Cenhank)	Names	11 (2)	
SE				INETLEST ING!	hbor (BlastX vs. Non-Redundant Pr	roteins)
П	-	ON DESCRIPTION			!	1
—	THEELOSIC	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		L.major mRNA for			(U78289) tylactone synthase	T
88	2 X93567	beta-tubulin (1404bp	0.007		modules 4 & 5 [Streptomyces	
	1273307		0.007	2317862	fradiae)	3.0
			1	ł	(AL032646) predicted using	
- 1	ł	ļ.	1	i	Genefinder; cDNA EST	i i
ı		•	ł		EMBL:D76407 comes from this	
1	İ		Ì	1	gene; cDNA EST	
ı	ł		ļ	1	EMBL:C08999 comes from this	
- 1	· I		}	İ	gene; cDNA EST yk199b12.5	ľ
1	ı	Brassica rapa mRNA	1	· .	comes from this gene; cDNA	
883	APOLOGO	for SRK45, complete			EST yk282a4.5 comes from this	
1 000	AB012106	cds	0.007.	3881103	gene; cDNA EST EMBL:C0	2.7
1	i	Homo sapiens			THROMBIN RECEPTOR	
	1	WSCR4 gene, exons		·	PRECURSOR human	1
884	AF041056		0.007	125012	>gi 339677 (M62424) thrombin	
		J and 4	0.007	135817	receptor [Homo sapiens]	2.2
1	i	Rattus norvegicus			HYPOTHETICAL 32.2 KD PROTEIN C22E12.04 IN	ľ
1		homer-1c mRNA.			CHROMOSOME I >gi 1220279	į.
885	AF093268	complete cds	0.007	1723518	(Z70043) unknown	a. 1
1	I	Hevea brasiliensis 3-			(C. 5543) dilatiowii	2.1
1	1	hydroxy-3-	ł		1	1
ł		methylglutaryl-	I			\ \ \ \ \
-	ł	coenzyme A	ı			
886	M74798	reductase gene. 3'	0.007		1	
	1114756	enu.	0.007	1001282	(D64003) polyA polymerase	1.9
ł	1				HYPOTHETICAL III.9 KD	
1	i		1		PROTEIN C34E10.8 IN CHROMOSOME III	j
1	j	H.sapiens CpG DNA.			>gi 500731 (U10402) weakly	i
1		clone 76g 1, reverse	1		similar to protein C kinase	- 1
887	Z62997	read cpg76g11.rtla.	0.007 ·	1176532	substrate [Caenorhabditis	1.8
					DVA-I POLYPROTEIN	1.0
			ŀ		PRECURSOR nematode	ı
			i	İ	polyprotein antigen precursor	1
		Sombura	ŀ	ĺ	[Dictyocaulus viviparus]	1
		Sambucus nigra hevein-like protein	i	·	>gi 1585421 prf 2124414A	
888	AF074386	mRNA, complete cds	0.007	0.1005:-	polyprotein antigen/allergen	J
		Synechocystis species	0.007	2498317	[Dictyocaulus viviparus]	1.2
		(strain PCC 6803)	1	1		
		drg.A gene. complete	1	1	(ABO18230) KI A 2005	
889		cds.	0.007		(AB018320) KIAA0777 protein	1
				300213	Homo sapiens]	1.1

13	Neares	Neighbor (BlastN vs. C	Genbank)	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEC			T	1.021036 14618	Hon-Redundant P	roteins)	
[ID	~	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION		
				1 ACCESSION	DESCRIPTION	P VALUE	
		Mus musculus DNA	 				
	1	for prostaglandin D2	ľ				
1	I	synthase, complete	ļ			1	
890	D83329	cds	0.007	1001741	(D64004) hypothetical protein	0.97	
1	i	1			HYPOTHETICAL 11.6 KD	0.57	
	Ĭ		1 1		PROTEIN IN NUTI-ARO2		
		Brassica rapa mRNA			INTERGENIC REGION	1	
891	AB012106	for SRK45, complete cds	0.007		PRECURSOR YGL149w -	1	
971	AB012100	cus	0.007	1723928	yeast (Saccharomyces	0.94	
1					GLUTENIN, HIGH		
	1	Sambucus nigra			MOLECULAR WEIGHT		
	ł	ribosome inactivating			SUBUNIT 12 PRECURSOR	l i	
		protein precursor	1		>gi 82606 pir A24266 glutenin high molecular weight chain 12		
892	U76524	mRNA, complete cds	0.007	121452	precursor - wheat >gi 21779	0.79	
					precursor - wheat >gr 21779	0.79	
l]	Arabidopsis thaliana	i				
		cellulose synthase	1				
l	j	catalytic subunit (Ath-	i			1 1	
893	AF027173	A) mRNA, complete			(U30294) ORF2 [Prevotella	1	
093	AF02/1/3	cds	0.007	927287	ruminicola]	0.35	
ĺ					(U40061) contains similarity to		
		H.sapiens IMAGE	1		transmembrane domains like	ŀ	
894	Y11918	cDNA clone 26881	0.007	1055188	those found in sugar transporter		
		Mus Musculus	0.007	1033100	proteins	0.26	
į		alphaA-crystallin-			(AF083061) ABC transporter	- 1	
895	L36827	binding protein [0.007	4063019	TliF [Pseudomonas fluorescens]	0.21	
		Mus Musculus			tradicacina)	<u> </u>	
201		alphaA-crystallin-			(AF083061) ABC transporter	1	
896	L36827	binding protein I	0.007	4063019	TliF [Pseudomonas fluorescens]	0.20	
		u		٠.			
		H.sapiens CpG DNA.				I	
897	_ 1	clone 54c10, reverse read cpg54c10.rt1a.	0.007	100000	1	- 1	
"	203/19	lead cpg34c10.rt1a.	0.007	1097307	HIC-1 gene [Homo sapiens]	0.20	
1				•	UTROPHIN (DYSTROPHIN-		
- 1	į,	Helianthus tuberosus	ĺ		RELATED PROTEIN 1) (DRP1) (DRP)	į	
I		ectin 1 mRNA,	ĺ	1	Sec 1 (DRP) Sec 1 Se	ļ	
898	AF064029	complete cds	0.007	1174915	protein) [Homo sapiens]	0.002	
	1	vlus musculus			Processis (Fronto adpletia)	0.002	
202		athepsin S (CatS)	ļ		(U78721) RNA helicase isolog	ļ	
899	AF051730 g	ene, exon 6	0.007	1707017	[Arabidopsis thaliana]	0.001	

	Neares	Nearest Neighbor (BlastN vs. Genbank)			Nearest Naighbox (Blook) on No. B. L. L.			
SEC	1 0 0 0 0 0		JCHOMIK)	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)				
ID ID	ACCESSIO	N DESCRIPTION	D.V					
	ACCESSION	Oryctolagus	PVALUE	ACCESSION	DESCRIPTION	P VALUE		
-	 	cuniculus		ļ				
		gp42/basigin/OX-	1					
1	i	47/HT7 mRNA.	1	ł		į.		
900	U62398	complete cds.	0.007	2270404	J	1		
	1 33370	M.musculus	0.007	2370494	(Z98944) hypothetical protein	2e-04		
l	1	glutathione reductase			() C005504) D06084 1 GT			
901	X76341	mRNA.	0.007	3513303	(AC005594) R26984_1 [Homo sapiens]	0.07.		
		Rat (lambda 20B0.5)	0.007	3313303	sapiens	8e-07		
	l	M-type 6-	l	İ		1		
	1	phosphofructo-2-	l)		
l		kinase/fructose-2, 6-		1 .		1		
902	M26215	bisphosphatase	0.007	3036809	(AL022373) putative protein	6e-15		
	1				(AB007902) HH0712 cDNA	00-13		
					clone for KIAA0442 has a 574-			
		Homo sapiens			bp insertion at position 1474 of			
003		KIAA0442 mRNA.			the sequence of KIAA0442.			
903	AB007902	partial eds	0.007	2662165	[Homo sapiens]	2e-17		
		Lactococcus lactis						
		cremoris plasmid						
		pNZ4000 insertion			1	{		
		sequence IS982			1	Ì		
		putative transposase						
		gene and eps gene	ł		(U28739) similar to alcohol			
ı		cluster			dehydrogenase/ribitol	I		
l		(epsRXABCDEFGHI	1		dehydrogenase [Caenorhabditis			
904	U93364	JKL), complete cds	0.007	2731377	elegans]	10.21		
		Rattus norvegicus		2.0.0.	ciegans	1e-31		
I		homer-1c mRNA,	ł		1			
905	AF093268	complete cds	0.006	<none></none>	<none></none>	<none></none>		
ſ		Mus musculus						
		Pontin52 mRNA,	1			· 1		
906	AF100694	complete cds	0.006	<none></none>	<none></none>	<none></none>		
- 1			Ī					
		Sambucus nigra	Į.					
907		hevein-like protein				i		
"	AF074386	mRNA, complete cds	0.006	<none></none>	<none></none>	<none></none>		
- 1	İ	Arabidopsis thaliana	j			7		
1		cellulose synthase	j					
- 1-		catalytic subunit (Ath	1		· .	1		
ł		B) mRNA, complete				[
908		eds	0.006	<none></none>	ALONIE-	NONTE		
		Arabidopsis thaliana	0.000	CHOINES		<none></none>		
1		nRNA for	1		***	J		
		eoxanthin cleavage		.		j		
909		nzyme	0.006	<none></none>	<none></none>	<none></none>		
					74104122	~~ ~~~		

	E Nearest	Neighbor (BlastN vs. C	:enhank)	Nagara Najal	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEC		Tieranoor (Blastiv Vs. C	T T	ivealest iveig	noor (Blasta Vs. Non-Redundant P	roteins)		
B	ACCESSION	DESCRIPTION	D.V.AT.TITE					
-	TACCESSION	DESCRIPTION	PVALUE	ACCESSION	DESCRIPTION	P VALUE		
-	+	Arabidopsis thaliana	 	<u> </u>				
1		cellulose synthase	l	ļ	1	ŀ		
	ł	catalytic subunit (Ath-		ł				
	į.	B) mRNA, complete	ĺ			i i		
910	AF027174	cds	0.006	<none></none>	NOVE	1		
		Rattus norvegicus	5.000	CHOILES	<none></none>	<none></none>		
1	ł	homer-1c mRNA.				ŀ		
911	AF093268	complete cds	0.006	<none></none>	<none></none>	<none></none>		
		Rattus norvegicus				TANDINES		
1		homer-1c mRNA.				1		
912	AF093268	complete cds	0.006	<none></none>	<none></none>	<none></none>		
ı]	Brassica rapa mRNA						
0.0		for SRK45, complete	••					
913	AB012106	cds	0.006	<none></none>	<none></none>	<none></none>		
1	1	Helianthus tuberosus						
i i		lectin 1 mRNA.				j l		
914	AF064029	complete cds	0.006	-NIONIT-		ii		
	14 004023	Mus musculus	0.008	<none></none>	<none></none>	<none></none>		
ł		Pontin52 mRNA.				i i		
915	AF100694	complete cds	0.006	<none></none>	<none></none>	<none></none>		
					(AF063866) ORF MSV064	CHOINES		
		Rattus norvegicus	j		hypothetical protein	[]		
		homer-1c mRNA.	- 1		[Melanoplus sanguinipes	1 1		
916	AF093268	complete cds	0.006	4049856	entomopoxvirus]	9.6		
			İ		(Z82070) predicted using			
•			1		Genefinder: similar to Lectin C-	ľ		
	i				type domain short and long	ļ.		
			l		forms (2 domains); cDNA EST	ľ		
1		ļ.	j		EMBL:C10633 comes from this			
1	[Mus musculus	1		gene: cDNA EST			
		Pontin52 mRNA,			EMBL C12424 comes from this			
917		complete cds	0.006	3880536	gene; cDNA EST yk191e7.3 comes from this	7.0		
			0.000	2000230	comes nom uns	7.9		
į	ł	Sambucus nigra	ł		(Z81552) F56G4.1	ĺ		
	[;	ribosome inactivating	j		[Caenorhabditis elegans]			
	T.	protein precursor	ì	i	>gi 3878615 gnl PID e1348240	1		
918	AF012899 i	nRNA, complete cds	0.006	3877761	(Z\$3118) F56G4.1	7.5		
1								
- 1		I.sapiens PTPL1		ł	CATHEPSIN E PRECURSOR			
919		nRNA for protein	0.005	ì	precursor - rabbit >gi 402729	į		
717	X80289 t	vrosine phosphatase	0.006	1168791	(LOS418) procathepsin E	7.4		

Little	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ						
ID	ACCESSION	DESCRIPTION	PVALUE	ACCESSION	DESCRIPTION	l
	1		1	I ACCESSION	DESCRIPTION	P VALUE
—	 				KINASE, BETA	
1	l			ł	DIACYLGLYCEROL	1
	1	İ		1	KINASE)	
1	1	1			>gi 477059 pir A47744	1
j		Sambucus nigra			diacylglycerol kinase (EC	
1	ł	hevein-like protein			2.7.1.107) beta - rat 90kDa-	
920	AF074386	mRNA, complete cds	0.006	1346371	diacylglycerol kinase [Rattus	5.5
1 1		Lycopersicon				1 !
}		esculentum class II	,			}
		small heat shock		•		1
J	117000	protein Le-HSP17.6			(D88588) lipoprotein	
921	U72396	mRNA, complete cds	0.006	2196567	[Escherichia coli]	4.3
i i		Sambucus nigra	İ		· I	
	İ	hevein-like protein			(783250) AmahiBaras	
922	AF074387	mRNA, complete cds	0.006	2113798	(Z83259) AmphiBrf38 [Branchiostoma floridae]	,,
	- <u> </u>	Brassica rapa mRNA	0.000	2113770	[[Dianemostoma floridae]	4.3
		for SRK45, complete	1		(U58282) Bowel [Drosophila	j i
923	AB012106	cds	0.006	1388166	melanogaster]	4.3
		Sambucus nigra	1			
924		hevein-like protein	0.001		HYPOTHETICAL 20.1 KD	
924	AF074386	mRNA, complete cds	0.006	2496785	PROTEIN Y4YS A-AGGLUTININ	4.2
	ļ				ATTACHMENT SUBUNIT	i
	1	ł	!	•	PRECURSOR	ŀ
ľ		Sambucus nigra	j		>gi 101170 pir A41258 a-	İ
		ribosome inactivating	ľ		agglutinin core protein AGA1 -	
j		protein precursor	ł		yeast (Saccharomyces	l
925		mRNA, complete cds	0.006	416592	cerevisiae)	2.7
				<u></u>	A-AGGLUTININ	
	.	,	-[ATTACHMENT SUBUNIT	į
	Į.				PRECURSOR	•
1	1.				>gi 101170 pir A41258 a-	
ł		Helianthus tuberosus	1		agglutinin core protein AGA1 -	Ì
926	1	ectin 1 mRNA,	0.005		yeast (Saccharomyces	i
720		Complete cds Arabidopsis thaliana	0.006	416592	cerevisiae)	2.5
ſ		nRNA for	i		(U41263) The 3' UTR of this	•
ł		neoxanthin cleavage	1		gene overlaps the 3' UTR of T19D12.6(confirmed by EST	ł
927		enzvme	0.006	3258584	hits) [Caenorhabditis elegans]	2.0
		Human Down		222004	into (Cachottiabditis cicgails)	- 2.0
1		Syndrome region of	[
j	le	rhromosome 21.	ļ			
ļ		enomic sequence.			(AF067150) beta-hydroxyacyl-	į
928	U33949 c	lone A12H1-1A6.	0.006	3850997	ACP dehydratase precursor	1.9

	Negrect	Neighbor (BlastN vs. C		Norma Visith (B) W N D			
		THEIGHDOLIDIASIN VS. C	renoank)	Nearest Neig	hbor (BlastX vs. Non-Redundant I	Proteins)	
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
	T					I VALUE	
		Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-					
1175	AF027173	A) mRNA, complete	2e-04	<none></none>	<none></none>) .vo.=	
	1	H.sapiens fertilin	20 07	CHORES	ENUNES	<none></none>	
1176	Y09232	alpha pseudogene	2e-04	<none></none>	<none></none>	<none></none>	
1177	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	2e-04	<none></none>	<none></none>	NONE	
		Mus musculus	20.04	CHOILES	<noine></noine>	<none></none>	
1178	AF100694	Pontin52 mRNA, complete cds	2e-04	<none></none>	<none></none>	<none></none>	
		Homo sapiens putative swelling- activated chloride channel (CLNS1A)				4.10.1.2	
1179	AF072847	gene, intron 6	2e-04	<none></none>	<none></none>	<none></none>	
1180	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete eds	2e-04	<none></none>	<none></none>	<none></none>	
1181		Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	2e-04	AIONE	·		
	370324	IIIKINA, complete cas		<none></none>	<none></none>	<none></none>	
		Arabidopsis thaliana cellulose synthase	·		(U50199) coded for by C. elegans cDNA yk89e9.5; coded for by C. elegans cDNA cm7g5; coded for by C. elegans cDNA cm14b9; coded for by C. elegans cDNA yk52g5.5; coded	·	
1182		catalytic subunit (Ath- A) mRNA, complete cds	2e-04	1213557	for by C. elegans cDNA yk76e5.5; coded for by C. elegans cDNA yk131f11.5; c	8.4	

	Neares	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEC			T T	Nearest Nei	gnbor (BlastX vs. Non-Redundant Pi	oteins)		
Ð	- 6	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE		
<u> </u>		<u> </u>			EPITHELIAL DISCOIDIN	1		
- [į	ļ			DOMAIN RECEPTOR I	 		
1	I		1		PRECURSOR (TYROSINE-	[
j	1			i .	PROTEIN KINASE CAK)			
1	1	Lycopersicon	ı	İ	(CELL ADHESION KINASE)	1		
i	1	esculentum cytosolic			(TYROSINE KINASE DDR)			
1		class II small heat	1		(DISCOIDIN RECEPTOR	ľ		
1	i	shock protein HCT2	}	i	TYROSINE KINASE) (TRK E)			
	j	(HSP17.4) mRNA,		l	(PROTEIN-TYROSINE			
1183	AF090115	complete cds	2e-04	729008	KINASE RTK 6) sapiens]	8.3		
1	l				HYPOTHETICAL 138.1 KD	0.5		
1				1	PROTEIN IN MOLR-BGLX			
1	1	Sambucus nigra	1	ľ	INTERGENIC REGION	ľ		
1		ribosome inactivating		i	>gi 1788436 (AE000300)	j		
1	i	protein precursor	,		putative regulator [Escherichia	- 1		
1184	AF012899	mRNA, complete cds	2e-04	2507582	colil	7.8		
1	i				collagen alpha 1(IX) chain -	7.6		
ł		1.	1 1		mouse musculus]	- 1		
1		Sambucus nigra	i l	,	>gi 744962 prf 2015346A	1		
1		hevein-like protein			collagen: SUBUNIT=alpha1:ISO	}		
1185	AF074386	mRNA, complete cds	2e-04	1085500	TYPE=IX [Mus musculus]	7.8		
1 1								
1 1		Arabidopsis thaliana			1	- 1		
1 1		cellulose synthase			1	- 1		
1 1		catalytic subunit (Ath-	ı		1	i		
1186		A) mRNA, complete	[(Y13942) GTN Reductase	1		
1130	AF027173	cds	2e-04	2623967	[Agrobacterium radiobacter]	7.4		
1 1			i		ADVANCED			
1 1					GLYCOSYLATION END	1		
1 1	I		į.		PRODUCT-SPECIFIC	ł		
1 1	ł		į		RECEPTOR PRECURSOR			
	i	.]	ľ		(RECEPTOR FOR	1		
	. 1	1			ADVANCED	- 1		
		. [· 1.		GLYCOSYLATION END			
	1	Arabidancie shaliana			PRODUCTS) products receptor	- 1		
		Arabidopsis thaliana	1		precursor - bovine >gi 163651	1		
1	1	nRNA for	i		(M91212) receptor for advanced]		
1187		neoxanthin cleavage			glycosylation end products (Bos	1		
	7,003013	nzyme	2e-04	2497316	taurusj	5.3		
1	[,	Arabidopsis thaliana	j					
1	ľ	ellulose synthase	ı			ł		
l		atalytic subunit (Ath-	- 1			j		
			1			ľ		
1188		ds mRNA, complete	2.01			1		
	0	u.,	2e-04	1001710	(D64004) hypothetical protein	3.5		

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEQ							
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
		Arabidopsis thaliana			(U41263) The 3' UTR of this	Ť	
		mRNA for			gene overlaps the 3' UTR of		
1		neoxanthin cleavage	İ	}	T19D12.6(confirmed by EST	ļ	
1189	AJ005813	enzyme	2e-04	3258584	hits) [Caenorhabditis elegans]	2.1	
	l	Arabidopsis thaliana					
1		cellulose synthase]	
1	i	catalytic subunit (Ath-					
1		A) mRNA, complete			(AF038623) contains similarity		
1190	AF027173	cds	2e-04	2736338	to RNA recognition motifs	0.89	
						0.07	
1		Lycopersicon		.,			
1		esculentum class II					
1		small heat shock	٠.		\	i .	
1		protein Le-HSP17.6			(D88588) lipoprotein]	
1191	<u>U72396</u>	mRNA, complete cds	2e-04	2196567	[Escherichia coli]	0.69	
		Lycopersicon					
1 i		esculentum cytosolic					
1		class II small heat					
		shock protein HCT2				<u> </u>	
1		(HSP17.4) mRNA.	-		(AJ006096) F-spondin		
1192	AF090115	complete cds	2e-04	3319874	[Branchiostoma floridae]	5e-04	
				-			
		Chlamydomonas				l	
1 .		reinhardtii dynein			l		
1 1		heavy chain alpha	i		(Z81077) predicted using		
1193	L26049	(ODA11) gene, exons 2-15, and partial cds.	2e-04	2074775	Genefinder; Similarity to Yeast	2- 00	
 	2-0049	Mus musculus	26-04	3876775	protein 8248 (TR:G587531)	2c-09	
		Pontin52 mRNA,				•	
1194		complete cds	1e-04	<none></none>	<none></none>	<none></none>	
		•					
		Helianthus tuberosus		•			
	. 1	lectin 1 mRNA,				j	
1195	AF064029	complete cds	1c-04	<none></none>	<none></none>	<none></none>	
		Hama andian	.				
		Homo sapiens retinaldehyde-binding	I]	
		protein (CRALBP)	1			.	
1196		gene, complete cds.	1e-04	<none></none>	<none></none>	<none></none>	
		Rhesus monkey		41.01.0	\(\text{110112}\)	-::0::-	
1197		interleukin-3 gene	1e-04	<none></none>	<none></none>	<none></none>	

	Nearest I	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEQ						T		
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE		
	1	Plasmodium		. reception		I VALUE		
		falciparum				· 		
	l .	chromosome 2.			1			
,		section 58 of 73 of						
]		the complete						
1198	AE001421	sequence	le-04	<none></none>	<none></none>	<none></none>		
						14101122		
		Lycopersicon			ĺ	1		
		esculentum cytosolic			İ	1		
j l	·	class II small heat				1		
i i		shock protein HCT2				1 1		
ŀ		(HSP17.4) mRNA.						
1199	AF090115	complete cds	le-04	<none></none>	<none></none>	<none></none>		
			• .					
li		Arabidopsis thaliana						
		cellulose synthase						
		catalytic subunit (Ath-						
		B) mRNA, complete			(Y15086) HepC protein			
1200	AF027174	cds	1e-04	2576287	[Cylindrotheca fusiformis]	4.7		
		Arabidopsis thaliana						
		mRNA for						
		neoxanthin cleavage			(AB016623) RWC-3 [Oryza			
1201	AJ005813	enzyme	le-04	3395673	sativa]	0.14		
		Homo sapiens	ľ			1 1		
1		BRCA1-associated	i			1		
		RING domain protein			1			
1202		(BARDI) gene,	0.07					
1202		exons 2 and 3 Arabidopsis thaliana	9e-05	<none></none>	<none></none>	<none></none>		
		mRNA for	1					
ĺ								
1203		neoxanthin cleavage	9e-05	<none></none>	NONE	<none></none>		
1203		enzyme Brassica rapa mRNA	96-03	< NOINE>	<none></none>	KNONES		
		for SRK45, complete		· .				
1204		cds	9e-05	<none></none>	<none></none>	<none></none>		
		Xenopus laevis		SHORES	CHOINE?	STONES		
ŀ		mitotic						
		phosphoprotein 44	i	•		ļ i		
1205		mRNA, partial eds	9e-05	<none></none>	<none></none>	<none></none>		
	22222				HYPOTHETICAL			
1	Ì		i		LIPOPROTEIN MG348			
			1		PRECURSOR	i I		
- 1		Laccaria bicolor	į		>gi 1361668 pir E64238			
ŀ		glyoxal malate	1		hypothetical protein MG348 -			
ı		synthase protein	1		Mycoplasma genitalium (SGC3)			
1206		mRNA, complete cds	9e-05	1351553	>gi]3844931	8.8		

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEQ							
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
		Human DNA for					
		alpha-platelet-derived			(AF056494) NADH		
		growth factor			dehydrogenase subunit 5		
1207	D50006	receptor, exon 6-10	9e-05	3063639	[Panorpa japonica]	5.1	
		Human Down			INHIBIN ALPHA CHAIN	1	
j .		Syndrome region of			PRECURSOR bovine		
	*****	chromosome 21.	0 - 06	10.4072	>gi 163195 (M13273) inhibin A	3.0	
1208	U50423	clone A41B8-1B7. Arabidopsis thaliana	9e-05	124273	subunit [Bos taurus] (X72850) 2.4-	3.0	
1 1		mRNA for			dihydroxybenzoate		
		neoxanthin cleavage			monooxygenase (Sphingomonas		
1209	AJ005813	enzyme	9e-05	4007782	sp.]	2.3	
1209		Homo sapiens clone	<u> </u>	4007702	39.1		
		fragment			İ		
]		UWGC:gap3 from			į		
		7q31.3, complete					
		sequence [Homo			(U60315) MC132L [Molluscum		
1210	AC005276	sapiens]	9e-05	1492075	contagiosum virus subtype 1]	1.0	
		Mus musculus					
	•	Pontin52 mRNA.			(AB007884) KIAA0424 [Homo		
1211	AF100694	complete cds	9e-05	2887423	sapiens	2e-10	
					(U83115) non-lens beta gamma-		
		C.fuscus gamma-M2-			crystallin like protein [Homo	7 25	
1212	X77772	1 crystallin mRNA.	9e-05	2072425	sapiens]	7e-25	
		Brassica rapa mRNA	1			ľ	
1213	A BO13104	for SRK45, complete	8e-05	<none></none>	<none></none>	<none></none>	
1213	AB012106	Apis mellitera	96-07	CHORES	\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	
]]		ligustica complete	ı				
		mitochondrial					
1214	L06178	genome	8e-05	<none></none>	<none></none>	<none></none>	
		Brassica rapa mRNA					
		for SRK45, complete		•			
1215	AB012106	cds	8e-05	<none></none>	<none></none>	<none></none>	
							
		Sambucus nigra	ļ				
		ribosome inactivating	ļ				
		protein precursor		.,			
1216	U76524	mRNA, complete cds	8e-05	<none></none>	<none></none>	<none></none>	
		Apis mellitera	1		· ·		
		ligustica complete	- 1			,	
1217	1.061.70	mitochondrial	82.05	NONE	<none></none>	<none></none>	
1217	L06178	genome Brassica rapa mRNA	8e-05	<none></none>	CHOINE	1101112	
		for SRK45, complete	1				
1218	AB012106	cds	8e-05	<none></none>	<none></none>	<none></none>	
	' 100			7	1		

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEO						ľ	
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
		Mus musculus				1	
		Pontinii mRNA.				 	
1219	AF100694	complete cds	8e-05	<none></none>	<none></none>	<none></none>	
<u> </u>		Brassica rapa mRNA				1	
i		for SRK45, complete				ļ	
1220	AB012106	cds	8e-05	<none></none>	<none></none>	<none></none>	
					WNT-11 PROTEIN		
ļ		Brassica rapa mRNA	i		PRECURSOR (XWNT-11)	ĺ	
		for SRK45, complete			clawed frog >gi 439108	ł	
1221	AB012106	cds	8e-05	1722841	(L23542) maternal protein	9.9	
	į	Arabidopsis thaliana		• •			
		cellulose synthase					
		catalytic subunit (Ath-	• •				
		B) mRNA, complete			(U35637) nebulin (Homo		
1222	AF027174	cds	8e-05	1205991	sapiens	9.6	
1 1		**	İ				
		Homo sapiens serine]				
		protease-like protease			(ATOSSES I)		
1222	A F02 1606	Sequence 2 from	ا م	22.42702	(AF055354) respiratory burst	0.4	
1223	AF024605	patent US 5736377 Rattus norvegicus	8e-05	3242783	oxidase protein B	8.6	
		mRNA for PAG608	ľ		(AE000616) alpha-ketoglutarate		
1224	Y13148	gene	8e-05	2314243	permease (kgtP)	8.1	
1224	113146	gene	86-05	2314243	RAS GTPASE-ACTIVATING-	6.1	
					LIKE PROTEIN IQGAPI		
1					(P195) (KIAA0051)		
					>gi 627594 pir A54854 Ras		
					GTPase activating-related		
		Arabidopsis thaliana	J.		protein - human sapiens]		
· •		mRNA for			>gi 536844 (L33075) ras		
ı		neoxanthin cleavage	1		GTPase-activating-like protein		
1225	AJ005813	enzyme	8e-05	1170586	[Homo sapiens]	7.8	
				•			
	}	ĺ	Ì		NADH-UBIQUINONE		
		1	i		OXIDOREDUCTASE CHAIN		
			ļ		4 >gi 1085185 pir S52968	į	
ı	İ	Arabidopsis thaliana	- 1		NADH dehydrogenase chain 4 -		
		cellulose synthase			honeybee mitochondrion		
	i	catalytic subunit (Ath-	i		(SGC4) >gi 552446 (L06178)		
		A) mRNA, complete	1		NADH dehydrogenase subunit 4		
1226		cds	8e-05	464239	[Apis mellifera ligustica]	3.5	
ľ		Mus musculus	ł			1	
		Pontin52 mRNA.				, , l	
1227	AF100694	complete cds	8e-05	544353	F-SPONDIN PRECURSOR	3. <i>5</i>	

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEQ							
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
		Sambucus nigra					
		ribosome inactivating					
1 1		protein precursor			apolipoprotein B-100 - chicken]	
1228	U76524	mRNA, complete cds	8e-05	483243	(fragment)	3.4	
		Rattus norvegicus					
		homer-1c mRNA.			proline-rich protein - mouse		
1229	AF093268	complete cds	8e-05	91207	(fragment) musculus]	2.2	
		Arabidopsis thaliana					
l I		cellulose synthase					
i I	!	catalytic subunit (Ath-		٠.			
1 1		A) mRNA, complete			ZONADHESIN PRECURSOR		
1230	AF027173	cds	8e-05 [.]	2499181	>gi 1066466	2.2	
		Arabidopsis thaliana					
i 1		cellulose synthase					
		catalytic subunit (Ath-					
1		A) mRNA, complete			ZONADHESIN PRECURSOR		
1231	AF027173	cds	8e-05	2499181	>gi 1066466	1.9	
<u> </u>		Brassica rapa mRNA					
		for SRK45, complete		0000010	(AF027972) flagelliform silk	,,	
1232	AB012106	cds	8e-05	2833647	protein [Nephila clavipes]	1.6	
		Rattus norvegicus homer-1c mRNA.			(Z49821) MYO2		
1233	AF093268		8e-05	1163063	[Saccharomyces cerevisiae]	0.90	
1233	AF093208	complete cds	8e-03	1103003	[[Saccharonivees celevisiae]	0.90	
		Arabidopsis thaliana	·		· ·		
] [cellulose synthase			1		
		catalytic subunit (Ath-					
		B) mRNA, complete]		
1234	AF027174	cds	8e-05	1653488	(D90914) hypothetical protein	0.30	
		Chicken nonmuscle					
		myosin heavy chain					
		(MHC) gene,	1		[
1235	M26510	complete cds.	8e-05	112159	plectin - rat	0.003	
		Human chromatin					
		structural protein			(AF003384) weak similarity to		
1236	U56402	homolog	8e-05	2088823	the peptidase family A2	le-13	
		Mus musculus	t				
		Pontin52 mRNA.	1		(U02289) GTPase-activating		
1237	AF100694	complete cds	8e-05	437181	protein [Caenorhabditis elegans]	2e-17	
	[Mus musculus			HYPOTHETICAL 80.8 KD	1	
		Pontin52 mRNA,			PROTEIN ZC21.4 IN	0. 37	
1238	AF100694	complete cds	8e-05	465983	CHROMOSOME III	8e-27	

	Nearest 1	Neighbor (BlastN vs. G	enbank)	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEQ]	
Œ	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
						<u> </u>	
		Lycopersicon esculentum cytosolic					
l		class II small heat					
		shock protein HCT2					
		(HSP17.4) mRNA,					
1239	AF090115	complete cds	7e-05	<none></none>	<none></none>	<none></none>	
					(AL031633) predicted using		
		Rattus norvegicus NF-		,	Genefinder; cDNA EST yk304f12.5 comes from this		
امريرا	1102/5/	KB gene, promotor	7e-05	3880858	gene [Caenorhabditis elegans]	9.3	
1240	U83656	region	76-03	3600636	gene [Caenornabultis elegans]	7.3	
l i		Sambucus nigra		• •			
		hevein-like protein			(AL022600) hypothetical		
1241	AF074387	mRNA, complete cds	7e-05	3080538	protein	9.2	
					HYPOTHETICAL 23.7 KD		
					PROTEIN IN MDHI-VMA5 INTERGENIC REGION		
					>gi 539182 pir S37908		
					hypothetical protein YKL083w -		
		H.sapiens ung gene			yeast (Saccharomyces		
		for uracil DNA-		•	cerevisiae) >gi 486120		
1242	X89398	glycosylase	7e-05	549700	(Z28082) ORF YKL083w	1.8	
	, , , , , , , , , , , , , , , , , , , ,	Bovine follicle					
		stimulating hormone-			() 10002 (2) DIADTI		
	1,000	beta subunit gene.	7- 06	2398621	(AJ000342) DMBT1 protein, 5.8 kb transcript [Homo sapiens]	1.8	
1243	M83753	complete cds. Rat troponin T	7 e -05	2398021	J.8 ko Galiscript [Homo sapiens]	1.0	
		cardiac isoform gene.			(X83413) U88 (Human		
1244	M80829	complete cds	5e-05	854065	herpesvirus 6]	2e-08	
				,			
		Sambucus nigra		ii	FLAGELLIN B2 PRECURSOR		
ا ـ ا		hevein-like protein	4.00	1202:10	Methanococcus voltae	5.2	
1245	AF074387	mRNA, complete cds	4e-05	120240	>gi 150063 (M72148) flagellin		
		Sambucus nigra					
		ribosome inactivating					
		protein precursor					
1246	AF012899	mRNA, complete cds	3e-05	<none></none>	<none></none>	<none></none>	
		Sambucus nigra					
		ribosome inactivating protein precursor					
1247	U76524	mRNA, complete cds	3e-05	<none></none>	<none></none>	<none></none>	
124/	070324	maxives, complete cus		4.01.02			
		Sambucus nigra			1		
		hevein-like protein	j		·.		
1248	AF074386	mRNA, complete cds	3e-05	<none></none>	<none></none>	<none></none>	

PCT/US00/18374

WO 01/02568

	Nearest N	Neighbor (BlastN vs. G	enbank)	Nearest Neigh	bor (BlastX vs. Non-Redundant Pr	oteins)
SEQ						
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Rattus norvegicus				
		homer-1c mRNA,		· · · · · · · · · · · · · · · · · · ·		
1249	AF093268	complete cds	3e-05	<none></none>	<none></none>	<none></none>
		Brassica rapa mRNA			(A FOROZIO Similar de accesio	
		for SRK45, complete	2.05	277722	(AF039716) Similar to protein kinase (Caenorhabditis elegans)	6.7
1250	AB012106	cds Mus musculus	3e-05	2773226	kinase [Caenornabattis etegans]	0.7
		Pontin52 mRNA.			(U93568) putative p150 [Homo	Ì
1251	AF100694	complete cds	3e-05	2072961	sapiens]	5.6
1-51	AI 100034	complete cus	- 5.0 5.5		EXOGLUCANASE II	
					PRECURSOR cellulose 1.4-beta	
1 !				,,	cellobiosidase (EC 3.2.1.91) II	
		Lycopersicon		:	precursor - fungus (Trichoderma	
		esculentum class II		•	reesei) 1,4-beta-cellobiosidase	
		small heat shock		-	(EC 3.2.1.91) II - fungus	•
		protein Le-HSP17.6	2.07	101055	cellobiohydrolase II	4.6
1252	U72396	mRNA, complete cds	3e-05	121855	[Trichoderma reesei]	4.0
	!	Sambucus nigra			(AL021572) similar to CTP	1
		ribosome inactivating		•	SYNTHASE (EC 6.3.4.2) (UTP-	
		protein precursor			-AMMONIA LIGASE) (CTP	
1253	U76524	mRNA, complete cds	3e-05	3880516	SYNTHETASE)	3.3
	0.0321	Mouse brain-1 POU-				
		domain protein,			(U66102) intimin [Escherichia	
1254	M88299	complete cds.	3e-05	1947048	coli]	3.0
					CELL-CYCLE NUCLEAR	
					AUTOANTIGEN SG2NA (S/G2 NUCLEAR ANTIGEN)	
		Xenopus laevis				
1		mitotic phosphoprotein 44			autoantigen - human >gi 805095	
1255	U95098	mRNA, partial cds	3e-05	3122872	(U17989) GS2NA	2.8
1233	093098	mixina, partial cus	30,00	J	CYTOCHROME C OXIDASE	
					POLYPEPTIDE I chain I -	
		Sambucus nigra			Thermus aquaticus >gi 155083	
		ribosome inactivating			(M84341) cytochrome c oxidase]
		protein precursor			subunits precursor (Thermus	
1256	U76524	mRNA, complete cds	3e-05	1352145	thermophilus]	2.6
					SEGMENTATION POLARITY	
		Lycopersicon			PROTEIN ENGRAILED	
		esculentum class II			>gi 2076747 (U42429) engrailed (Anopheles gambiae)	
		small heat shock			>gi 2148918 (U42214)	
	1172224	protein Le-HSP17.6	3-05	2811015	engrailed (Anopheles gambiae)	2.0
1257	U72396	mRNA, complete cds	3e-05	2011013	Tenstanea (wnobueies gamorae)	

	Nanrect N	Neighbor (BlastN vs. Ge	nhank)	Nearest Neigh	bor (BlastX vs. Non-Redundant Pro	oteins)
050	i tearest i	Totalion (Diabit - 13. Of				
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Arabidopsis thaliana				
		cellulose synthase			· ·	
		catalytic subunit (Ath-			(MARCONE) EE 45 like protein	
		B) mRNA, complete	2 25	1/57750	(U62325) FE65-like protein	1.7
1258	AF027174	cds	3e-05	1657752	[Homo sapiens]	1/
		Mus musculus			(U93568) putative p150 [Homo	
	1510000	Pontin52 mRNA.	3- 05	2072961	sapiens!	1.5
1259	AF100694	complete cds	3e-05	2072901	CYTOCHROME C OXIDASE	
					POLYPEPTIDE I chain I -	
					Thermus aquaticus >gi 155083	٠. ٠
		Sambucus nigra lectin			(M84341) cytochrome c oxidase	
		precursor mRNA,			subunits precursor [Thermus	
1260	U76523	complete cds	3e-05	1352145	thermophilus]	1.1
1200	010323	H.sapiens regulatory			Sxr (Bkm-homolog) sex-	
		region of HOXA7			determining region protein -	
1261	X91890	gene	3e-05	111013	mouse	1.0
		Homo sapiens metase			(D84239) IgG Fc binding	
1262	L36936	gene, partial cds.	3e-05	1944352	protein [Homo sapiens]	0.99
					SMP2 PROTEIN	
-					>gi 320853 pir S30911 SMP2	
					protein - yeast (Saccharomyces	
	ì	Brassica rapa mRNA			cerevisiae) gene	1
1,263	ABOLOLOS	for SLG45, complete	3e-05	- 417782	[Saccharomyces cerevisiae]	0.89
1263	AB012105	cds	26-02	417702	(Saccination) vess core vesses	
:		Sambucus nigra				i
İ		ribosome inactivating			INTEGRIN ALPHA CHAIN-	
		protein precursor			LIKE PROTEIN alpha Intlp	
1264	U76524	mRNA, complete cds	3e-05	1708501	[Candida albicans]	0.39
	f					
		Lycopersicon				
		esculentum cytosolic				
	ĺ	class II small heat				
		shock protein HCT2			Lie Calai municipa annia CM120	
		(HSP17.4) mRNA.		1.500003.	cis-Golgi matrix protein GM130	0.20
1265	AF090115	complete cds	3e-05_	1587031	[Rattus norvegicus]	0.20
		Human DNA				
		sequence from cosmid U65A4.				
		between markers				
1	1	DXS366 and DXS87			(U93569) putative p150 [Homo	
1266	Z81014	on chromosome X *	3e-05	2072964	sapiens)	0.049
1.700	Z31UI#	Tou chiomosome A	20.00	20.2707	1	

	Nearest	Neighbor (BlastN vs. C	enbank)	Nearest Neigh	bor (BlastX vs. Non-Redundant P	roteins)
SEQ						T T
ΙD	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					glycosylated and myristilated	†
					smaller surface antigen -	
			1		Plasmodium falciparum	
ł	i				>gi 836640 (X76298)	}
		H.sapiens telomeric	ŀ		glycosylated and myristilated	
1		DNA sequence, clone			smaller surface antigen gallus]	1
1		7PTEL001, read	[>gi 1092178 prf 2023165B	
1267	Z96668	7PTELOO001.seq	3e-05	542429	surface antigen	0.029
					(Z70310) predicted using	
					Genefinder; Similarity to Mouse	ŀ
					ankyrin (PIR Acc. No. S37771);	
					cDNA EST EMBL:T01923	
		ĺ			comes from this gene; cDNA	
					EST EMBL:D32335 comes	
					from this gene; cDNA EST	
					EMBL:D32723 comes from this	
					gene; cDNA ES Genefinder;	
				•	Similarity to Mouse ankyrin	1
					(PIR Acc. No. S37771); cDNA	[
					EST EMBL:T01923 comes	
l			1		from this gene; cDNA EST	
					EMBL:D32335 comes from this	
		Brassica rapa mRNA	1		gene; cDNA EST	
		for SLG45, complete			EMBL:D32723 comes from this	
1268	AB012105	cds	3e-05	3879121	gene; cDNA ES	2e-13
l		Sambucus nigra			ZVVINI (ZVVVINI 2)	
ł		hevein-like protein	I		ZYXIN (ZYXIN 2) sapiens]	ſ
1269	AF074385	mRNA, complete cds	3e-05	2407677	>gi 1545954 gn1 PID e223417	
1207	AL 074303	mkivA, complete cus	36-03	2497677	(X95735) zyxin	2e-23
1		Arabidopsis thaliana	Ī]	
		cellulose synthase]	
1		catalytic subunit (Ath-	· ·			
	İ	B) mRNA, complete	1			i
1270	AF027174	cds	1e-05	<none></none>	<none></none>	<none></none>
- 1			İ		PITUITARY HOMEOBOX 3	
- 1	į.	Carina mDNA for	i		(HOMEOBOX PROTEIN	
		Canine mRNA for	J		PITX3) >gi 2645427	i
127.	1	signal recognition			(AF005772) homeobox protein	ŀ
1271	X16318	particle 54k protein	1e-05	3122612	Pitx3 [Mus musculus]	4.4
- 1		Brassica rapa mRNA	f		(D90905) DNA mismatch repair	ł
1272		or SLG45, complete	1-0-	1/20/20	protein MutL (Synechocystis	I
14/4	AB012105	ds .	1e-05	1652458	sp.	0.62

	Nearest N	Veighbor (BlastN vs. G	enbank)	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEQ							
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
		Human					
i i		phosphatidylinositol					
		3-kinase delta		•	(1557000) ODF1 1 (15)	1	
		catalytic subunit		455000	(X67098) ORF1A [Homo	0.00	
1273	U57843	mRNA, complete cds	le-05	475909	sapiens]	0.22	
} !		H.sapiens telomeric					
		DNA sequence, clone				l	
f l		2QTEL054, read			unknown protein - rabbit	!	
1274	Z96569	2QTELOO054.seq	le-05	2137043	(fragment) cuniculus]	0.005	
					()	· · · · · · · · · · · · · · · · · · ·	
			. [kinensin-like protein KIF4 (SW:P33174); cDNA EST		
			٠. [EMBL:D27320 comes from this		
					gene; cDNA EST		
					EMBL:D27322 comes from this	1	
	·				gene; cDNA EST		
			`		EMBL:D27321 comes from this	•	
		•			gene; cDNA EST		
					EMBL:D35764 comes Mouse		
j					kinensin-like protein KIF4		
				•	(SW:P33174); cDNA EST		
					EMBL:D27320 comes from this		
		Methanobacterium			gene; cDNA EST		
		thermoautotrophicum			EMBL:D27322 comes from this]	
		from bases 172512 to			gene; cDNA EST		
		182957 (section 16 of			EMBL:D27321 comes from this		
		148) of the complete			gene; cDNA EST		
1275	AE000810	genome	le-05	3877579	EMBL:D35764 comes	6e-27	
		Homo sapiens gene	į				
		for CC chemokine	i				
1000	4 BO10113	PARC precursor,	9e-06	<none></none>	<none></none>	<none></none>	
1276	AB012113	complete cds Homo sapiens Xp22-	96-00	CHOMES	SHOINES	ZHONES	
		154-155 BAC GSHB-	l				
		52411 (Genome	l		1		
		Systems Human BAC	ļ				
		Library), complete					
		sequence [Homo	Į				
1277	AC005830	sapiens)	9e-06	<none></none>	<none></none>	<none></none>	
		Human MHC (HLA)					
		DRB intron I DNA,	l		(U37531) mucin apoprotein		
1278	D86245	partial sequence	9e-06	1051253	[Mus musculus]	1.3	
		Human mRNA for			LINE OF LETTICAL PROTECTS		
		KIAA0176 gene.	0.04	00222	HYPOTHETICAL PROTEIN	40.00	
1279	D79998	partial cds	9e-06	2833253	KIAA0176 sapiens]	4e-06	

	Nearest !	Neighbor (BlastN vs. G	enbank)	Nearest Neight	oor (BlastX vs. Non-Redundant Pr	oteins).
SEQ						
ΙĐ	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					(Z69655) Similarity to Yeast	
					uridine kinase	
					(SW:URK1_YEAST); cDNA	
					EST EMBL:Z14695 comes	
				,	from this gene; cDNA EST	
i I		Toxoplasma gondii			CEMSE17F comes from this	
		RH uracil			gene; cDNA EST	ł
		phosphoribosyl			EMBL:D67355 comes from this	
		transferase gene.			gene; cDNA EST yk209h1.5	
1280	U10246	complete cds.	9e-06	3876090	comes from this ge	7e-33
					(Z69635) Similarity to Yeast	
		• •		• •	uridine kinase	
	-				(SW:URK1_YEAST); cDNA	
			•••		EST EMBL:Z14695 comes	
					from this gene; cDNA EST	1
		Toxoplasma gondii			CEMSE17F comes from this	
		RH uracil			gene; cDNA EST EMBL:D67355 comes from this	l i
		phosphoribosyl			gene; cDNA EST yk209h1.5	
100	1110046	transferase gene,	9e-06	3876090	comes from this ge	7e-34
1281	U10246	complete cds.	9e-06	3870090	comes from this ge	76-34
		Sambucus nigra				1
		ribosome inactivating			Ì	}
		protein precursor				į i
1282	AF012899	mRNA, complete cds	8e-06	<none></none>	<none></none>	<none></none>
		Sambucus nigra				
		ribosome inactivating			1	
		protein precursor				1 1
1283	AF012899	mRNA, complete cds	8e-06	<none></none>	<none></none>	<none></none>
1203	111 012079	Human Rh blood		4,01.05		
		group C antigen				
		(RHCE) gene, exon			(U80837) F07E5.6 gene product	
1284	U66340	2. partial cds	8e-06	17.07 155	[Caenorhabditis elegans]	9.6
		Sambucus nigra				
		ribosome inactivating				
1205		protein precursor	70.04	MONE	<none></none>	<none></none>
1285	AF012899	mRNA, complete cds Human insulin	7e-06	<none></none>	ZIAOIAE>	~14014E>
		receptor (allele 2)				
		gene. exons 14, 15,				
1286	M29930	16 and 17.	4e-06	<none></none>	. <none></none>	<none></none>
	1-1-///	Homo sapiens				
	l	(subclone 5_d3 from				
	,	P1 H25) DNA	l			
1287		sequence.	3e-06	<none></none>	: <none></none>	<none></none>

PCT/US00/18374

SEQ ID ACCESSION DESCRIPTION P VALUE ACCESSION ACCES		Nearest	Neighbor (BlastN vs. C	Genbank)	Nearest Neigh	nbor (BlastX vs. Non-Redundant F	Proteins)
D ACCESSION DESCRIPTION P VALUE ACCESSION	SEO		T	T	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	isor (Siasac is: Iven recommant	Totellis
Mus musculus Cerberus-like (Cer-l) gene, complete cds 3e-06 NONE NONE NONE NONE	1 -		DESCRIPTION				1
1288 AF012244 cerberus-like (Cer-l) gene. complete cds 3e-06 <none></none>	12	ACCESSION		PVALUE	ACCESSION	DESCRIPTION	P VALUE
1288 AF012244 gene. complete cds 3e-06 NONE> NONE> NONE	_			<u> </u>			T
Human DNA Sequence from Cosmid L96F8, Huntington's Disease Region, chromosome 4p16.3 contains EST. 3e-06 < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE < NONE	1		cerberus-like (Cer-l)	1			
Human DNA sequence from cosmid L96F3 Humington's Disease Region chromosome 4p16.3 contains EST 3e-06 NONE	1288	AF012244	gene, complete cds	3e-06	<none></none>	<none></none>	<none></none>
Sequence from cosmid L96F8,	1						1
1289 Z69366 Huntington's Disease Region, chromosome ap16.3 contains EST. 3e-06 NONE> NONE> NONE>	1	j	1				İ
Huntington's Disease Region. chromosome 4p16.3 contains EST. 3e-06 NONE> NONE> NONE	ļ		sequence from				}
1289 Z69366 Region. chromosome 4p16.3 contains EST. 3e-06 <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none< td=""><td>i</td><td>i</td><td></td><td></td><td></td><td>• -</td><td>1</td></none<></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none>	i	i				• -	1
1289 Z69366	1						
Human DNA sequence from cosmid L96F3. Huntington's Disease Region, chromosome 4pl6.3 contains EST. 3e-06 <none> <none> <none> <none <n<="" <none="" td="" =""><td>1</td><td>ŀ</td><td>Region, chromosome</td><td>]</td><td></td><td></td><td></td></none></none></none></none>	1	ŀ	Region, chromosome]			
1290 Z69366 Huntington's Disease Region, chromosome 4p16.3 contains EST. 3e-06 NONE> NONE> NONE	1289	Z69366	4p16.3 contains EST.	3e-06	<none></none>	<none></none>	<none></none>
1290 269366 4p16.3 contains EST. 3e-06 4NONE>			Human DNA	i			
1290 Z69366 Huntington's Disease Region, chromosome 4p16.3 contains EST. 3e-06 <none> <none> <none> <none < ="" < <="" none="" td="" =""><td>1</td><td></td><td>_</td><td></td><td>• .</td><td></td><td>1 ' 1</td></none></none></none></none>	1		_		• .		1 ' 1
Huntington's Disease Region, chromosome 4p16.3 contains EST. 3e-06 <none> <none> <none <<="" <none="" td="" =""><td>1</td><td></td><td>4 -</td><td></td><td></td><td></td><td></td></none></none></none>	1		4 -				
Region, chromosome			i i			1	
1290 Z69366				1			
H.sapiens Chromosome 3 Sequences Sequences Sequences Sequences Sequences Sequences Sequences Sequences Sequences Sequences Sequences Sequence Sequ	1200	760266		3.00			
1291 X85232 sequences 3e-06 <none> <none> <none> <none td="" ="" <=""><td>1290</td><td>209300</td><td></td><td>3e-06</td><td><nune></nune></td><td><none></none></td><td><none></none></td></none></none></none></none>	1290	209300		3e-06	<nune></nune>	<none></none>	<none></none>
1291 X85232 sequences 3e-06 <none> <none> <none td="" ="" <=""><td></td><td></td><td></td><td>ı</td><td></td><td></td><td>1</td></none></none></none>				ı			1
Human platelet glycoprotein IIIa. exons 7. 8 and 9. 3e-06 NONE> NONE> NONE	1201	Y95222		3- 06	NONE		
1292 M32674 exons 7. 8 and 9. 3e-06 <none> <none> <none> <none td="" ="" <=""><td>1271</td><td>X03232</td><td></td><td>3e-06</td><td><nune></nune></td><td>· <none></none></td><td><none></none></td></none></none></none></none>	1271	X03232		3e-06	<nune></nune>	· <none></none>	<none></none>
1292 M32674 exons 7.8 and 9. 3e-06 NONE> NONE> NONE> NONE>	1 1	٠	_				
Human HepG2 3' region cDNA, clone hmd2a01 3e-06 998296 (U33484) ependymin Hemiodus sp.] 5.6	1292		_ * •	30.06	-NONE-	11017	I
region cDNA. clone hmd2a01 Lagothrix lagotricha interphotoreceptor retinoid-binding protein (IRBP) gene. intron 1, complete sequence 1294 U18614 Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA. 1295 AF090115 AF090115 AF016898 region cDNA. clone hmd2a01 3e-06 998296 (U71440) polyprotein [Rice (U		14132074		36-00	<none></none>	<none></none>	<none></none>
1293 D16879 hmd2a01 3e-06 998296 [Hemiodus sp.] 5.6						(7172404)	i i
Lagothrix lagotricha interphotoreceptor retinoid-binding protein (IRBP) gene. intron 1, complete sequence 3e-06 1613846 (U71440) polyprotein [Rice tungro spherical virus] 5.0 Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds 3e-06 1477646 plectin [Homo sapiens] 4.0 1296 AF016898 gene. complete cds 3e-06 1085177 [Drosophila yakuba] 3.0	1293	D16870	•	70.06	000004	• •	
interphotoreceptor retinoid-binding protein (IRBP) gene. intron 1, complete sequence 3e-06 I613846 (U71440) polyprotein [Rice tungro spherical virus] 5.0 Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA. complete cds 3e-06 I477646 plectin [Homo sapiens] >gi[1477651 (U63610) plectin [Homo sapiens] 4.0 Homo sapiens B-ATF gene. complete cds 3e-06 I085177 [Drosophila yakuba] 3.0				36-00	990290	[Hemiodus sp.]	3.6
retinoid-binding protein (IRBP) gene, intron 1, complete sequence 3e-06 I613846 (U71440) polyprotein [Rice tungro spherical virus] 5.0 Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA. complete cds 3e-06 I477646 plectin [Homo sapiens] >gi[1477651 (U63610) plectin [Homo sapiens] 4.0 Homo sapiens B-ATF gene, complete cds 3e-06 I085177 [Drosophila yakuba] 3.0	i						1
1294 U18614 protein (1RBP) gene, intron 1, complete 3e-06 1613846 (U71440) polyprotein [Rice tungro spherical virus] 5.0							1
1294 U18614 Intron 1, complete 3e-06 1613846 Intron 1, complete sequence 3e-06 I613846 Intron 1, complete Sequence 3e-06 I613846 Intron 1, complete Sequence 3e-06 I613846 Intron 1, complete Sequence 5.0 Lycopersicon			- 1			i	
1294 U18614 sequence 3e-06 1613846 tungro spherical virus 5.0				İ		(U71440) polyprotois (Disc	
Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA. complete cds 3e-06 1477646 Homo sapiens B-ATF gene. complete cds 3e-06 1085177 Interpretation of things spherical virial virial viria	1294		•	30-06	16139.16		50
esculentum cytosolic class II small heat shock protein HCT2 (U53204) plectin [Homo sapiens] >gi[1477651 (U63610) plectin [Homo sapiens] >gi[1477651 (U63610) plectin [Homo sapiens] 4.0 Homo sapiens B-ATF gene. complete cds 3e-06 1085177 [Drosophila yakuba] 3.0		<u> </u>		30.00	1017040	italigio spherical virus	J.U
esculentum cytosolic class II small heat shock protein HCT2 (U53204) plectin [Homo sapiens] >gi[1477651 (U63610) plectin [Homo sapiens] >gi[1477651 (U63610) plectin [Homo sapiens] 4.0 Homo sapiens B-ATF gene. complete cds 3e-06 1085177 [Drosophila yakuba] 3.0	ł	.]	Lycopersicon		,		
class II small heat (U53204) plectin [Homo sapiens] >gi[1477651 (U63610) plectin [Homo sapiens] >gi[1477651 (U63610) plectin [Homo sapiens] 4.0	J],	esculentum cytosolic	.			ľ
Shock protein HCT2	i						
(HSP17.4) mRNA. 1295 AF090115 complete cds 3e-06 1477646 sapiens] >gi[1477651 (U63610) plectin [Homo sapiens] 4.0 reverse transcriptase - fruit fly reverse transcriptase 1296 AF016898 gene. complete cds 3e-06 1085177 [Drosophila yakuba] 3.0	1					(U53204) plectin (Homo	1
1295 AF090115 complete cds 3e-06 1477646 plectin [Homo sapiens] 4.0 reverse transcriptase - fruit fly reverse transcriptase 1296 AF016898 gene. complete cds 3e-06 1085177 [Drosophila yakuba] 3.0	ŀ						l l
Homo sapiens B-ATF Homo sapiens B-ATF gene. complete cds 3e-06 1085177 Teverse transcriptase - fruit fly reverse transcriptase	1295			3e-06	1477646		40
Homo sapiens B-ATF reverse transcriptase 1296 AF016898 gene, complete cds 3e-06 1085177 [Drosophila yakuba] 3.0							
1296 AF016898 gene. complete cds 3e-06 1085177 [Drosophila yakuba] 3.0		ļī.	Homo sapiens B-ATF	j	-		i
	1296			3e-06	1085177		3.0
[(∠81522) predicted using						(Z81522) predicted using	
Genefinder; similar to RNA	- 1	1		j			
Homo sapiens DNA, recognition motif. (aka RRM,	- 1	Į.	Homo sapiens DNA.	j			i
trinucleotide repeats RBD, or RNP domain)	- 1	Į t	rinucleotide repeats	ľ	ļ		1
1297 AB018490 region 3e-06 3876572 [Caenorhabditis elegans] 3.0	1297	AB018490 r	egion	3e-06		- 1	3.0

		tricks and all and C	bank)	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
	Nearest N	Neighbor (BlastN vs. G	епоапк)	ivearest iveight	Joi (Blasta vs. 14011-1400undalii Fit	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
		,					
	-	Arabidopsis thaliana					
		cellulose synthase				•	
		catalytic subunit (Ath-					
		B) mRNA, complete			(AB020631) KIAA0824 protein	J	
1298	AF027174	cds	3e-06	4240137	[Homo sapiens]	2.7	
		Homo sapiens					
		adenosine				[
	-	monophosphate			(DOOLS) of the district of	Į.	
		deaminase l			(D90916) thiol:disulfide		
_		(AMPD1) gene,			interchange protein DsbD	1.7	
1299	M37929	exons 11-12.	3e-06	1653775	[Synechocystis sp.]	1./	
		Homo sapiens		1	Ì		
		adenosine					
1		monophosphate			(D90916) thiol:disulfide		
		deaminase 1			interchange protein DsbD		
		(AMPD1) gene.	3e-06	1653775	[Synechocystis sp.]	1.7	
1300	M37929	exons 11-12.	36-00	1033773	ACTIN-LIKE PROTEIN ARPS		
		Glycine max actin (Soy86) gene, partial			Ynl2430p [Saccharomyces	Į.	
ا ا	U60496	cds	3e-06	1730738	cerevisiael	2e-05	
1301	060496	Yersinia	30-00	1750750			
		pseudotuberculosis		1		i	
1		rplC, rplD, rplW,			·		
1		rplB and rpsS genes			1		
1	i	for ribosomal proteins			50S RIBOSOMAL PROTEIN	1	
1		L3, L4, L23, L2 and			L2 maritima >gi 437926		
1302	X14363	S19 ·	3e-06	585879	(Z21677) ribosomal protein L2	2e-12	
1502	322.00	H.sapiens DNA for				Ì	
		microsatellite	l i		İ	1	
1303	Z34969	polymorphism	2e-06	<none></none>	<none></none>	<none></none>	
		H.sapiens BBC1				1,101,175	
1304	X64707	mRNA	1e-06	<none></none>	<none></none>	<none></none>	
		Homo sapiens Xp22-				ļ	
!	j	154-155 BAC GSHB-			· .		
		524I1 (Genome					
	1	Systems Human BAC	[<u>'</u>		
		Library), complete	ļ :	ı			
	1	sequence [Homo		NONE	NIONES	<none></none>	
1305	AC005830	sapiens]	1e-06	<none></none>	<none></none>	12,0,1,2	
1							
1		Human electron transfer flavoprotein					
1300	104059	alpha-subunit mRNA.	1e-06	<none></none>	<none></none>	<none></none>	
1306	J04058	Jeompiele cus.	10-00		1		

	Nearest 1	Neighbor (BlastN vs. G	enbank)	Nearest Neigh	bor (BlastX vs. Non-Redundant Pr	oteins)
SEQ						
[D]	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens		i		
1 1		fibroblast growth factor receptor gene				
		(located in the central				
		MHC) signal peptide			mxcQ gene [Methylobacterium	1
1307	L25647	and consecutive exon	le-06	1586734	organophilum]	5.4
					(U20633) NADH	
		Human MHC class III		160400#	dehydrogenase subunit	١., ١
1308	L26261	HLA-RP1 gene.	1e-06	1684985	[Neuwiedia veratrifolia]	1.8
		Mus musculus alpha-				
		actinin-2 associated				
		LIM protein mRNA.			(AF053367) carboxyl terminal	
		alternatively spliced			LIM domain protein [Mus	
1309	AF002283	product, complete cds Human haptoglobin	le-06	2996196	musculus]	4e-17
		gene (alpha-2 allele),				
	•	complete cds and				
		haptoglobin-related				
		gene, exon 1 and				
1310	M10935	three Alu repeats.	6e-07	<none></none>	<none></none>	<none></none>
		Homo sapiens			· ·	
		(subclone 1_g6 from BAC H76) DNA			coagulation factor Xa (EC	
1311	AC002251	sequence	4e-07	2144491	3.4.21.6) precursor norvegicus]	4.2
	AC002251	sequence	, , , ,			
lli		Streptomyces				
		chrysomallus				
i í		actinomycin				
	A 50 17717	synthetase II (acmB)	4e-07	699196	(U15181) 4-coumarate-coA	le-06
1312	AF047717	gene, complete cds	46-07	099190	ligase [Mycobacterium leprae] GUANINE NUCLEOTIDE	16-00
					DISSOCIATION	
}					STIMULATOR RALGDS	
					FORM A (RALGEF)	
					>gi 321257 pir S28415 guanine	
		Human Ral guanine		•	nucleotide dissociation	
		nucleotide			stimulator ralGDS - mouse >gil193573 (L07924) guanine	
		dissociation stimulator mRNA.	ŀ		nucleotide dissociation	
1313	U14417	partial eds.	4e-07	544402	stimulator [Mus musculus]	8e-08
בוני	014417	H.sapiens flow-sorted	3007	J-7402	ominator (mas mas ares)	
		chromosome 6			1	
		HindIII fragment.		•]	
1314	Z79027	SC6pA20G8	3e-07	<none></none>	<none></none>	<none></none>

	Nearest N	Neighbor (BlastN vs. G	enbank)	Nearest Neight	oor (BlastX vs. Non-Redundant Pr	oteins)
SEQ						T T
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
	ACCESSION	Homo sapiens	1 TALUE	ACCESSION		11 1.4202
		intestinal mucin				<u> </u>
			ļ			}
		(MUC2) gene.				l
1,2,6	*******	promoter region and	3e-07	ANONES	NONE	NONT
1315	U67167	partial cds	3e-07	<none></none>	<none></none>	<none></none>
		Homo sapiens full			•	
	A E004044	length insert cDNA	2. 07	MONE	<none></none>	<none></none>
1316	AF086256	cione ZD41C11	3e-07	<none></none>	(U97003) contains similarity to	KINOINES
					C4-type zinc fingers and a]
		** -1 (10) 41			ligand-binding domain of	
	1147000	Human clone HS4.61	2- 07	1020427		2.3
1317	U67228	Alu-Ya5 sequence	3e-07	1938437	nuclear hormone receptors	2.3
		YY				
		Human calpain-like			(AF047659) No definition line	1
	******	protease (htra-3)	2 07	2011060	1.	0.70
1318	U94346	mRNA, complete cds	3e-07	2911858	found [Caenorhabditis elegans]	0.39
		• •				
		Homo sapiens				
		SERCA3 gene. exons				21027
1319	Y15724	1-7 (and joined CDS)	1e-07	<none></none>	<none></none>	<none></none>
		Bean DNA tor			1	i i
		glycine-rich cell wall				,,,o,,,,,,
1320	X13596	protein GRP 1.8	1e-07	<none></none>	<none></none>	<none></none>
		IT			İ	
Į I		Homo sapiens				
1 1		cytosolic selenium-]
l 1		dependent glutathione			(U58751) C07G1.7 gene	
i I		peroxidase gene,				
l I		complete cds, and	. 07	122/206	product [Caenorhabditis	8.0
1321	M83094	rhoh 12 gene. 3' end.	1e-07	1326385	elegans]	8.0
		Harrison CaC DNA				
		H.sapiens CpG DNA.			laytonsin tilsa neotsin maiza	
,,,,,		clone 71f4, forward	· 1e-07	1076802	extensin-like protein - maize >gi 600118 mays	0.61
1322	Z55905	read cpg71f4.ft1a . Human mRNA of trk	1e-0/	1070802	>griout to mays	0.01
		oncogene > ::			(M74509) [Human endogenous	
					retrovirus type C oncovirus	
		gb I96186 I96186 Sequence 23 from			sequence.], gene product [Homo	
.,,,,			1.07	205.166	sequence.j, gene product (riomo	3e-04
1323		patent US 5734039	1e-07	325465	sapiens]	JC-U4
l		Canis familiaris Y-			(D10628) sing finger protein	
ا ا		linked zinc finger	1. 07	2207.12	(D10628) zinc finger protein	7, 00
1324	AF027766	protein Bovine mRNA for	le-07	220643	[Mus musculus]	7e-08
1	•					
		rabphilin-3A.			(ACOO 1082) sale2 affinatos 19-a-	
		complete cds > ::			(AC004082) rab3 effector-like;	
i !		dbj E07809 E07809		• •	35% Similarity to AF007836	
		cDNA encoding			(PID:g2317778) [Homo	, ,,
1325	D13613	rabphilin-3A	1e-07	2822161	sapiens]	6e-1!

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
	Nearest i	Neighbor (BlastN vs. G	enbank)	Nearest Neigh	oor (Blasta vs. Non-Redundant Pro	Jieins)	
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
		Human mRNA for c-			(J04169) gag-one fusion protein		
1326	X57110	cbi proto-oncogene	le-07	323270	[Cas NS1 retrovirus]	3e-14	
					PROTO-ONCOGENE C-CBL		
	;	Human mRNA for c-			human >gi 29731 (X57110) c-		
1327	X57110	cbl proto-oncogene	le-07	115855	cbl protein [Homo sapiens]	4e-19	
		Homo sapiens					
		(subclone 2_g12 from					
		BAC H94) DNA				ł	
1328	AC001178	sequence	4e-08	<none></none>	<none></none>	<none></none>	
		Human interleukin-8					
		receptor type B					
		(ILSRB) gene,		1.		·	
		promoter and exons 1-					
1329	U11866	6	4e-08	<none></none>	<none></none>	<none></none>	
		Homo sapiens					
		(subclone 2_e6 from					
		BAC H94) DNA			histone H1 II-1 (clone L95) -		
1330	AC001225	sequence	4e-08	478184	midge	6.5	
					HYPOTHETICAL 32.6 KD PROTEIN IN TRANSPOSON		
					1		
		Human modulator			TN4556 >gi 80758 pir JQ0428 hypothetical 32.6K protein -		
		recognition factor 2					
1		(MRF-2) mRNA.			Streptomyces fradiae transposon	4.7	
1331	M73837	complete cds.	4e-08	141448	Tn4556	4.7	
i l		Homo sapiens clone					
		UWGC:y28gap from			(AF000996) ubiquitous TPR		
		6p21, complete			motif, Y isoform [Homo		
		sequence (Homo	4e-08	2580578	sapiens]	1.2	
1332	AC006164	sapiens]	4e-08	2360378	T-CELL RECEPTOR BETA	<u>1:=</u>	
ĺ		III			CHAIN PRECURSOR		
1222	V01060	Human mRNA for	4e-08	135514	precursor (ANA 11) - rabbit	0.61	
1333	X01060	transferrin receptor	46-09	177714	INSULIN RECEPTOR-		
		1			RELATED PROTEIN		
					PRECURSOR (IRR) (IR-		
		H.sapiens INE2			RELATED RECEPTOR)		
1334	Y10697	mRNA	4e-08	124909	>gi 186555 sapiens	0.14	
1534	110097	Rattus norvegicus	40-00	154707	- 6-11-00000 000-0-0-0-1		
		myr 6 myosin heavy					
		ichain mRNA.			myosin I, high molecular weight		
1335	U60416	complete cds	4e-08	102189	- Acanthamoeba sp	3e-08	

	Nearest N	Neighbor (BlastN vs. G	enbank)	Nearest Neigh	bor (BlastX vs. Non-Redundant Pr	oteins)
SEQ						
ΙD	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					HYPOTHETICAL 33.2 KD	T T
					TRP-ASP REPEATS	
		Drosophila	1		CONTAINING PROTEIN	
		melanogaster putative			T10F2.4 IN CHROMOSOME	
		GTP-binding_			III protein; similar to G-Beta	ļ
		regulatory protein			repeat region (Trp-Asp	1
		beta chain (GPB)			domains) of guanine nucleotide	
1336	U23804	mRNA, partial cds.	4e-08	2494916	binding protein	le-28
		Escherichia coli K-12			(AL022325) tF27C3.1.1	
		MG1655 section 103			(protein similar to C. elegans	1
		of 400 of the			protein B0035.16) (isoform 1)	
1337	AE000213	complete genome	4e-08	3294172	[Homo sapiens]	2e-67
					RHO-RELATED GTP-	
		Mus musculus mRNA	٠.		BINDING PROTEIN RHOD	ļ. :
		for RhoM, complete			(RHO-RELATED PROTEIN	
1338	D89821	cds	2e-08	3024539	HP1) (RHOHP1) sapiens]	1e-04
1 1						
		Human telomeric				
		repeat DNA-binding				
		protein (PIN2)	1. 00	-MONTS	NONES	<none></none>
1339	U74382	mRNA, complete cds	le-08	<none></none>	<none></none>	KNONES
		Homo sapiens (subclone H8 5_a10				
		from Pt 35 H5 C8)				
1340	L35657	DNA sequence.	le-08	<none></none>	<none></none>	<none></none>
1340	L33037	Human succinate	10-00	THORIES	(AF060886) adenine	
		dehydrogenase			phosphoribosyltransferase	l
1341	L21936	flavoprotein subunit	1e-08	3201678	[Leishmania tarentolae]	4.0
	221730	Homo sapiens gene				
		for osteonidogen.			tritin - wheat	
1342	AB009777	promoter region	le-08	479388	>gi 391929 gnl PID d1003454	2.2
					GLUCOSE-6-PHOSPHATE	
		Human heparin			ISOMERASE, CYTOSOLIC 2	
} }		cofactor II (HCF2)		•	(GPI) (PHOSPHOGLUCOSE	
i		gene, exons 1 through			ISOMERASE) (PGI) isomerase	
1343	M58600	5.	le-08	1730173	[Clarkia concinna]	1.9
					GLUCOSE-6-PHOSPHATE	
		Human heparin			ISOMERASE, CYTOSOLIC 2	
		cofactor II (HCF2)			(GPI) (PHOSPHOGLUCOSE	
		gene, exons I through			ISOMERASE) (PGI) isomerase	
1344	M58600	5	le-08	1730173	[Clarkia concinna]	1.7
T		Homo sapiens				
		(subclone 1_g2 from				
		PI H31) DNA			(L27428) reverse transcriptase	,,
1345	AC000980	sequence	le-08	439877	[Homo sapiens]	1.1

	Negreet N	leighbor (BlastN vs. G	enbank)	Nearest Neigh	bor (BlastX vs. Non-Redundant Pro	oteins)
	14earest 1	Cignool (Diasir vs. C				
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1346	U48734	Human non-muscle alpha-actinin mRNA. complete cds	le-08	168237	(M76546) hydroxyproline-rich protein [Helianthus annuus]	0.19
1347	M76724	Human leukocyte adhesion receptor alpha subunit	te-08	1177607	(X92485) pval [Plasmodium vivax]	0.19
1348	AF067959	Gallus gallus homeodomain protein HOXD-3 mRNA, complete cds	le-08	3165574	(AF067942) No definition line found [Caenorhabditis elegans]	0.15
1349	Z 81014	Human DNA sequence from cosmid U65A4. between markers DXS366 and DXS87 on chromosome X *	le-08	2072964	(U93569) putative p150 [Homo sapiens]	0.001
		Human h-lys gene for lysozyme (upstream	i	VONE	NONE	<none></none>
1350	X57103	region)	7e-09	<none></none>	<none></none>	KNONES
1351	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	7e-09	231629	BILE-SALT-ACTIVATED LIPASE PRECURSOR ESTER LIPASE) (STEROL ESTERASE) (CHOLESTEROL ESTERASE) salt-activated lipase [Homo sapiens] sapiens]	0.22
1352	L34741	Aplysia californica prohormone convertase (PC2) mRNA, complete cds.	5e-09	322054	cytochrome-c oxidase (EC 1.9.3.1) chain II precursor - Synechocystis sp. (PCC 6803) >gi[581739 sp.]	5.0
1353	AF052959	Homo sapiens type XV collagen (COL15A1) gene. exon 6	4e-09	131269	PHOTOSYSTEM II P680 CHLOROPHYLL A APOPROTEIN (CP-47 PROTEIN) >gi 72708 pir QJLV6A photosystem II chlorophyll a- binding protein psbB - liverwort (Marchantia polymorpha) chloroplast >gi 11700	1.8

	Nearest 1	Veighbor (BlastN vs. G	enbank)	Nearest Neigh	bor (BlastX vs. Non-Redundant Pr	oteins)
SEQ						
ID	ACCESSION	DESCRIPTION	PVALUE	ACCESSION	DESCRIPTION	P VALUE
					FOSSIBLE AGMATIMASE	
					AGMATINE	
1 1	,				UREOHYDROLASE) (AUH)	1
1 1					(PROCLAVAMINIC ACID	
					AMIDINO HYDROLASE)	[]
1 1					>gi 1361423 pir S57669	i
				:	Proclavaminic acid amidino	
					hydrolase - Streptomyces	1
1		Streptomyces		•	clavuligerus >gi 295171	
i		clavuligerus (NRRL			Proclavaminic acid amidino	[
i I	-	3585) clavulanic acid			hydrolase [Streptomyces	
1 1		biosynthesis protein		•	clavuligerus]	
		(cla) gene, complete			>gi 1586122 prf 2203286B]
	!	cds and clavaminate	•		proclavaminic acid amidino	
ارمدرا	115170	synthase 2 (cs2) gene.	4e÷09	586028	hydrolase [Streptomyces clavuligerus]	4e-13
1354	L15470	partial cds.	46-09	380028	clavungerus	46-13
l I					GENERAL SECRETION	
1 1		Human mRNA for			PATHWAY PROTEIN L	
1 1		KIAA0304 gene.			product [Klebsiella pneumoniae]	
1355	AB002302	complete cds	2e-09	131600	>gi 149311 (M32613) pulL	2.5
1333	.12002302	complete cos				
		Homo sapiens]
		retinaldehyde-binding				
		protein (CRALBP)			1	
1356	L34219	gene, complete cds.	le-09	<none></none>	<none></none>	<none></none>
		Human mRNA for				
		KIAA0304 gene.			(AB002302) KIAA0304 [Homo	
1357	AB002302	complete cds	le-09	2224549	sapiens]	5.0
		Homo sapiens				
		HSPAIL gene for	J			
	•	Heat shock protein 70 testis variant, 5'UTR.			(U58658) unknown [Homo	
1358	D85731		1e-09	1389766	[sapiens]	1.3
1338	ונונטע	partial sequence	10-07	1307700	Jupienoj	
] 						
 		Homo sapiens natural	ļ			
i I		resistance-associated	ı			
		macrophage protein 2				
		(NRAMP2) gene.	}			
		exon 17, alternatively	j		1	
		spliced non-IRE			!!!! ALU CLASS F WARNING	
1359	AF064483	form, complete cds	8e-10	113671	ENTRY !!!!	0.72

	Nearest N	Neighbor (BlastN vs. G	enbank)	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEQ							
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
,		No Lucalmba			1	1	
		Mus musculus alpha- actinin-2 associated			1		
		LIM protein mRNA.			(AF053367) carboxyl terminal	i i	
		alternatively spliced			LIM domain protein [Mus		
1360	AF002283	product, complete cds	6e-10	2996196	musculus]	4e-21	
1300	14 002203	African green					
		monkey origin of			gene DMR-N9 protein - mouse	1	
1361	M26220	replication	5e-10	2143455	(fragment)	8.8	
		H.sapiens flow-sorted					
	:	chromosome 6		•		· ·	
		HindIII fragment,			(U93574) putative p150 [Homo	0.005	
1362	Z78006	SC6pA7F10	4e-10	2072977	sapiens] (U88183) similar to the	0.005	
					immunoglobulin superfamily,		
1 1		Homo sapiens			most similar to nerual cell		
		unknown protein			adhesion proteins		
1363	U82303	mRNA, partial cds	2e-10	1825711	[Caenorhabditis elegans]	0.031	
		Drosophila					
		melanogaster			(AF079764) enhancer of	1	
] [,	enhancer of			polycomb [Drosophila		
1364	AF079764	polycomb	2e-10	3757890	melanogaster	1e-10	
1 1					(AC004520) similar to NFE2- related transcription factors;		
		II NDEI			similar to I48694		
		Homo sapiens NRF1 protein (NRF1)	1		(PID:g2137676) [Homo		
1365	L24123	mRNA.	2e-10	3004573	sapiens]	4e-53	
1303	L24(2)	HUXIAN.		300 +3.3	- Supremor		
					NADH-UBIQUINONE		
					OXIDOREDUCTASE CHAIN		
					4 >gi 1085185 pir S52968	• 1	
					NADH dehydrogenase chain 4 -		
			·	•	honeybee mitochondrion		
		Orangutan alpha-			(SGC4) >gi 552446 (L06178) NADH dehydrogenase subunit 4		
12.5	2501.55	globin gene duplicate	10.10	464220	[Apis mellifera ligustica]	6.0	
1366	M91454	region. House mouse;	le-10	464239	[[Apis meilifera figustica]	U.U	
		Musculus domesticus				1	
		brain mRNA for					
		SAP102, complete			(L31961) phosphoprotein [Mus		
1367	D87117	cds	6e-11	473912	cookii]	2.2	
		Homo sapiens					
		(subclone 2_h9 from			1		
	_	P1 H39) DNA			NOVE:	MONTE	
1368	AC001002	sequence	5e-11	<none></none>	<none></none>	<none></none>	

	Nearest	Neighbor (BlastN vs. C	ienbank)	Negreet Main	hbor (BlastX vs. Non-Redundant F	
SEC			1	rearest rely	into (Blaset vs. Non-Redundant F	roteins)
ΙĐ	ACCESSION		P VALUE	ACCESSION	DESCRIPTION	P VALUE
<u> </u>		Homo sapiens		I		1
1		(subclone 2_h9 from				
1	İ	P1 H39) DNA	ł			1
1369	AC001002		5e-11	<none></none>	<none></none>	<none></none>
1	}	Homo sapiens				
1270	4 D003074	KIAA0414 mRNA.			1	1
1370	AB007874	partial cds	5e-11	<none></none>	<none></none>	<none></none>
Į.		Homo sapiens				1
1		(subclone 2_h9 from				
1371	AC001002	P1 H39) DNA			i	
13/1	AC001002	sequence Homo sapiens	5e-11	<none></none>	<none></none>	<none></none>
1		(subclone 2_h9 from		• •		
1		PI H39) DNA				
1372	AC001002	sequence	5e-11	-NONTE-		
	110001002	Homo sapiens	26-11	<none></none>	<none></none>	<none></none>
1		(subclone 2_h9 from		۳		ľ
1	ł	P1 H39) DNA				1
1373	AC001002	sequence	5e-11	<none></none>	NONE	
		Homo sapiens		VI ONE	<none></none>	<none></none>
		(subclone 2_h9 from				
1		P1 H39) DNA	1		} .	
1374	AC001002	sequence	5e-11	<none></none>	<none></none>	<none></none>
1 1		H.sapiens mRNA for				1
[]		HERV-K long	j		gag polyprotein - human	i i
1375	Z21852	terminal repeat	5e-11	419481	endogenous virus S71	4.6
i		Homo sapiens mRNA	I			
		for KIAA0459	i		(AF051782) diaphanous 1	
1376	AB007928	protein, partial cds	5e-11	2947238	[Homo sapiens]	2.8
		House mouse:	1			
ĺ	1	Musculus domesticus	ŀ			
· . [7	brain mRNA for	. 1			l. 1
1377		SAP102, complete	l		(L31961) phosphoprotein [Mus]	
13//		eds Homo Sapiens DNA	5e-11	473912	cookii]	1.8
		sequence between				l
1		•	1		l	
1378		two AML1 gene promoters, 6423 BP	50.11	720021	!!!! ALU SUBFAMILY J	!
	.13131301	profitoters, 0423 BP	5e-11	728831	WARNING ENTRY	0.20
ł	i,	Human endogenous	I			ľ
I	1	etroviral protease	1			j
1379		nRNA, complete cds.	5e-11	88558	retroviral proteinase-like protein	
		complete cus.j	20-11	00330	- human	0.002

	Nearest	Neighbor (BlastN vs. G	enbank)	Nearest Neigh	ibor (BlastX vs. Non-Redundant Pi	oteins)
SEQ		T	1		I Sol (Blastit Vs. Ivon-Reddingant I)	l l
ID	ACCESSION	DESCRIPTION	PVALUE	ACCESSION	DESCRIPTION	P VALUE
	T			1,011,01	HYPOTHETICAL 55.2 KD	1
					TRP-ASP REPEATS	
i	1	Drosophila			CONTAINING PROTEIN	j
l] .	melanogaster putative			T10F2.4 IN CHROMOSOME	1
1	I	GTP-binding			III protein; similar to G-Beta	
i		regulatory protein			repeat region (Trp-Asp	l
i		beta chain (GPB)			domains) of guanine nucleotide	
1380	U23804	mRNA, partial cds.	5e-11	2494916	binding protein	le-30
		M.musculus troponin			(AF072889) transcription	
1381	Z22784	I gene.	_3e-11	3892202	repressor brain factor 2	0.053
		Homo sapiens				
		KIAA0420 mRNA,			1	
1382	AB007880	complete cds	2e-11	<none></none>	<none></none>	<none></none>
		9 Homo sapiens BAX				
		gene, exon 6, partial	I	•		
1383	AF020361	sequence	2e-11	<none></none>	<none></none>	<none></none>
					GLYCOPROTEIN D	
		Homo sapiens DNA			PRECURSOR gD (Bovine	
1384	L35600	sequence.	2e-11	1174952	herpesvirus []	0.25
		Human organic anion				
1206	F101010	transporting			(U95011) brain-specific organic	
1385	U21943	polypeptide	2e-11	2738223	anion transporter	9e-19
j		Homo sapiens			(AF053367) carboxyl terminal	
1386	U90878	carboxyl terminal LIM domain protein	2e-11	2006106	LIM domain protein [Mus	
-300		Human orphan		2996196	musculus]	4e-23
		nuclear receptor	1			
		(DAXI) gene,			1	
1387		complete cds	6e-12	<none></none>	· <none></none>	<none></none>
		Human von		VI ONE	CHOILE	CHOILE
I		Willebrand factor	1		[
	j	gene, exon 1, 2, and	[1
J		3, and three Alu				
1388	M25828	repetitive elements.	6e-12	<none></none>	<none></none>	<none></none>
			1			
1		Homo sapiens mRNA		•		J
ĺ	Į:	for KIAA0841	i			Į
1389		protein, partial cds	3e-12	<none></none>	<none></none>	<none></none>
		H sapiens genes for				
1	3	umor necrosis factor	1	. أ		
		(Tnfa) and	1			
1390		ymphotoxine (Tnfb)	2e-12	<none></none>	<none></none>	<none></none>
		Homo sapiens	1			1
		callistatin (PI4) gene.	ļ			į
201		exons 1-4, complete				
1391		ds	2e-12	<none></none>	<none></none>	<none></none>
1392		Human cosmid QLL2C9 from Xq28	20.12	∠NONE-		NONE:
277	2-7040	Sersea nom vd-9	2e-12	<none></none>	<none></none>	<none></none>

	Nearest	Neighbor (BlastN vs. G	ienhank)	Nanage Maint	ibor (BlastX vs. Non-Redundant Pr	
SEV			I	ivearest iveign	I I I I I I I I I I I I I I I I I I I	oteins)
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		H.sapiens tlow-sorted				
		chromosome 6				
		HindIII fragment,	i		hypothetical protein (L1H 3'	
1393	Z79007	SC6pA20E2	2e-12	106322	region) - human	1.5
ł	i	Human tyrosine				
1		kinase TXK (txk)			(M55524) ORF 4; putative	
1394	U34377	gene, exon 13.	le-12	151484	[Pseudomonas aeruginosa]	4.3
ļ		Mus musculus apg-1 gene for novel	, ,		ALKALDE DOGEDA GE	
1		member of heat shock			ALKALINE PROTEINASE	
		protein 110, promoter			PRECURSOR (ALP) precursor	1
1395	D70845	region	le-12	. 113658	fungus (Acremonium	3.5
1323	D70843	1681011	16-12	113038	chrysogenum)	3.5
		Human vascular			(AF069731) calmodulin-	
	!	endothelial growth			dependent protein kinase II beta	
1396	M63978	factor gene, exon 8.	le-12	3982737	M isoform [Rattus norvegicus]	0.083
					(**************************************	0.003
		Homo sapiens				
		lysosomal alpha-	1		1	
		mannosidase (manB)	ļ	•		
1397	U60266_	mRNA, complete cds	8e-13	<none></none>	<none></none>	<none></none>
		Caenorhabditis	1	,		
		elegans cosmid			(AC002542) similar to C.	
1 1		F11A10. complete	j		elegans F11A10.5; 80%	
	1	sequence [Caenorhabditis	1		similarity to Z68297	
1398		elegans)	7e-13	2393734	(PID:g1130619) [Homo	5. 3.
1370		Caenorhabditis	/e-13	2393734	sapiens]	5e-34
		elegans cosmid	1		(AC002542) similar to C.	
		FIIAIO, complete]		elegans F11A10.5; 80%	
		sequence	1		similarity to Z68297	
		[Caenorhabditis	i		(PID:g1130619) [Homo	
1399	Z68297	elegans]	7e-13	2393734	sapiens]	3e-38
		Human DNA				
i		sequence from	}			1
	4	cosmid L21F12B,				
		Huntington's Disease	- 1			
J		Region, chromosome	j			
1400		4p16.3, contains	, l	AIOE TO		
1400		EST. H.sapiens DAP-	6e-13	<none></none>	<none></none>	<none></none>
1401		kinase mRNA	6e-13	2911154	(AB007143) ZIP-kinase [Mus	0.007
		H.sapiens flow-sorted	00.13	2711134	mu <u>s</u> culus	0.007
ŀ		chromosome 6 TagI	l			ŀ
ļ		ragment.	1	,	hypothetical protein (L1H 3'	1
1402		SC6pA13G4	5e-13	106322	region) - human	2e-06
		Homo sapiens DNA			(AC004136) hypothetical	
1403	L35600 s	sequence.	3e-13	3184290	protein [Arabidopsis thaliana]	1.7

	Nearest	Neighbor (BlastN vs. G	enbank)	Nearest Neigh	ibor (BlastX vs. Non-Redundant Pr	Oteins)
SEQ						1
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Cloning vector				
		pKODT complete			(Z49966) F35C11.4	
1404	AF090452	sequence	2e-13	3876730	[Caenorhabditis elegans]	7.8
		Human gene for ATP				
	l	synthase alpha				ļ
		subunit, complete cds			gag polyprotein - human	1
1405	D28126	(exon 1 to 12)	2e-13	419481	endogenous virus S71	3.4
		Homo sapiens				
		transcription factor			(AC004080) transcription factor	
1406	AF005219	HOXD13	2e-13	2822166	HOXA13 [Homo sapiens]	5e-09
		·				
1	i	Homo sapiens mRNA			1	
		for KIAA0758		•	(AB018301) KIAA0758 protein	
1407	AB018301	protein, partial cds	2e-13	3882237	[Homo sapiens]	le-23
		Mus musculus apg-l				
1 1		gene for novel			ALKALINE PROTEINASE	:
		member of heat shock			PRECURSOR (ALP) precursor	
		protein 110, promoter			fungus (Acremonium	
1408	D70845	region	le-13	113658	chrysogenum)	3.1
		Homo sapiens				
		genomic DNA, 21q	<u> </u>			
		region, clone:	1		(X15332) alpha-1 (III) collagen	
1409	AG000691	T171BG33	8e-14	930045	[Homo sapiens]	3e-04
		Mouse mRNA for				
1 1		neuropsin, complete	ı		(AJ005641) serine protease	
1410	D30785	cds	8e-14	3559978	[Rattus rattus]	2e-12
1 1						
		Haemophilus	1			1
		influenzae Rd section			(AL035064) queuine trna-	
1 1		25 of 163 of the	ľ		ribosyltransferase	1
1411	U32710	complete genome	Se-14	4106673	[Schizosaccharomyces pombe]	2e-38
] [ſ		T		hypothetical protein 2 - North	
l i		Homo sapiens	İ		American opossum (fragment)	· }
		genomic DNA, 21q	1		>gi 897721 (Z48955) ORF-2,	Ī
	1	region, clone:	1		putative RT [Didelphis	ļ
1412	AG000886	64E11X19	7e-14	1363925	virginiana)	1.1
! [. 1		ļ			7
		H.sapiens CpG DNA.	į.			- 1
أدينا		clone 71d11, forward	1		(AC002328) F20N2.6	· · · · · · · · · · · · · · · · · · ·
1413	Z62664	read cpg71d11.ft1a.	7c-14	3953461	[Arabidopsis thaliana]	0.085
	1.		- !			
		Homo sapiens mRNA	- 1			
1,1	T I	for KIAA0632	7.).	112660	!!!! ALU CLASS C WARNING	
1414	AB014532	protein, partial cds	7e-14	113668	ENTRY !!!!	0.040

	Nearest	Neighbor (BlastN vs. G	enbank)	Nearest Naigh	nbor (BlastX vs. Non-Redundant P	rotains)
SEO				TVCMCSt : Vergi	loof (Blasta Vs. 140n-Redundant P	Toteins)
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
<u></u>	<u> </u>	<u> </u>				T
-		H.sapiens telomeric				
1		DNA sequence, clone		•		İ
1415	706 170	20PTEL004, read		1	(AB012223) ORF2 [Canis	1
1413	Z96478	20PTELOO004.seq Mus musculus	7e-14	2981631	familiaris]	2e-04
		Pontin52 mRNA.				
1416	AF100694	complete cds	4e-14	-NONEs	NOVE	1
<u> </u>	10 100034	complete cus	46-14	<none></none>	<none></none>	<none></none>
ĺ		Sambucus nigra			1	l i
ļ.,		ribosome inactivating		Ì		j
l		protein precursor		! ,	1	
1417	AF012899	mRNA, complete cds	4e-14	<none></none>	<none></none>	<none></none>
ł			• •			
		Homo sapiens MLL			1	j
1		gene breakpoint	` ;		1	
	1 50300 40	cluster region, intron			!!!! ALU SUBFAMILY J	1
1418	AF033349	1. partial sequence	3e-14	728831	WARNING ENTRY	9.3
		Homo sapiens				
	,	(subclone 4_f6 from P1 H54) DNA				ļ
1419	AC001526	sequence	3e-14	99861	extensin - almond >gi 20420	
	110001520	sequence	36-14	77001	(X65718) extensin	9.2
		Sambucus nigra				1
		ribosome inactivating				i
İ		protein precursor	•		!!!! ALU SUBFAMILY SB	1
1420	AF012899	mRNA, complete cds	3e-14	728832	WARNING ENTRY	0.15
1						
		[i		EPHRIN-A2 PRECURSOR	
1			i		(EPH-RELATED RECEPTOR	l l
ſ			1		TYROSINE KINASE LIGAND	1
1		Mus musculus	- 1		6) (LERK-6) sapiens]	
1421	1	Pontin52 mRNA, complete cds	2e-14	2012672	>gi 2924761 (AC004258)	
1421	AI 100094	complete cas		3913573	EPL6_HUMAN (Homo sapiens) EIB PROTEIN, SMALL 1-	8.7
- 1	İ	•	Ĭ		ANTIGEN (E1B 19K)	
1	1		1	i	>gi 74142 pir Q1AD25 early	
		1			E1B 21K protein II - human	
- 1	į]		adenovirus 5 >gi 58489	
					(X02996) mRNA 5 first reading	
1	į:	Sambucus nigra	İ		frame [Human adenovirus type	1
ł		ribosome inactivating	j		5] adenovirus type 5]	i
	1.	protein precursor			>gi 209797 (J01969) 21 kD	j
1422	AF012899	nRNA, complete cds	9e-15	119040	protein	1.5

	Nearest	Neighbor (BlastN vs. G	enbank)	Nearest Neigh	nbor (BlastX vs. Non-Redundant Pr	roreins)
SEO					- Diabet 13: Hon-Redandant Fi	J. C.C.IIIST
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
<u></u>					transcription factor GATA-4,	
1	ł	Sambucus nigra			retinoic acid-inducible - mouse	
Ī	İ	ribosome inactivating		l	>gi 293345 (M98339) GATA-	1
		protein precursor			binding transcription factor	
1423	AF012899	mRNA, complete cds	8e-15	477102	[Mus musculus]	0.57
		Conin fomiliaria I DIE			·}	
i i		Canis familiaris LINE 1 element ORF2				ļ
1424	AB012223	mRNA, complete cds	00.15	02205	hypothetical protein - rat	
1424	ABOLIZZI	Mus musculus	8e-15	92385	(fragment)	0.003
		Pontin52 mRNA.			ì	
1425	AF100694	complete cds	3e-15	· · <none></none>	<none></none>	<none></none>
		Human pHS1-2		CITOTIVES.	CHONES	KNONES
		mRNA with ORF	• •			
1	1	homologous to			1	
		membrane receptor			collagen alpha 3(IV) chain - sea	
1426	X12433	proteins	3e-15	422532	urchin	8.9
					PROBABLE NUCLEAR	0.7
					HORMONE RECEPTOR	
i Į					E02H1.7	
! I		Sambucus nigra			>gi 3875431 gnl PID e1344980	
		ribosome inactivating			(Z47075) similar to Zinc finger,	
1427		protein precursor			C4 type (two domains)	
1427	AF012899	mRNA, complete cds Human DNA	3e-15	1353143	[Caenorhabditis elegans]	5.0
		sequence from				
		cosmid L75B9.	Í			
i		Huntington's Disease				ł
I		Region, chromosome			(L24521) transformation-related	i
1428	1	4p16.3	3e-15	403460	protein [Homo sapiens]	0.60
				,05.00	Ig heavy chain precursor	0.00
		Sambucus nigra	ł		(B/MT.4A.17.H5.A5) - bovine	į
.		ribosome inactivating	[>gi 440 (X62916) anti-	ĺ
- 1		protein precursor	1		testosterone antibody [Bos	1
1429		mRNA, complete cds	2c-15	108750	taurus]	1.1
	1	H.sapiens SMA3			(X83299) SMA3 gene product	
1430	X83299	mRNA	2e-15	671530	[Homo sapiens]	0.32
	į.					
		Human p300 protein]	i
		mRNA, complete cds.	1			Į
1		> :: gb 162297 162297 Sequence 1 from	ł			1
1431		•	20.15	20242 + 1	E1A-ASSOCIATED PROTEIN	0010
1421	0013//	patent US 5658784	2e-15	3024341	P300	0.019

	Near	est Neighbor (BlastN	vs. Genb	ink)	Negroes M	aighter (D)	<u> </u>
SEQ	2				rearest No	eighbor (BlastX vs. Non-Redundant P	roteins)
ID	ACCESS	ON DESCRIPTION	N P	VALUE	ACCESSIO		P VALI
						HYPOTHETICAL 45.1 KD	
1	1		1		1	PROTEIN CIECIO.6 IN	
l			i		Ī	CHROMOSOME III	1
l	1	1	j		ſ	>gi 3874384 gnI PID e1344078	1
1			[EST EMBL: C08256 comes	ł
1	f	İ	ł			from this gene; cDNA EST	ł
	i	ļ.				EMBL:C09941 comes from this	l
]	Mouse MHC (Qa)	001			gene; cDNA EST yk340a10.3	i
	1	k gene for class I	, Q2			comes from this gene; cDNA	ĺ
1432	X16516	antigen, exons 4-8				EST yk340a10.5 comes from	1
	1110010	antigen, exons 4-6	1	e-15	2496897	this gene [Ca	7e-08
- 1		Chicken tensin		ł	٠.		
1433	M74165		cde l	. re.		tensin - chicken >gi 212752	
		H.sapiens gene for	10	-15	283920	(M74165) tensin	2e-19
ł		immunoglobulin	1	l			
- 1		kappa light chain		1			
1		variable region O4	j	j			
1434	X71893	and O5		-16	ALONE	1	
- f				··	<none></none>	<none> (284479) match: multiple</none>	<none:< td=""></none:<>
ł				ł		proteins; match: O00407	
- 1		1		- 1		Q12829 P22127 P36861	
- 1			- 1			Q40219; match: P70550	
- 1			1	- 1		Q41022 P22125 Q08155	
j				i		P35286; match: P51148 P51147	
- 1				1		P35293 P36861 P35289; match:	
125		Human Rar protein				P35284 Q40217 P51152	
435	U05227	mRNA, complete co	ls. 9e-	16	3036779	P51157 P51158; match: Q41022	2- 04
- 1						131137131138, Haten: Q41022	3e-06
		Chicken erythrocyte	1	- 1		1	
- 1		anion transport	1	1		(U23175) similar to anion	
436	M22404	protein (band3)	1	1		exchange protein	
÷30	M23404	mRNA, complete cd	s. 9e-1	6	726403	[Caenorhabditis elegans]	le-28
ĺ			1			alpha-L-fucosidase (EC	16-28
1		Rat mRNA for liver		- 1		3.2.1.51) 1 precursor, tissue	
		L-Fucosidase (EC	7	- 1		human >gi 178409 (M29877)	1
37	X16145	3.2.1.51)		_		alpha-L-fucosidase precursor	[
_	-3.0173	ا (۱۰٫۵۰۰	9e-1	<u> </u>	67502	VEC 3 3 1 3 2 2 2	2e-29
-		Sambucus nigra	1	I			
		ribosome inactivating	.1	- 1			1
-		protein precursor	1	- 1			•
38 · A		mRNA, complete cds	0.1/	.	Nov-		ı
		Mus musculus brain	8e-16	' _	<none></none>	<none> <n< td=""><td>NONE></td></n<></none>	NONE>
- 1		mitochondrial carrier	l	- 1			
		protein BMCP1	l				•
1	I -	Bmcpl) mRNA,	I	- 1	j		1
9 A		complete cds	8e-16	- 1	20747/-	(AF078544) brain mitochondrial	1
			96-10		3851540	carrier protein-1 [Homo sapiens]	e-13

	Nearest	Neighbor (BlastN vs. G	enbank)	Nearest Neigh	abor (BlastX vs. Non-Redundant Pr	oteins)_
SEQ						
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		H.sapiens MN/CA9			!!!! ALU SUBFAMILY J	
1440	Z54349	GENE	5e-16	728831	WARNING ENTRY	0.002
		Non-mandus SU2		•		
1		Mus musculus SH3 domain-containing			(M35526) complement	
		adapter protein			component C5D [Mus	
1441	AF077003	mRNA, complete cds	3e-16	309123	musculus]	3.1
		M.musculus mRNA			glycoprotein - rat >gi 986943	
		for splicing factor			(L08134) glycoprotein [Rattus	
1442	X64587	U2AF (65 kD)	3e-16	2143767	norvegicus] norvegicus]	0.003
		Homo sapiens mRNA				
		for KIAA0661		•	(AB014561) KIAA0661 protein	
1443	AB014561	protein, complete cds	3e-16	3327136	[Homo sapiens]	1e-20
		Human DNA			[220.00 0000.00]	.0.20
		sequence from			1	
1 1		cosmid N120B6 on	İ			
		chromosome 22 Contains ESTs.				Ì
		complete sequence	· ` '		·	
1444	Z73987	(Homo sapiens)	le-16	<none></none>	<none></none>	<none></none>
	273307	Homo sapiens ala	- 10 .0	ALTO ITES	THORIZ TO THE PART OF THE PART	CITOLIC
1445	M58318	gene.	le-16	<none></none>	<none></none>	<none></none>
		Human small GTP				
¦		binding protein Rab9			(Z80233) hypothetical protein	
1446	U44103	mRNA, complete cds	le-16	1552584	Rv0029	1.3
			i			
		Homo sapiens mRNA				1
		for KIAA0661	0 17	2227126	(AB014561) KIAA0661 protein	2 20
1447		protein, complete cds Mus musculus	9e-17	3327136	[Homo sapiens]	2e-20
	ı	Pontin52 mRNA.				
1448		complete cds	le-17	<none></none>	<none></none>	<none></none>
		Mus musculus	- 1		1	į
		ribosomal protein (Ke	1		1	1
1449		3) gene, exons 1 to 5. and complete cds.	le-17	1073048	pupR protein - Pseudomonas	0.36
****	27,0702	and complete cus.	10-17	107,5040	putida >gi 525260	-0.50
	1	Human DNA.	j		LINE-I REVERSE]
	ļ	replication enhancing	l		TRANSCRIPTASE	
1450		element (REE1)	4e-18	126295	HOMOLOG	0.78
- 1		Human mRNA for	Ì			i
İ		hepatoma-derived growth factor,				
1451		complete cds	4e-18	3242079	(AJ006984) proline-rich protein	0.018
	D 10-01	complete eds	70-10	J=7=U/9	Ityronosom) bronne-tren brotein I	0.010

	Nearest	Neighbor (BlastN vs. C	ienbank)	Nearest Neigh	bor (BlastX vs. Non-Redundant Pr	
SEO		T T	T		Visit Visit Visit Von-Reddingant Pr	T (terns)
Ð	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
<u> </u>						
Ĭ					(Z73102) Similarity to B.subtilis	
1					DNAJ protein	
1		Mus musculus heat			(SW:DNAJ_BACSU); cDNA	
1		shock protein hsp40-3			EST yk437a1.5 comes from this	ļ
1452	AF088983	mRNA, complete cds	4e-18	3873707	gene [Caenorhabditis elegans]	9e-25
1						
1		Human methyl sterol				}
	****	oxidase (ERG25)				
1453	U60205	mRNA, complete cds	3e-18	<none></none>	<none></none>	<none></none>
		f ·				
İ.		Mana anni ana alama		•	G protein-coupled receptor 74 -	
		Homo sapiens clone 23899 mRNA	• •		equine herpesvirus 2 >gi 695246	
1454	AF038177		, , , ,	1260776	(U20824) G protein-coupled	
1434	A1036177	sequence	le-18	1360775	receptor [Equine herpesvirus 2]	5.1
		Homo sapiens mRNA	ı			
		for KIAA0661	l l		(ABOL1561) KIA AO661	
1455	AB014561	protein, complete cds	le-18	3327136	(AB014561) KIAA0661 protein	
1	112014301	protetti. complete cus	10-13	3327130	[Homo sapiens]	le-21
		Homo sapiens mRNA	I			
		for KIAA0661	ŀ		(AB014561) KIAA0661 protein	
1456	AB014561	protein, complete cds	le-18	3327136	[Homo sapiens]	le-22
				3327.530	[Tromo sapiens]	16-22
		Human tyrosine	1			
] }		kinase TXK (txk)	1			
1457	U34374	gene, exons 9 and 10.	le-19	NONE	<none></none>	<none></none>
		Homo sapiens				
	İ	hGAA1 mRNA.	1		(AF102855) synaptic SAPAP-	i
1458		complete cds	le-19	4151809	interacting protein Synamon	0.19
		Human mR:NA for				
		KIAA0295 gene.	ļ		(AB002293) KIAA0295 [Homo	İ
1459	AB002293	partial cds .	le-19	2224531	sapiens]	6e-17
1	1		·	•	·	
		H.sapiens CpG DNA.	- 1			l
		clone 168t9, reverse			(Z82055) predicted using	ı
1460		read cpg168f9.rt1a.	5e-20	3880251	Genefinder	6.5
		Human modulator	1			Ī
- 1		recognition factor 2	ļ		.	ļ
1461		MRF-2) mRNA.	1		modulator recognition factor 2 -	
1461	M73837	complete cds.	5e-20	284313	human factor 2 [Homo sapiens]	0.019

 	Near	rest Neighbor (BlastN vs.	Genbank)	Nearest Ne	ighbor (Blass V	
SEQ	2			11021031146	ighbor (BlastX vs. Non-Redundant I	roteins)
ΙD	ACCESSI	ON DESCRIPTION	P VALUE	ACCESSION	N DESCRIPTION	P VALI
				 	DELLA	
1	1		1	ł	DELTA-1-PYRROLINE-3- CARBOXYLATE	
İ	1		1	1 .	DEHYDROGENASE	i
	j		1	1	PRECURSOR (P5C	1
	J				DEHYDROGENASE)	1
		j	1	1	>gi 1353248 sapiens]	l
		1	1		ogili 353250 (Tradoca)	ł
	1		1	i	>gi 1353250 (U24267) pyrroline 5-carboxylate dehydrogenase	1
		}			[Homo sapiens]	l
		Human pyrroline-5-		l	>gi 1589585 prf 2211355A	Ī
1462	710.00.00	carboxylate	1	i	Delta 1-pyrroline-5-carboxylate	
1402	U24267	dehydrogenase	5e-20	2506350	dehydrogenase [Homo sapiens]	
ı		Mus musculus myelin			(U13262) myelin gene	5e-04
1463	1112262	gene expression	į .		expression factor [Mus	
1403	U13262	factor	4e-20	536926	musculus]	7-07
- 1		Mus musculus myelin				3e-07
1464	U13262	gene expression factor			(AF061832) M4 protein	
		idetoi	4e-20	3126878	deletion mutant [Homo sapiens]	le-08
		H.sapiens CpG DNA.				
ł		clone 48f10, forward	ľ			
465	Z61239	read cpg48f10.ft1a.	4e-20	1660/01	(D88747) AR401 [Arabidopsis	
			- 40-20	1669601	(thaliana)	8e-19
ſ		Mus musculus	ľ		1	
		junctional adhesion	i		1	
		molecule (Jam)			(U89915) junctional adhesion	•
166	U89915	mRNA, complete cds	le-20	3462455	molecule [Mus musculus]	
- 1		G-11 11				7e-11
		Gallus gallus p52 pro-	i]	
167	AF029071	apototic protein			(AF029071) p52 pro-apototic	
	. 11 0290/1	mRNA, complete cds Figure 4. Nucleotide	7e-22	2599492	protein [Gallus gallus]	le-15
- 1		sequence of the	1			10-15
- 1		pKS36 1.797 kb	ı			- 1
68	M25636	insert.	6- 22		(M21305) unknown protein	ľ
			6e-22	1196398	[Homo sapiens]	0.65
	į	Homo sapiens mRNA	1	1		
1		for KIAA0848	1			1
59 A		protein, complete cds	6e-22	4240225	(AB020725) KIAA0918 protein	1
		F-5-5-5-5-5	<u> </u>	4240325	[Homo sapiens]	le-19

	Nearest	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEQ		T T	T					
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE		
					PROCOLLAGEN ALPHA	T		
1					I(IV) CHAIN PRECURSOR			
	l		ļ		>gi 84917 pir A31893 collagen			
1					alpha I(IV) chain precursor -	1		
1	<u> </u>]			fruit fly (Drosophila	1 .		
ł					melanogaster) melanogaster]	1		
1		chorionic			>gi 157078 (M96575) type IV			
		gonadotropin beta 1			collagen pro-collagen	ŀ		
1470	S80935	(CG beta 1) subunit	5e-22	115310	[Drosophila melanogaster]	0.027		
1		Homo sapiens						
1471	4.5063066	microsatellite			!!!! ALU SUBFAMILY J			
14/1	AF053066	D5S2926 sequence	2e-22	728831	WARNING ENTRY	3e-04		
1		Danio rerio carbonic	٠.		CARBONIC ANHYDRASE			
		anhydrase homolog CAH-Z mRNA,			(CARBONATE			
1472	1166177		2. 22	2102100	DEHYDRATASE) >gi 2576335			
14/2	<u>U55177</u>	complete cds Gallus gallus	2e-22	3123190	(U55177) CAH-Z [Danio rerio]	5e-14		
		ubiquitin specific			(AF016107) his idease:6	ļ		
1473	AF064250	protease 66	2e-22	2736064	(AF016107) ubiquitin specific			
1111	711 004230	protease oo	26-22	2730004	protease 41 [Gallus gallus] DRA PROTEIN (DOWN-	7e-37		
í l					REGULATED IN ADENOMA)			
1 1			İ		>gi 2135020 pir A47456 down-			
					regulated in adenoma (DRA) -			
i I			ı		human >gi 291964 (L02785)			
l i		ļ	i		Nuclear localization signal at			
ļ I					AA 569-573, 576-580, 579-583;			
! !		Homo sapiens			acidic transer, activ. domain 620-			
		pendrin (PDS)	1		640,; homeobox motif 653-676			
1474	AF030880	mRNA, complete cds	2e-22	729367	[Homo sapiens]	4e-53		
1		Mus musculus						
		Pontin52 mRNA,						
1475		complete cds	6e-23	<none></none>	<none></none>	<none></none>		
		Human mRNA for	i		Pm5 protein - human			
1476	X57398	pM5 protein	3e-23	107350	>gi 1335273 gn1 PID e362+1	1e-04		
l		Rattus norvegicus	Ì					
I	1	PAD-R11 mRNA for	1					
		Peptidylarginine	į		1	1		
1477		deiminase type I,	2- 22	MONT				
- 17/		complete cds Human h NAT allele	2e-23	<none></none>	<none></none>	<none></none>		
j		2-2 gene for						
1		arylamine N-	I		(10 173 t) CDC6			
1478		acetyltransferase	2e-23	171200	(J04734) CDC6 protein			
		Human h NAT allele	26-23	1/1/200	[Saccharomyces cerevisiae]	9.8		
1		2-2 gene for	ı			ļ		
J		arylamine N-	i		(J04734) CDC6 protein	ľ		
1479		ncetyltransferase	2e-23	171200	(Saccharomyces cerevisiae)	8.3		
				171200	[[Saccuatomyces cerevisiae]	د.د		

		Near	est Neighbor (BlastN	vs. Genbank)	Nearest Ne	eighbor (BlastX vs. Non-Redundant		_
	SI	EQ				Marioti (Blasek Vs. (Non-Redundant)	roteins)	_
		D ACCESSI			E ACCESSION	N DESCRIPTION	P VALU	_
	-		Homo sapiens MI				1. 1.7.	_
	1	80 AF02454	AF4 fusion protein			serine/proline-rich FEL protein	+	_
	14	80 AF02454	1 mRNA, partial cd	s 2e-23	2136142	splice form 1 - human		
			, <u> </u>			- Indinan	le-20	_
	14		Human AF-4 mRN	NA.		(AF031404) MLL-AF4 fusion	1.	
	1.4	BL L13773		2e-23	3063962	protein [Homo sapiens]	1- 20	
	1		Mus musculus			(=====================================	le-20	_
	148	15100c0	Pontin52 mRNA,	. 1			i	Į
	146	32 AF10069		8e-24	<none></none>	<none></none>	NONT	I
	1	ľ	Drosophila	1			<none></none>	4
	1	1	melanogaster Rga		j	1	l	J
	1		Atu genes, complet	te	1 '	(U75467) Atu [Drosophila	1 .	ı
	148	3 U75467	cds	8e-24	1658503	melanogaster!	2- 27	Į
	ł		Human HepG2 par	tial			2e-37	ł
	١		cDNA, clone			ļ	ĺ	ł
	148	4 D17076	hmd5a09m5	7e-24	<none></none>	<none></none>		ı
	1			·		FMRFAMIDE-RELATED	<none></none>	Į
	İ	1		1	1	NEUROPEPTIDES	i .	ı
	Ī	1			l	PRECURSOR >gi 416208	i l	ı
		J	Mus musculus	j		(U03137) neuropeptide		l
ı		. #	Pontin52 mRNA,	ļ	1	precursor FMRFamide-related	i	l
I	1485	AF100694	complete cds	7e-24	1169643	peptide [Lymnaea stagnalis]		İ
1		1				(Z81054) predicted using	7e-10	
1		ł	Human 28S	1		Genefinder; Similarity to UDP-	1	
ŀ	1486	M11167	ribosomal RNA gen	e. 2e-24	3875481	glucoronosyltransferases		
1			Mus musculus		5515161	gracoronosymransierases	5.1	
ı		ł	Pontin52 mRNA,			USPI PROTEIN PRECURSOR	l.	
Ļ	1487	AF100694	complete cds	2e-24	549173	>gi 169623		
l			Cloning vector		347173	>gi1109023	1.2	
ı			pAP3neo DNA.	1 1		(Y65335) la 27 man a mal	J	
L	1488	AB003468	complete sequence	2e-24	987050	(X65335) lacZ gene product		
l			Human mRNA of trk		207030	[unidentified cloning vector]	0.058	
l		. •	oncogene > ::	1		(M74509) [Human endogenous	1	
l			gb 196186 196186	1 ' '		retrovirus type C oncovirus		
	ł		Sequence 23 from	1 1		retiovirus type C oncovirus	j	
\subseteq	1489	X03541	patent US 5734039	2e-24	325465	sequence.], gene product [Homo	. [
			Homo sapiens	 	323403	sapiens]	3e-04	
	- 1		(subclone 2_gll from	۱ ا		1	1	
	i		PI H43) DNA	1 1		L	1	
ı	490	L81652	sequence	2e-24	225047	reverse transcriptase related	i	
	- 1		Drosophila		223047	protein [Homo sapiens]	4e-12	
	J		melanogaster	1 1		1	- 1	
	- 1		strawberry notch	1 1			1	
	- 1		(sno) mRNA,	 		1,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	Į	
ı.	491	1	complete cds	2e-24	2070202	(U95760) Sno [Drosophila		
	T		Mus musculus		2078282	melanogaster)	2e-∔1	
	ı	ľ	Pontin52 mRNA,			(AF004835) tyrocidine		
l۷	192		complete cds	8e-25	242222	synthetase 3 [Brevibacillus		
			picic cus	06.23	2623773	brevis]	8.6	

	<u>_</u>	Neare	est Neighbor (BlastN vs.	Genbank)	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
	SE	Q				The state of the s	roteins)	
	II	ACCESSIO	ON DESCRIPTION	PVALUE	ACCESSION	DESCRIPTION		
					1	DESCRIPTION	PVALUE	
				 		HYPOTHETICAL 127.3 KD	 	
	ı			}	ľ	PROTEIN B0416.1 IN	1	
	1	ľ	Homo sapiens mRNA	A.	•	CHROMOSOME X >gi 746502		
		į	for LAK-4p.	1		(U23516) B0416.1 gene product		
	149	3 AB00240:		8e-25	2496822	[Caenorhabditis elegans]		
			Human mRNA from			(Cachornabditis elegans)	9e-11	
		1	chromosome 15 gene	.]			ł	
			with homology to		İ			
	نہ ا	. [MHC-HLA-SB-I			(X92842) nuclear protein [Mus		
	1494	K03002	intron A.	8e-25	1514614	musculus]	le-13	
1		I			٠,		16-13	
-			Human tubulin-	j i				
- 1	1406		folding cofactor E			(U61232) cofactor E [Homo		
ŀ	1495	U61232	mRNA, complete cds	7e-25	1465772	sapiens]	2e-05	
1		ſ	A					
ł		1	Arabidopsis thaliana	1 1			ĺ	
1			Col-O putative RNA	l i		(U10245) putative RNA		
1	1496	U10245	helicase A mRNA,			helicase A [Arabidopsis	1	
H	1470	010243	complete cds.	5e-25	1353239	thaliana]	le-37	
		ł	H.sapiens DNA for	. [
1		i	endogenous retroviral				I	
	1497	X89211	like element	3- 35	20672.4	(Y12713) Pro-Pol-dUTPase	Į	
Γ			Homo sapiens	3e-25	2065210	polyprotein	5e-06	
ł		Ĭ	(subclone 2_g11 from	1				
Ĺ		1	P1 H43) DNA	ł		11:025.01	1	
L	498	L81652	sequence	3e-25	2072961	(U93568) putative p150 (Homo	J	
Г				- 30-23	2072901	sapiens MAGUK P55 SUBFAMILY	5e-16	
				ł			1	
1			H.sapiens mRNA for	ł		MEMBER 2 (MPP2 PROTEIN) (DISCS, LARGE HOMOLOG	i	
L	499	X82895	DLG2	2e-25	2497511	(DISCS, LARGE HOMOLOG		
	ı		Mouse homeo box		5477511	21	le-34	
	_	• •	2.6 (Hox-2.6) mRNA.			(AE001255) T. pallidum	[]	
1	500	M36654	complete cds.	9e-26	3323169	predicted coding region TP0854		
		-	Mus musculus (clone			Proceed couring region 170834	1.9	
			pMILZ-1) zinc finger	j		(Z67747) zinc finger protein	1	
1.	501	L36315	protein	9e-26	1806134	[Mus musculus]	4e-05	
	- [i					40-03	
	- 1		Homo sapiens mRNA	l			j	
1 4	502	A BOLOGO:	for KIAA0738	1		!!!! ALU SUBFAMILY J	J	
-	702	AB018281	protein, complete cds	9e-26		WARNING ENTRY	le-07	
		i	Homo societa	ŀ				
			Homo sapiens	1		1	[
15	03		putative transcription	2	1	ZINC FINGER PROTEIN ZFP-	1	
		01/433	factor CR53	9e-26	3219985	29	le-17	

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEQ		Tiergardor (Brasia v vs. C	Jenounk)	Nearest Neignbor (BlastX vs. Non-Redundant Proteins)			
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
		Homo sapiens	T T	1		IF VALUE	
		(subclone 2_e6 from					
1	1	BAC H94) DNA	1	1	(U91823) small S protein	1	
1504	AC001225	sequence	8e-26	2653713	[Hepatitis B virus]	4.3	
		Mus musculus			cyteine-rich surface antigen 72,	+	
1	J	Pontin52 mRNA,	İ ,		CRP72 - Giardia lamblia	1	
1505	AF100694	complete cds	8e-26	283446	(fragment)	3.4	
1,500					!!!! ALU SUBFAMILY SQ		
1506	X94912	H.sapiens Pr22 gene	3e-26	728837	WARNING ENTRY	4e-09	
1	J	Mus musculus	ł I				
1507	AF100694	Pontin52 mRNA,					
1307	AF100694	complete cds	2e-26	· <none></none>	<none></none>	<none></none>	
l i		Human small GTP	٠.		•		
1 1		binding protein Rab9				1 1	
1508	U44103	mRNA, complete cds	le-26	2227020	(AB014512) KIAA0612 protein		
	0.4103	matra, complete cus	16-20	3327038	[Homo sapiens] (AC005990) Contains repeated	8.7	
1 1					region with similarity to	ł !	
					gb U+3627 extensin (atExt1)	1 1	
1 1				•	gene from Arabidopsis thaliana.		
		Mus musculus	1		ESTs gb Z34165 and gb Z18788		
1 1		Pontin52 mRNA,	- 1		come from this gene.	1	
1509	AF100694	complete cds	9e-27	4056454	[Arabidopsis thaliana]	0.14	
1 1		Homo sapiens			LINE-I REVERSE	0.14	
		genomic DNA, 21q			TRANSCRIPTASE	i	
		region. clone:	I		HOMOLOG protein		
1510	AG001212	9H11N46	9e-27	126296	[Nycticebus coucang]	0.012	
1 1	į		i				
1 1		Mus musculus mucin	1			j	
1511	AF027131	glycoprotein MUC3			(U76551) mucin Muc3 [Rattus		
1311	AI-02/131	mRNA, partial cds	9e-27	2589172	norvegicus)	2e-14	
	ľ	Rattus norvegicus	1		1		
1		CTD-binding SR-like			. !	1	
J		protein r.A9 mRNA.	İ		(THOOSE) AND IN		
1512		complete cds	5e-27	1438534	(U49057) rA9 [Rattus		
		op.oto eas		1436334	norvegicus)	1e-0-1	
i i	Į i	Human, plasminogen		•	·		
- 1	;	ectivator inhibitor-1					
1513		zene, exons 2 to 9.	3e-27	<none></none>	<none></none>	<none></none>	
		vl.musculus partial	<u>_</u>		110112	-11-011-L2	
		ochlear mRNA	1		(Z78160) unknown (Mus	ŀ	
1211	Z78160 (clone 28D2)	3e-27	1490362	musculus)	2e-05	
- 1	1						
J	_		1		(AB004538) LIPOIC ACID		
- 1		Lapiens CpG DNA.	1		SYNTHETASE	. [
1515	i i	lone 99b4, reverse	1		PRECURSOR(LIP-SYN)		
	Z64210 r	ead cpg99b4.ntla.	3e-27	2257538	[Schizosaccharomyces pombe]	1e-06	

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEQ							
ID	ACCESSION	DESCRIPTION	PVALUE	ACCESSION	DESCRIPTION	P VALUE	
		Homo sapiens				1	
		(subclone H8 6_h6				 	
		from P1 35 H5 C8)	·	İ	I	ļ	
1516	L35659	DNA sequence.	le-27	<none></none>	<none></none>	<none></none>	
		Mus musculus					
		Pontin52 mRNA.			(U72686) odorant receptor 4	1	
1517	AF100694	complete cds	1e-27	1644471	[Danio rerio]	7.5	
		Mus musculus			(AF003534) hypothetical		
		Pontin52 mRNA,			protein 004L (Chilo iridescent		
1518	AF100694	complete cds	1e-27	2738388	virus	6.7	
		II			(AL 032(26) X (0D (D 2]	
1519	AB009271	Homo sapiens gene for BCNT, partial cds	le-27	3880909	(AL032636) Y40B1B.3	1 46	
1319	AB009271	Mus musculus	16-27	3000909	[Caenorhabditis elegans]	4.6	
		Pontin52 mRNA.			spermatophorin Sp23 - yellow		
1520	AF100694	complete cds	le-27	2133579	mealworm molitor)	0.85	
	112 100074	Mus musculus		2133377	inearworm montor)	0.05	
		Pontin52 mRNA,			ENDOGLUCANASE A		
1521	AF100694	complete cds	1e-27	121805	PRECURSOR	0.58	
		Mus musculus					
•		Pontin52 mRNA.			(AF035323) survival motor		
1522	AF100694	complete cds	le-27	3722000	neuron protein [Bos taurus]	0.10	
ľ		Mus musculus	1				
		Pontin52 mRNA,			(AF074902) laminin alpha chain		
1523	AF100694	complete cds	le-27	3328188	[Caenorhabditis elegans]	0.083	
		Homo sapiens IkB			(AE074392) IkB kingga gamma		
1524		kinase gamma subunit	le-27	3641280	(AF074382) IkB kinase gamma subunit [Homo sapiens]	0.041	
.,,,,,	A1 074362	Kinase gamma subumi	10-17	3041230	(AC005990) Contains repeated	0.041	
					region with similarity to		
f			ł		gb[U43627 extensin (atExt1)		
]			ľ		gene from Arabidopsis thaliana.		
1		Mus musculus	i		ESTs gb Z34165 and gb Z13788		
		Pontin52 mRNA.		•	come from this gene.		
1525		complete cds	le-27	4056454	[Arabidopsis thaliana]	6e-04	
		Homo sapiens	ŀ				
1		(subclone 2_e10 from					
ایی		P1 H49) DNA			reverse transcriptase related		
1526	L78778	sequence	1e-27	225047	protein [Homo sapiens]	2e-09	
[[.	Human zinc finger	ſ		į	i	
		protein basonuclin	- 1		(U59694) zinc finger protein		
1527		mRNA, complete cds.	le-27	1488275	basonuclin [Homo sapiens]	9e-22	
	,	Human ribosomal			(AB004538) LIPOIC ACID		
		protein L9 gene, 5'	į		SYNTHETASE	ļ	
	1	region and complete	i		PRECURSOR(LIP-SYN)	ŀ	
1528	U09954	eds.	4e-28	2257538	[Schizosaccharomyces pombe]	2e-04	

	Nearest Neighbor (BlastN vs. Genbank)			Nessest Naighbor (Blast V. vo. Nov. Bada da D			
GEO		TACIBIDOL I DIASILA VS. C	lenoank)	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEQ	1	DESCRIPTION		l .		İ	
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
<u> </u>		 					
1]	1	(Z46381) similar to lipoic acid		
1			ļ	}	synthase; cDNA EST yk283b6.3		
Į.					comes from this gene; cDNA	ŀ	
			·	ļ	EST yk283b6.5 comes from this		
1			f	1	gene; cDNA EST yk472f5.3	1	
	j	H.sapiens CpG DNA,	İ		comes from this gene; cDNA	ł	
1529	761212	clone 99b4, reverse			EST yk472f5.5 comes from this	l	
1329	Z64210	read cpg99b4.rt1a . Danio rerio carbonic	4e-28	3878570	gene; cDNA EST yk476e7.3	7e-11	
ł					CARBONIC ANHYDRASE		
1		anhydrase homolog			(CARBONATE		
1530	HEELTT	CAH-Z mRNA,	4 20		DEHYDRATASE) >gi 2576335		
1330	U55177	complete cds	4e-28	3123190	(U55177) CAH-Z [Danio rerio]	5e-21	
l i		Human mRNA for		i.	1.077.004		
		very-long-chain acvl-			ACYL-COA		
ł		CoA dehydrogenase			DEHYDROGENASE, VERY-		
		(VLCAD), complete			LONG-CHAIN SPECIFIC		
1531	D43682	cds	4e-28	1251020	PRECURSOR (VLCAD)		
1.33.	D-3002	cus	46-28	1351839	>gi 930358 taurus	3e-27	
		Homo sapiens			· ·		
	•	survival motor neuron					
	•	pseudogene, complete			!!!! ALU SUBFAMILY I	i	
1532	AF016591	sequence	3e-28	728831	WARNING ENTRY	3e-08	
		Mus musculus	- 33.30	720051	WARNING ENTRY	JE-08	
ĺ		Pontin52 mRNA,	į		!!!! ALU SUBFAMILY SB	ł	
1533	AF100694	complete cds	2e-28	728832	WARNING ENTRY	2.5	
					DEHYDRIN DHN3		
1		İ	ſ		>gi 100035 pir \$18139 dehydrin	ı	
		Mus musculus	1		DHN3 - garden pea >gi 20709		
		Pontin52 mRNA,	i i		(X63063) pea dehydrin DHN3		
1534	AF100694	complete cds	2e-28	118588	[Pisum sativum]	0.004	
					FMRFAMIDE-RELATED		
ľ		•	l	•	NEUROPEPTIDES	ſ	
J		1	1		PRECURSOR >gi 416208	1	
1		Mus musculus	i		(U03137) neuropeptide]	
i		Pontin52 mRNA,	ŀ		precursor FMRFamide-related		
1535	AF100694	complete cds	2e-28	1169643	peptide [Lymnaea stagnalis]	6e-04	
i	ı				(AC005990) Contains repeated		
- 1	ł	1	[region with similarity to	i	
- 1	j	1	ŀ		gb U43627 extensin (atExt1)	ŀ	
I			i		gene from Arabidopsis thaliana.		
1		Mus musculus	i		ESTs gb Z34165 and gb Z18788		
	1	Pontin52 mRNA.	[come from this gene.		
1536	AF100694	complete cds	2e-28	4056454	[Arabidopsis thaliana]	9e-05	

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEQ							
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
					(AC005990) Contains repeated	1	
					region with similarity to	 	
]]					gb U43627 extensin (atExt1)	1	
1 1					gene from Arabidopsis thaliana.		
]		Mus musculus	ľ		ESTs gb Z34165 and gb Z18788		
1 1		Pontin52 mRNA.	1		come from this gene.	1 ·	
1537	AF100694	complete cds	2e-28	4056454	[Arabidopsis thaliana]	2e-06	
				***************************************	(AC005990) Contains repeated		
					region with similarity to]	
	!		!		gb U43627 extensin (atExt1)	1	
1 1			[]		gene from Arabidopsis thaliana.		
]		Mus musculus	ļ I		ESTs gb Z34165 and gb Z18788		
1		Pontin52 mRNA,	† 		come from this gene.		
1538	AF100694	complete cds	2e-28	4056454	[Arabidopsis thaliana]	2e-09	
					(AC005990) Contains repeated		
					region with similarity to		
1	1		İ		gb U43627 extensin (atExt1)		
			<u> </u>		gene from Arabidopsis thaliana.		
		Mus musculus			ESTs gb Z34165 and gb Z18788	l	
		Pontin52 mRNA,			come from this gene.	ļ	
1539	AF100694	complete cds	2e-28	4056454	[Arabidopsis thaliana]	le-09	
					(AC005990) Contains repeated	ì	
			ŀ		region with similarity to		
					gb U43627 extensin (atExt1)	<u> </u>	
			l		gene from Arabidopsis thaliana.	l	
		Mus musculus	i i		ESTs gb Z34165 and gb Z18788	l	
ر د د د	A 5100404	Pontin52 mRNA,	2. 20	1056151	come from this gene.	5e-10	
1540	AF100694	complete cds	2e-28	4056454	[Arabidopsis thaliana] (AC005990) Contains repeated	36-10	
					region with similarity to		
	į				gb U43627 extensin (atExt1)]	
			}		gene from Arabidopsis thaliana.		
		Mus musculus			ESTs gb Z34165 and gb Z18788		
Ì		Pontin52 mRNA.		•	come from this gene.		
1541		complete cds	2e-28	4056454	[Arabidopsis thaliana]	le-11	
		complete eas			(AC002131) Strong similarity to		
		Mus musculus			extensin-like protein gb Z34465		
		Pontin52 mRNA.			from Zea mays. [Arabidopsis		
1542		complete cds	2e-28	3157926	thaliana]	8c-12	
		Mus musculus					
		Pontin52 mRNA.					
1543		complete cds	le-28	<none></none>	<none></none>	<none></none>	
		Mus musculus					
	ł	Pontin52 mRNA.					
1544		complete cds	le-28	<none></none>	<none></none>	<none></none>	
		Mus musculus					
		Pontin52 mRNA.	ſ		· .		
1545	AF100694	complete cds	1e-28	<none></none>	<none></none>	<nove></nove>	

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEQ	1						
ID	ACCESSION	DESCRIPTION	PVALUE	ACCESSION	DESCRIPTION	P VALUE	
		Mus musculus	1	ACCESSION .		IF VALUE	
-		Pontin52 mRNA.	 				
1546	AF100694	complete cds	le-28	ANONT-	NONE	2/02/75	
1340	AF100694	Mus musculus	1e-20	<none></none>	<none></none>	<none></none>	
1		Pontin52 mRNA.					
1547	AF100694	complete cds	le-28	NOMES	NONE	NONT	
134,	AP100094	Mus musculus	16-20	<none></none>	<none></none>	<none></none>	
}		Pontin52 mRNA.	1			1 .	
1548	AF100694	complete cds	le-28	<none></none>	MONTES	ANONTE	
1346	AT 100094	Mus musculus	16-20	CNOINES	<none></none>	<none></none>	
		Pontin52 mRNA.	1		1		
1549	AF100694	complete cds	le-28	· · <none></none>	NONTE:	- NONT	
1349	AF100094	Mus musculus	16-26	KINONES	<none></none>	<none></none>	
	i	Pontin52 mRNA.			1		
1550	AF100694	complete cds	le-28	NOME	ALCONES.	ANCONT	
	At 100094	Mus musculus	16-20	<none></none>	<none></none>	<none></none>	
	į	Pontin52 mRNA.					
1551	AF100694	complete cds	le-28	<none></none>	NONE	ANONE	
1331	AL 100094	Mus musculus	16-20	CAOMES	<none></none>	<none></none>	
		Pontin52 mRNA.					
1552	AF100694	complete cds	le-28	<none></none>	<none></none>	-NONTE:	
1332	AI 100094	Mus musculus	16-20	CHONES	KNUNES	<none></none>	
		Pontin52 mRNA.					
1553		complete cds	1e-28	<none></none>	<none></none>	<none></none>	
1333	111100034	Mus musculus	10-20	CHOILE	CNONE	KINONES	
		Pontin52 mRNA.				i i	
1554		complete cds	le-28	<none></none>	<none></none>	<none></none>	
		Mus musculus		4.10.12	31,01,25	Q.VO.V.Z	
ĺ		Pontin52 mRNA.	ſ		·	1	
1555	1	complete cds	1e-28	<none></none>	<none></none>	<none></none>	
		Mus musculus				1111111111	
ł		Pontin52 mRNA.	l				
1556	Į.	complete cds	le-28	<none></none>	<none></none>	<none></none>	
		Mus musculus					
	1	Pontin52 mRNA,		Ì		1	
1557		complete cds	le-28	<none></none>	<none></none>	<none></none>	
		Mus musculus				1	
	1:	Pontin52 mRNA.		.]			
1558	AF100694	complete cds	le-28	<none></none>	<none></none>	<none></none>	
		Mus musculus					
		Pontin52 mRNA,	i i				
1559	AF100694	complete cds	le-28	<none></none>	<none></none>	<none></none>	
		Mus musculus					
	į į	Pontin52 mRNA.	1	j			
1560	AF100694	complete cds	1e-28	<none></none>	<none></none>	<none></none>	
		Mus musculus					
ŀ		Pontin52 mRNA.	ļ		٠.	1	
1561	AF100694	complete cds	1e-28	<none></none>	NONE	<none></none>	

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEQ						T	
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
		Mus musculus	L			T	
		Pontin52 mRNA.					
1562	AF100694	complete cds	le-28	<none></none>	<none></none>	<none></none>	
		Mus musculus					
1,573	. 5. 65. 65.	Pontin52 mRNA,			1	ľ	
1563	AF100694	complete cds	1e-28	<none></none>	<none></none>	<none></none>	
1 .		Mus musculus				[
1564	AF100694	Pontin52 mRNA, complete cds	10.20	-MONTE-	NOVE		
1307	A1-100094	Mus musculus	le-28	<none></none>	<none></none>	<none></none>	
1 1		Pontin52 mRNA.					
. 1565	AF100694	complete cds	1e-28	, <none></none>	<none></none>	<none></none>	
					3.13.132	Q. (O. (L.)	
		Human simple repeat	٠.				
1566	M87708	polymorphism.	1e-28	<none></none>	<none></none>	<none></none>	
1 1		Mus musculus					
		Pontin52 mRNA,				ĺ	
1567	AF100694	complete cds	le-28	<none></none>	<none></none>	<none></none>	
1					B; cDNA EST yk450d8.5 comes		
]					from this gene; cDNA EST		
					yk249a6.5 comes from this		
1 1					gene; cDNA EST yk219a2.5		
		·			comes from this gene; cDNA		
			Ĭ		EST yk355e4.5 comes from this		
			1		gene; cDNA EST yk224f4.5		
					comes fr		
			ı		>gi 3924881 gn1 PID e1354569		
			1		from this gene; cDNA EST	İ	
	ĺ		ļ		yk249a6.5 comes from this		
			1		gene; cDNA EST yk219a2.5		
	ļ	Mus musculus	f		comes from this gene; cDNA EST yk355e4.5 comes from this		
		Pontin52 mRNA.	. [gene; cDNA/EST yk224f4.5		
1568		complete cds	le-28	3924779	comes from	3.0	
				- J/24/1/	FMRFAMIDE-RELATED		
	1		1		NEUROPEPTIDES		
	İ		I		PRECURSOR >gi 416208		
	1	Mus musculus	ŀ		(U03137) neuropeptide	1	
1	i i	Pontin52 mRNA,	1		precursor FMRFamide-related		
1569	AF100694	complete cds	1e-28	1169643	peptide [Lymnaea stagnalis]	0.66	

PCT/US00/18374

Nearest Neighbor (BlastN vs. Genbank) Nearest Neighbor (BlastX vs. Non-Redundant) SEQ ID ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION R. CDNA EST yk±50d8.5 com from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk224f4.5 comes from this gene; cDNA EST yk249a6.5 comes from this gene; cDNA EST yk249a	P VALUE
ID ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION 1. C.	is 0.65
	is 0.65
from this gene; cDNA EST yk249a6.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk355e4.5 comes from the gene; cDNA EST yk224f4.5 comes from this gene; cDNA EST yk249a6.5 comes from this gene; cDNA EST yk249a6.5 comes from this gene; cDNA EST yk249a6.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk224f4.5 comes from the gene; cDNA EST yk224f4.5 comes from the gene; cDNA EST yk224f4.5 comes from the gene; cDNA EST yk224f4.5 comes from the gene; cDNA EST yk224f4.5 comes from the gene; cDNA EST yk224f4.5 comes from the gene; cDNA EST yk224f4.5 comes from the gene; cDNA EST yk224f4.5 comes from the gene; cDNA EST yk224f4.5 comes from the gene; cDNA EST yk224f4.5 comes from the gene; cDNA EST yk224f4.5 comes from the gene; cDNA EST yk224f4.5 comes from the gene; cDNA EST yk224f4.5 comes from the gene; cDNA EST yk224f4.5 comes from the gene; cDNA EST yk224f4.5 comes from the gene; cDNA EST yk224f4.5 comes from the gene; cDNA EST yk224f4.5 comes from the gene; cDNA EST yk224f4.5 comes from the gene; cDNA EST yk219a2.5 co	is 0.65
yk249a6.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk224f4.5 comes fr >gi]3924881[gn] PID e135456 from this gene; cDNA EST yk249a6.5 comes from this gene; cDNA EST yk249a6.5 comes from this gene; cDNA EST yk249a6.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk224f4.5 comes from the gene; cDNA EST yk249a6.5 comes from the gene; cDNA EST yk249a6.5 comes from the gene; cDNA EST yk249a6.5 comes from the gene; cDNA EST yk249a6.5 comes from the gene; cDNA EST yk249a6.5 comes from the gene; cDNA EST yk249a6.5 comes from the gene; cDNA EST yk249a6.5 comes from the gene; cDNA EST yk249a6.5 comes from the gene; cDNA EST yk249a6.5 comes from the gene; cDNA EST yk249a6.5 comes from the gene; cDNA EST yk249a6.5 comes from the gene; cDNA EST yk249a6.5 comes from the gene; cDNA EST yk2	0.65
gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk355e4.5 comes from th gene; cDNA EST yk224f4.5 comes fr >gi 3924881 gn PID e135456 from this gene; cDNA EST yk249a6.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk2355e4.5 comes from th gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk355e4.5 comes from th gene; cDNA EST yk224f4.5 comes from th gene; cDNA EST yk224f4.5 comes from th gene; cDNA EST yk224f4.5 comes from th gene; cDNA EST yk355e4.5 comes from th gene; cDNA EST yk224f4.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk355e4.5 comes from th gene; cDNA EST yk355e4.5 comes from this gene; cDNA EST yk355e4.5 comes from th gene; cDNA EST yk355	0.65
comes from this gene; cDNA EST yk355e4.5 comes from the gene; cDNA EST yk224f4.5 comes fr >gi 3924881 gn PID e135456 from this gene; cDNA EST yk249a6.5 comes from this gene; cDNA EST yk249a6.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA Mus musculus Pontin52 mRNA, complete cds Pontin52 mRNA, pontin52 mRNA, spermatophorin Sp23 - yellow mealworm molitor Mus musculus Pontin52 mRNA, spermatophorin Sp23 - yellow mealworm molitor Mus musculus Pontin52 mRNA, spermatophorin Sp23 - yellow mealworm molitor Mus musculus Pontin52 mRNA, spermatophorin Sp23 - yellow mealworm molitor Mus musculus Pontin52 mRNA, spermatophorin Sp23 - yellow mealworm molitor Cyteine-rich surface antigen 72	0.65
EST yk355e4.5 comes from the gene; cDNA EST yk224f4.5 comes fr >gi 3924881 gn PID e135456 from this gene; cDNA EST yk249a6.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk219a2.5 comes from the gene; cDNA EST yk219a2.5 comes from the gene; cDNA EST yk219a2.5 comes from the gene; cDNA EST yk224f4.5 comes from the gene; cDNA EST yk	0.65
gene; cDNA EST yk224f4.5 comes fr >gi]3924881 gn PID e135456 from this gene; cDNA EST yk249a6.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk355e4.5 comes from th gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk355e4.5 comes from th gene; cDNA EST yk224f4.5 complete cds le-28 3924779 comes from Mus musculus Pontin52 mRNA, pontin52 mRNA, l571 AF100694 complete cds le-28 2133579 spermatophorin Sp23 - yellow mealworm molitor Mus musculus Pontin52 mRNA, l572 AF100694 complete cds le-28 2133579 mealworm molitor Cyteine-rich surface antigen 72	0.65
comes fr >gi 3924881 gn PID e135456 from this gene; cDNA EST yk249a6.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk355e4.5 comes from th gene; cDNA EST yk224f4.5 EST yk355e4.5 comes from th gene; cDNA EST yk224f4.5 complete cds	is 0.65
>gi 3924881 gn PID e135456 from this gene; cDNA EST yk249a6.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk355e4.5 comes from th gene; cDNA EST yk224f4.5 EST yk355e4.5 comes from th gene; cDNA EST yk224f4.5 complete cds le-28 3924779 comes from Mus musculus Pontin52 mRNA, pontin52 mRNA, l571 AF100694 complete cds le-28 2133579 spermatophorin Sp23 - yellow mealworm molitor Mus musculus Pontin52 mRNA, l572 AF100694 complete cds le-28 2133579 mealworm molitor Mus musculus Cyteine-rich surface antigen 72	is 0.65
from this gene; cDNA EST yk249a6.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk355e4.5 comes from the gene; cDNA EST yk355e4.5 comes from the gene; cDNA EST yk224f4.5 comes from the gene; cDNA EST yk224f4.5 comes from the gene; cDNA EST yk224f4.5 comes from the gene; cDNA EST yk224f4.5 comes from the gene; cDNA EST yk224f4.5 comes from the gene; cDNA EST yk224f4.5 comes from the gene; cDNA EST yk224f4.5 comes from the gene; cDNA EST yk224f4.5 comes from the gene; cDNA EST yk224f4.5 comes from the gene; cDNA EST yk224f4.5 comes from the gene; cDNA EST yk224f4.5 comes from the gene; cDNA EST yk224f4.5 comes from the gene; cDNA EST yk219a2.5 comes from the gene; cDNA EST yk219a2.5 comes from the gene; cDNA EST yk219a2.5 comes from the gene; cDNA EST yk224f4.5 comes fr	is 0.65
yk249a6.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk355e4.5 comes from the gene; cDNA EST yk355e4.5 comes from the gene; cDNA EST yk224f4.5 complete cds 1570 AF100694 complete cds Pontin52 mRNA, 1571 AF100694 complete cds Pontin52 mRNA, 1572 AF100694 complete cds Pontin52 mRNA, 16-28 2133579 mealworm molitor Mus musculus Pontin52 mRNA, 1572 AF100694 complete cds Pontin52 mRNA, 16-28 2133579 mealworm molitor Mus musculus Pontin52 mRNA, 1572 AF100694 complete cds Pontin52 mRNA, 16-28 2133579 mealworm molitor Cyteine-rich surface antigen 72	0.65
gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk355e4.5 comes from the gene; cDNA EST yk355e4.5 comes from the gene; cDNA EST yk355e4.5 comes from the gene; cDNA EST yk224f4.5 complete cds Ie-28 1570 AF100694 Mus musculus Pontin52 mRNA, complete cds Ie-28 16-28	0.65
Mus musculus Pontin52 mRNA, complete cds Pontin52 mRNA, pontin52 mRNA, complete cds Pontin52 mRNA, pontin52 mRNA, l571 AF100694 Mus musculus Pontin52 mRNA, l572 AF100694 Mus musculus Pontin52 mRNA, l572 AF100694 Mus musculus Pontin52 mRNA, l6-28 L6-2	0.65
Mus musculus Pontin52 mRNA, 1570 AF100694 complete cds Ie-28 3924779 comes from Mus musculus Pontin52 mRNA, 1571 AF100694 complete cds Ie-28 2133579 mealworm molitor Mus musculus Pontin52 mRNA, 1572 AF100694 complete cds Ie-28 2133579 mealworm molitor Mus musculus Pontin52 mRNA, 1572 AF100694 complete cds Ie-28 2133579 mealworm molitor Mus musculus Cyteine-rich surface antigen 72	0.65
Pontin52 mRNA, complete cds le-28 3924779 gene; cDNA EST yk224f4.5 comes from Mus musculus Pontin52 mRNA, complete cds le-28 2133579 mealworm molitor] Mus musculus Pontin52 mRNA, spermatophorin Sp23 - yellow mealworm molitor] Mus musculus Pontin52 mRNA, spermatophorin Sp23 - yellow mealworm molitor] Mus musculus Pontin52 mRNA, spermatophorin Sp23 - yellow mealworm molitor] Mus musculus Mus musculus Cyteine-rich surface antigen 72	0.65
1570 AF100694 complete cds 1e-28 3924779 comes from Mus musculus Pontin52 mRNA, spermatophorin Sp23 - yellow Complete cds 1e-28 2133579 mealworm molitor Mus musculus Pontin52 mRNA, spermatophorin Sp23 - yellow Pontin52 mRNA, spermatophorin Sp23 - yellow Complete cds 1e-28 2133579 mealworm molitor Mus musculus cyteine-rich surface antigen 72	
Mus musculus Pontin52 mRNA, complete cds Pontin52 mRNA, le-28 2133579 Mus musculus Pontin52 mRNA, spermatophorin Sp23 - yellow mealworm molitor Spermatophorin Sp23 - yellow spermatophorin Sp23 - yellow mealworm molitor Mus musculus Le-28 2133579 mealworm molitor cyteine-rich surface antigen 72	
Pontin52 mRNA, complete cds le-28 2133579 spermatophorin Sp23 - yellow mealworm molitor] Mus musculus Pontin52 mRNA, spermatophorin Sp23 - yellow mealworm molitor] AF100694 complete cds le-28 2133579 mealworm molitor] Mus musculus cyteine-rich surface antigen 72	0.49
1571 AF100694 complete cds 1e-28 2133579 mealworm molitor	0.49
Mus musculus Pontin52 mRNA, 1572 AF100694 complete cds le-28 2133579 mealworm molitor cyteine-rich surface antigen 72	0.49
Pontin52 mRNA, complete cds le-28 2133579 spermatophorin Sp23 - yellow mealworm molitor cyteine-rich surface antigen 72	1 1
1572 AF100694 complete cds le-28 2133579 mealworm molitor cyteine-rich surface antigen 72	1
Mus musculus cyteine-rich surface antigen 72	0.00
1 1 1 5	0.49
	' [
1573 AF100694 complete cds 1e-28 283446 (fragment)	0.45
SPERMATOPHORIN SP23	+ 5.43
Mus musculus PRECURSOR mealworm	
Pontin52 mRNA, >gi 161725 (M92928) structur	ıl
1574 AF100694 complete cds 1e-28 2498937 protein	0.33
Mus musculus	
Pontin52 mRNA, (U60315) MC107L [Molluscu	n
1575 AF100694 complete cds 1e-28 1492050 contagiosum virus subtype 1]	0.18
Mus musculus	
Pontin52 mR:NA, spermatophorin Sp23 - yellow	
1576 AF100694 complete cds 1e-28 2133579 mealworm molitor	0.088
DEHYDRIN DHN3	_
>gi 100035 pir S18139 dehydr Mus musculus	"] 1
	1
Pontin52 mRNA. (X63063) pea dehydrin DHN3 1577 AF100694	0.018
DEHYDRIN DHN3	10.013
>gi 100035 pir S18139 dehydr	, l
Mus musculus DHN3 - garden pea >gi 20709	"] ·]
Pontin52 mRNA. (X63063) pea dehydrin DHN3	
1578 AF100694 complete cds 1e-28 118588 [Pisum sativum]	



E		Neare	st Neighbor (BlastN vs	- Genbank)	Names Ma	inhhas / Plaus V	
5	EQ				thearest Nei	ighbor (BlastX vs. Non-Redundant F	roteins)
1	ID,	ACCESSIC	DESCRIPTION	P VALUE	ACCESSION		P VALUE
<u> </u>					 	DEHYDRIN DHN3	
			Mus musculus	j		>gi 100035 pir S18139 dehydrii	1
- !		•	Pontin52 mRNA.	- 1	1	DHN3 - garden pea >gi 20709	ł
11:	579	AF100694			1	(X63063) pea dehydrin DHN3	1
<u> </u>		AL 100094	complete cds	1e-28	118588	[Pisum sativum]	0.012
į	- 1					(AC005990) Contains repeated	
- 1	- 1			1	1	region with similarity to	1
- 1				1		gb U43627 extensin (atExt1)	l l
- }	- 1		Mus musculus	1	1	gene from Arabidopsis thaliana.	I .
ļ	- 1		Pontin52 mRNA.	ļ	ł	ESTs gb Z34165 and gb Z18788	1
_15	80	AF100694	complete cds	le-28	1056151	come from this gene.	i 1
	\Box			16-20	4056454	[Arabidopsis thaliana]	0.010
1	- 1				1	DEHYDRIN DHN3	1
	i		Mus musculus		1	>gi 100035 pir S18139 dehydrin	l l
	- 1		Pontin52 mRNA,	ł	ĺ	DHN3 - garden pea >gi 20709	1
15	81	AF100694	complete cds	le-28	118588	(X63063) pea dehydrin DHN3	ľ
1 -				10.20	110300	[Pisum sativum] FMRFAMIDE-RELATED	0.002
- 1	ſ					NEUROPEPTIDES	
- 1	- [1 .		PRECURSOR >gi 416208	- 1
-	ł		Mus musculus	1		(U03137) neuropeptide	i
_ [Pontin52 mRNA,			precursor FMRFamide-related	1
158	2	AF100694	complete cds	le-28	1169643	peptide [Lymnaea stagnalis]	0.000
- 1						(AC005990) Contains repeated	0.002
]	- 1		·	1 1		region with similarity to	1
1	1					gb U43627 extensin (atExt1)	
- 1	1			1		gene from Arabidopsis thaliana.	1
1			Mus musculus	1		ESTs gb Z34165 and gb:Z18788	ľ
158	,		Pontin52 mRNA,	1 1		come from this gene.	i
138	' '	AF100694	complete cds	1e-28	4056454	[Arabidopsis thaliana]	0.002
			ı	1 . 1		DEHYDRIN DHN3	
1	j	ĺ	Mus museul	1		>gi 100035 pir S18139 dehydrin	
1	1		Mus musculus Pontin52 mRNA,			DHN3 - garden pea >gil20709	i
1584	1 4		complete cds			(X63063) pea dehydrin DHN3	ł
1	+	- 100074	complete cas	1e-28	118588	[Pisum sativum]	0.002
	1	j				(AC005990) Contains repeated	
1	1			1		region with similarity to	1
1			1	í		gb U43627 extensin (atExt1)	. [
1	1	h	Mus musculus	į		gene from Arabidopsis thaliana.	1
			Pontin52 mRNA,	ı		ESTs gb Z34165 and gb Z18788	
1585	A		complete cds	1e-28	1056.45	come from this gene.	
				16-20	4056454	[Arabidopsis thaliana]	0.002
1	l		,	ĺ		DEHYDRIN DHN3	
		IN	lus musculus	f	İ	>gi 100035 pir S18139 dehydrin	
			ontin52 mRNA,	- 1		DHN3 - garden pea >gi 20709	
1586	A		omplete cds	le-28		(X63063) peu dehydrin DHN3	
	_				.10300	[Pisum sativum]	i 00.0

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEC		T ************************************	1	Tremest (Vergnoof (Blasex Vs. : Noti-Redditidant Proteins)			
В	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
<u> </u>					(AC005990) Contains repeated	i i	
ł			1		region with similarity to	 	
		Ĭ			gb U43627 extensin (atExt1)		
				ľ	gene from Arabidopsis thaliana.	[
1	1	Mus musculus	1	Į.	ESTs gb Z34165 and gb Z18788		
1		Pontin52 mRNA,	Î		come from this gene.		
1587	AF100694	complete cds	le-28	4056454	[Arabidopsis thaliana]	0.001	
1	l				(AC005990) Contains repeated		
			1		region with similarity to		
	1		1	•	gb U43627 extensin (atExt1)		
f			1		gene from Arabidopsis thaliana.		
i	1	Mus musculus		٠.	ESTs gb Z34165 and gb Z18788		
		Pontin52 mRNA.	1	ļ	come from this gene.		
1588	AF100694	complete cds	le-28	4056454	[Arabidopsis thaliana]	6e-04	
1		Ì			(AC005990) Contains repeated		
ŀ	ľ				region with similarity to		
l					gb U43627 extensin (atExt1)		
ł	i				gene from Arabidopsis thaliana.		
1		Mus musculus			ESTs gb Z34165 and gb Z18788		
1589	4510000	Pontin52 mRNA,			come from this gene.		
1389	AF100694	complete cds .	le-28	4056454	[Arabidopsis thaliana]	5e-04	
l	i				(AC005990) Contains repeated		
f			!		region with similarity to		
l			i i		gb U43627 extensin (atExt1)	1	
}		Mus musculus			gene from Arabidopsis thaliana.	ı	
		Pontin52 mRNA.			ESTs gb Z34165 and gb Z18788	Ī	
1590	AF100694	complete cds	le-28	4056454	come from this gene.		
		compiete cus	10-20	4020424	[Arabidopsis thaliana] DEHYDRIN DHN3	5e-04	
			1 1		>gi 100035 pir S18139 dehydrin		
		Mus musculus	: !		DHN3 - garden pea >gi 20709		
		Pontin52 mRNA.	1 1		(X63063) pea dehydrin DHN3	j	
1591	1	complete cds	1e-28	118588	[Pisum sativum]	2e-04	
			10.00	110300	(AC005990) Contains repeated	26-04	
Ī					region with similarity to		
ĺ	J		ļ		gb U43627 extensin (atExt1)		
	1				gene from Arabidopsis thaliana.	- 1	
l	Ī	Mus musculus			ESTs gb Z34165 and gb Z18788		
ļ	[:	Pontin52 mRNA,			come from this gene.	1	
1592	AF100694	complete cds	le-28	4056454	[Arabidopsis thaliana]	2e-04	
I				·····	(AC005990) Contains repeated		
	İ		Ì		region with similarity to		
		ļ	i		gb U43627 extensin (atExt1)	-	
	I		ſ		gene from Arabidopsis thaliana.		
i		Mus musculus	1		ESTs gb Z34165 and gb Z18788		
		Pontin52 mRNA,	. !		come from this gene.		
1593	AF100694	complete cds	le-28	4056454	[Arabidopsis thaliana]	5e-05	



E	Nearest	Neighbor (BlastN vs.	Genbank)	Nearpet Naia	hbor (BlastX vs. Non-Redundant Pr	
SEQ				ricalest Neig	itol (Blasta Vs. 140n-Redundant Pr	oteins)
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
<u> </u>	ļ				(AC005990) Contains repeated	
1	j				region with similarity to	
i		1	i		gb U43627 extensin (atExt1)	
ı	i		1		gene from Arabidopsis thaliana.	1
1	1	Mus musculus	1	ļ	ESTs gb/Z34165 and gb/Z18788	ļ
1		Pontin52 mRNA,		ł	come from this gene.	ľ
1594	AF100694	complete cds	le-28	4056454	[Arabidopsis thaliana]	5e-05
I			4		(AC005990) Contains repeated	
ı	1.				region with similarity to	
1	Í	,			gb U43627 extensin (atExt1)	
ı				ĺ	gene from Arabidopsis thaliana.	
	•	Mus musculus			ESTs gb Z34165 and gb Z18788	·
1606	1 F100404	Pontin52 mRNA,	1		come from this gene.	
1595	AF100694	complete cds	le-28	4056454	[Arabidopsis thaliana]	le-05
	ł		1		(AC005990) Contains repeated	
•	ļ		ł		region with similarity to	
ł					gb U43627 extensin (atExt1)	
ĺ		Mus musculus	1		gene from Arabidopsis thaliana.	
1		Pontin52 mRNA.			ESTs gb Z34165 and gb Z18788	
1596	AF100694	complete cds	le-28	1056454	come from this gene.	
1370	711 100094	complete cus	16-28	4056454	[Arabidopsis thaliana] (AC005990) Contains repeated	le-05
ļ			1		region with similarity to	ļ
			1 1		gb[U43627 extensin (atExt1)	
]		gene from Arabidopsis thaliana.	1
		Mus musculus]		ESTs gb Z34165 and gb Z18788	
		Pontin52 mRNA.	i		come from this gene.	ŀ
1597	AF100694	complete cds	le-28	4056454	[Arabidopsis thaliana]	9e-06
					(AC005990) Contains repeated	96-00
					region with similarity to	
]]		gb U43627 extensin (atExt1)	
ı			1 1		gene from Arabidopsis thaliana.	
*		Mus musculus			ESTs gb Z34165 and gb Z18788	I
1		Pontin52 mRNA,		,	come from this gene.	i
1598	AF100694	complete cds	1e-28	4056454	[Arabidopsis thaliana]	6e-06
- 1					(AC005990) Contains repeated	
1					region with similarity to	i
1					gb U43627 extensin (atExt1)	l l
- 1	l				gene from Arabidopsis thaliana.	ł
İ		Mus musculus			ESTs gb Z3+165 and gb Z18788	i
		Pontin52 mRNA.			come from this gene.	}
1599	AF100694	complete cds	le-28	4056454	[Arabidopsis thaliana]	5e-06
i	1.	Mus musculus	1		[7
- 1			ĺ		RNA-BINDING PROTEIN	1
1600		Pontin52 mRNA,	1. 20	5	FUS/TLS protein [human.	Į
1000	AF100694	omplete cds	le-28	544357	Peptide, 526 aa] [Homo sapiens]	4e-06



1:	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEQ			<u> </u>				
Ð	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
					(AC005990) Contains repeated		
					region with similarity to		
1 1			i		gb U43627 extensin (atExt1)]	
					gene from Arabidopsis thaliana.	1	
•		Mus musculus			ESTs gb Z34165 and gb Z18788	l	
		Pontin52 mRNA,			come from this gene.	į	
1601	AF100694	complete cds	le-28	4056454	[Arabidopsis thaliana]	2e-06	
				1	(AC005990) Contains repeated	ł	
					region with similarity to	ļ	
					gb U43627 extensin (atExt1)	İ	
					gene from Arabidopsis thaliana.	İ	
		Mus musculus			ESTs gb Z34165 and gb Z18788	•	
	4 F100 40 4	Pontin52 mRNA.		4056454	come from this gene.	2-06	
1602	AF100694	complete cds	le-28.	4056454	[Arabidopsis thaliana] (AC005990) Contains repeated	2e-06	
]		region with similarity to		
					gb[U43627 extensin (atExt1)		
				:	gene from Arabidopsis thaliana.		
	·	Mus musculus	ļ.		ESTs gb Z34165 and gb Z18788	ł	
ĺĺ		Pontin52 mRNA.			come from this gene.		
1603	i i	complete cds	1e-28	4056454	[Arabidopsis thaliana]	9e-07	
1005	111 100024	complete cus	10 20	4030434	(AC005990) Contains repeated	70 07	
					region with similarity to		
					gb U43627 extensin (atExt1)		
					gene from Arabidopsis thaliana.		
		Mus musculus			ESTs gb Z34165 and gb Z18788		
l		Pontin52 mRNA,			come from this gene.		
1604	AF100694	complete cds	1e-28	4056454	[Arabidopsis thaliana]	8e-07	
					FMRFAMIDE-RELATED		
			ŀ		NEUROPEPTIDES		
1	ł		İ		PRECURSOR >gi 416208		
		Mus musculus			(U03137) neuropeptide		
l		Pontin52 mRNA,			precursor FMRFamide-related		
1605	AF100694	complete cds	le-28	1169643	peptide [Lymnaea stagnalis]	7e-07	
l					(AC005990) Contains repeated		
·					region with similarity to		
1		,			gb U43627 extensin (atExt1)		
ı		M1 -			gene from Arabidopsis thaliana.		
ŀ		Mus musculus	1		ESTs gb Z34165 and gb Z18788		
1607		Pontin52 mRNA,		1066151	come from this gene.	6e-07	
1606	AF100694	complete cds	le-28	4056454	[Arabidopsis thaliana] (AC005990) Contains repeated	oe-∪.	
1	İ				region with similarity to		
l		Ì	ļ		gb U43627 extensin (atExt1)		
l			I		gene from Arabidopsis thaliana.		
- 1	- 1	Mus musculus	ļ		ESTs gb Z34165 and gb Z18788		
- 1		Pontin52 mRNA.	ľ		come from this gene.		
1607			10.20	4056154	_	5e-0~	
1607	AF100694	complete cds	1e-28	4056454	[Arabidopsis thaliana]	Je-U	



- 25.4	Nearest I	Neighbor (BlastN vs. C	ienbank)	Nearest Neigh	bor (BlastX vs. Non-Redundant Pr	oteins)
SEQ						
D D	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					(AC005990) Contains repeated	
					region with similarity to	
			1		gb U43627 extensin (atExt1)	
i l					gene from Arabidopsis thaliana.	1
l i		Mus musculus	1		ESTs gb Z34165 and gb Z18788	:
		Pontin52 mRNA.			come from this gene.	
1608	AF100694	complete cds	le-28	4056454	[Arabidopsis thaliana]	3e-07
1 1			į i		(AC005990) Contains repeated	
					region with similarity to	
					gb U43627 extensin (atExt1) gene from Arabidopsis thaliana.	
		3.6	1		ESTs gb Z34165 and gb Z18788	
		Mus musculus	[• •	come from this gene.	•
1600	4.5100404	Pontin52 mRNA,	1c-28	4056454	[Arabidopsis thaliana]	. le-07
1609	AF100694	complete cds	16-28	4030434	(AC005990) Contains repeated	. 1e-07
			1		region with similarity to	
		·			gb U43627 extensin (atExt1)	
i					gene from Arabidopsis thaliana.	
		Mus musculus	İ		ESTs gb Z34165 and gb Z18788	
		Pontin52 mRNA,			come from this gene.	
1610	AF100694	complete cds	1e-28	4056454	[Arabidopsis thaliana]	le-07
					(AC005990) Contains repeated	
					region with similarity to	
					gb U43627 extensin (atExt1)	
1 1					gene from Arabidopsis thaliana.	
f [Mus musculus			ESTs gb Z34165 and gb Z18788	·
j		Pontin52 mRNA.			come from this gene.	
1611	AF100694	complete cds	le-28	4056454	[Arabidopsis thaliana]	7e-08
1 1					(AC005990) Contains repeated	
 					region with similarity to	
					gb U43627 extensin (atExt1)	
1		,			gene from Arabidopsis thaliana.	
		Mus musculus			ESTs gb Z34165 and gb Z18788	
	. =	Pontin52 mRNA,		1056161	come from this gene.	2- 00
1612	AF100694	complete cds	1e-28	4056454	[Arabidopsis thaliana] (AC005990) Contains repeated	2e-08
					region with similarity to	
i			l l		gb U43627 extensin (atExt1)	•
			1		gene from Arabidopsis thaliana.	
		Mus musculus			ESTs gb/Z34165 and gb/Z18788	Ī
		Pontin52 mRNA.			come from this gene.	
1613	AF100694		le-28	4056454		6e-09
1613	AF100694	complete cds	le-28	4056454	[Arabidopsis thaliana]	6e-09

*:	Nearest i	Neighbor (BlastN vs. C	Genbank)	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEO		1	Γ		Total Control Control	O(C)(1.5)	
D D	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
			-		(AC005990) Contains repeated	I VALUE	
\vdash			 		region with similarity to		
j l			1		gb U43627 extensin (atExt1)]	
			·		gene from Arabidopsis thaliana.		
		Mus musculus			ESTs gb Z34165 and gb Z18788	ĺ	
ł i		Pontin52 mRNA.			come from this gene.		
1614	AF100694	complete cds	le-28	4056454	[Arabidopsis thaliana]	5e-09	
					(AC005990) Contains repeated	30 07	
					region with similarity to		
1 1					gb U43627 extensin (atExt1)		
1 1					gene from Arabidopsis thaliana.		
		Mus musculus	[ESTs gb Z34165 and gb Z18788		
i		Pontin52 mRNA,			come from this gene.		
1615	AF100694	complete cds	le-28	4056454	[Arabidopsis thaliana]	4e-09	
					(AC005990) Contains repeated		
					region with similarity to		
					gb U43627 extensin (atExt1)		
					gene from Arabidopsis thaliana.		
! I		Mus musculus]		ESTs gb Z34165 and gb Z18788		
}		Pontin52 mRNA,]		come from this gene.		
1616	AF100694	complete cds	le-28	4056454	[Arabidopsis thaliana]	7e-10	
					(AC005990) Contains repeated		
			1		region with similarity to		
	İ				gb U43627 extensin (atExt1)		
	i				gene from Arabidopsis thaliana.		
		Mus musculus	1		ESTs gb Z34165 and gb Z18788		
1617		Pontin52 mRNA,	1 - 20	1057.151	come from this gene.	6.10	
101/	AF100694	complete cds	1e-28	4056454	[Arabidopsis thaliana] [(AC005990) Contains repeated	6e-10	
			l l		region with similarity to		
			l		gb U43627 extensin (atExt1)	Į	
					gene from Arabidopsis thaliana.	1	
]	Mus musculus	ĺ		ESTs gb Z34165 and gb Z18788		
		Pontin52 mRNA.			come from this gene.		
1618		complete cds	1e-28	4056454	[Arabidopsis thaliana]	5e-10	
	22220074			.000757	(AC005990) Contains repeated		
j			. 1		region with similarity to	ľ	
	Ì				gb U43627 extensin (atExt1)		
1					gene from Arabidopsis thaliana.	l	
	 	Mus musculus	İ		ESTs gb Z34165 and gb Z18788		
	į.	Pontin52 mRNA,	1		come from this gene.	i	
1619	AF100694	complete cds	le-28	4056454	[Arabidopsis thaliana]	4e-10	

	Nearest	Neighbor (BlastN vs. C	lenbank)	Nanaga Maiak	nbor (BlastX vs. Non-Redundant Pr	
250		radigitor (Diagra 45. C	Titodik)	ivearest iveigh	iour (Diasex vsvon-Redundant Pr	oteins)
SEQ	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
			L	T The state of the	(AC005990) Contains repeated	<u> </u>
					region with similarity to	
1	[gb U43627 extensin (atExt1)	ł
					gene from Arabidopsis thaliana.	
]	ł	Mus musculus	ļ		ESTs gb Z34165 and gb Z18788	
		Pontin52 mRNA.	ļ]	come from this gene.	
1620	AF100694	complete cds	1e-28	4056454	[Arabidopsis thaliana]	2e-10
1					(AC005990) Contains repeated	
]			}		region with similarity to	
1			1		gb U43627 extensin (atExt1)	
ĺ			1.	1	gene from Arabidopsis thaliana.	
	1	Mus musculus			ESTs gb Z34165 and gb Z18788	,
		Pontin52 mRNA,	}	•	come from this gene.	
1621	AF100694	complete cds	1e-28	4056454	[Arabidopsis thaliana]	5e-11
Ĭ			ļ		(AC005990) Contains repeated	
1					region with similarity to	
l				1	gb U43627 extensin (atExt1)	
1 .					gene from Arabidopsis thaliana.	
		Mus musculus			ESTs gb Z34165 and gb Z18788	
		Pontin52 mRNA,			come from this gene.	
1622	AF100694	complete cds	1e-28	4056454	[Arabidopsis thaliana]	2e-12
i		Petromyzon marinus				
1623	AF032896	polyadenylate binding	100	1000000	polyadenylate binding protein II	
1023	AF032896	protein	1e-28	1082703	human DEHYDRIN DHN3	2e-27
			`		>gi 100035 pir S18139 dehydrin	
		Mus musculus			DHN3 - garden peå >gi 20709	[
		Pontin52 mRNA.	}		(X63063) pea dehydrin DHN3	
1624		complete cds	9e-29	118588	[Pisum sativum]	0.013
	12.50074	Mus musculus	70 47	110300	It izani zanvani)	0.013
		Pontin52 mRNA,	ł		spermatophorin Sp23 - yellow	,
1625	1	complete cds	9e-29	2133579	mealworm molitori	6e-04
					instruction months	-
·		.]			(Z81071) predicted using	· [
ı		ļ]	•	Genefinder; Similarity to	
ľ			j		Human small nuclear	
l			Ĭ		ribonucleoprotein E cDNA EST	j
I		Mus musculus	· i		yk375g7.5 comes from this	- 1
1	ľ	Pontin52 mRNA,	ł		gene; cDNA EST yk435f5.3	ł
1626	AF100694	complete cds	9e-29	3876465	comes from this gen	9e-06
					(AC005990) Contains repeated	
	ļ	ļ	į		region with similarity to	
- 1	i	ĺ	i	•	gb U43627 extensin (atExt1)	
		ł	i		gene from Arabidopsis thaliana.	i
		Mus musculus	1	i	ESTs gb Z34165 and gb Z18788	
]		Pontin52 mRNA,	1		come from this gene.	
1627	AF100694	complete cds	8e-29	4056454	[Arabidopsis thaliana]	2e-06

TO !

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
CEO	1.04.050	Vergiloor (Brasil 13: C	I	14cmest [4e18]:	ibbi (Blastic Vs. 14011-Redutidatit Fi	T	
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
					ADP-RIBOSYLATION	<u> </u>	
1					FACTOR 3 truit tly (Drosophila		
i					melanogaster) >gi 507234	1	
1	ľ	Mus musculus			(L25063) ADP ribosylation	ł	
1		Pontin52 mRNA.			factor 3 [Drosophila		
1628	AF100694	complete cds	4e-29	728883	melanogaster]	0.016	
İ							
		Mus musculus			RNA-BINDING PROTEIN		
1620	4510000	Pontin52 mRNA.			FUS/TLS protein [human,	l	
1629	AF100694	complete cds	4e-29	544357	Peptide, 526 aa] [Homo sapiens] (AC005990) Contains repeated	2e-07	
					region with similarity to	l	
					gb U43627 extensin (atExt1)		
		Mus musculus			gene from Arabidopsis thaliana.		
		Pontin52 mRNA.	i		ESTs gb Z34165 and gb Z18788		
1630	AF100694		4- 20	4056454	come from this gene.		
1030	AP100094	complete cds	4e-29	4036434	[Arabidopsis thaliana] ACYL-COA	1e-08	
		,			DEHYDROGENASE, VERY-		
		Human mRNA for	i		LONG-CHAIN SPECIFIC		
		very-long-chain acyl-			PRECURSOR (VLCAD)		
	,	CoA dehydrogenase	:		dehydrogenase precursor - rat		
1 1		(VLCAD), complete			Acyl-CoA dehydrogenase		
1631	D43682	cds	4e-29	1168287	[Rattus norvegicus]	6e-37	
		M.tuberculosis accBC			(Z95556) accD1	00 37	
1632	Y07660	gene	4e-29	2113935	[Mycobacterium tuberculosis]	3e-47	
		Human alpha-satellite					
		DNA from clone	1		1		
1633	X55367	pTRA-2.	le-29	<none></none>	<none></none>	<none></none>	
		Homo sapiens					
)	(subclone 1_f1 from	1				
		PI H54) DNA	i		1		
1634		sequence	le-29	<none></none>	<none></none>	<none></none>	
1		{Alu repeats, clone	1				
ı		52H10} [human,	í		l	ı	
		colonic mucosa.			!!!! ALU SUBFAMILY J		
1635	S75940	Genomic, 943 nt]	1e-29	728831	WARNING ENTRY	1e-07	
İ	[,	Homo sapiens	J		!!!! ALU SUBFAMILY J		
1636		PACE4 gene, exon 13	1c-29	728831]	2e-09	
.050	715001907	ACL4 gene. exon 13	16-29	120031	WARNING ENTRY	26-03	
ĺ	[1	Mus musculus SH3					
l		domain-containing	1				
1		adapter protein	1				
1637	- I	nRNA, complete cds	5e-30	<none></none>	<none></none>	<none></none>	



12.	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEQ						ł	
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
					(AC005990) Contains repeated		
					region with similarity to		
1 1					gb U43627 extensin (atExt1)		
					gene from Arabidopsis thaliana.		
		Mus musculus .			ESTs gb Z34165 and gb Z18788		
		Pontin52 mRNA.			come from this gene.		
1638	AF100694	complete cds	4e-30	4056454	[Arabidopsis thaliana]	3e-10	
]					POLYADENIA ATT		
		Xenopus laevis			POLYADENYLATE- BINDING PROTEIN		
		poly(A)-binding			polyadenylate-binding protein -		
1,500	1.600000	protein (ABP-EF)	4- 70	1252700	African clawed frog laevis	5e-21	
1639	M27072	mRNA, complete cds.	4e-30	1352709	African clawed frog faevis	26-71	
		B.taurus mRNA for bovine vacuolar	• .		(AF039573) abscisic acid- and		
1640	X58386	ATPase subunit A	2e-30	2773154	stress-inducible protein	4.3	
1040	V20200	M.tuberculosis accBC	26-30	2113134	(Z95556) accD1	4.5	
1641	Y07660	gene	1é-30	2113935	[Mycobacterium tuberculosis]	4e-47	
1041	10/000	gene	10-50	2113733	[MVcoodeterram taceralisas]		
		Sus scrofa mRNA for			į		
		hypothetical protein		!	(AF007561) delta 6-desaturase		
1642		(5'; clone 7C+)	4e-31	4102021	[Borago officinalis]	7.4	
		Homo sapiens					
		calcium-dependent					
		chloride channel- l					
1 1		(hCLCAI) mRNA.			(AB017156) gob-5 [Mus		
1643	AF039400	complete cds	2e-31	3721912	musculus]	7e-08	
					BOMBYXIN B-2 HOMOLOG		
		Homo sapiens			PRECURSOR silkmoth		
		(subclone 5_d9 from			>gi 217385 gnl PID d1003528		
		PI HI9) DNA			(D13924) Samia bombyxin		
1644	L77036	sequence.	le-31	461663	homolog B-2 [Samia cynthia]	1.1	
1 1		H.sapiens mRNA for	1		(X61971) macropain subunit		
, , , ,	W61071	macropain subunit	10.21	296734	delta [Homo sapiens]	3e-06	
1645	X61971	delta human mitochondrial	1e-31	270/34	(AC005990) Contains repeated	36-00	
		trnas and partial	1		region with similarity to		
		proteins 4 & 5;			gb U43627 extensin (atExt1)		
		histidyl-, seryl-,	1		gene from Arabidopsis thaliana.		
		leucyl-trna genes:	1		ESTs gb Z34165 and gb Z18788		
		urf4 and urf5			come from this gene.	İ	
1646	L00016	(partial).	5e-32	4056454	[Arabidopsis thaliana]	0.002	
		VF	<u>-</u>		(AC005990) Contains repeated		
(I		1			region with similarity to		
 			į		gb U43627 extensin (atExt1)		
 	·	Human acidic	ļ		gene from Arabidopsis thaliana.		
		ribosomal	Ī		ESTs gb Z34165 and gb Z18788		
		phosphoprotein P2	4		come from this gene.		
1647	M17887	mRNA, complete cds.	5e-32	4056454	[Arabidopsis thaliana]	1e-05	

4	Nearest N	Neighbor (BlastN vs. G	enbank)	Nearest Neight	oor (BlastX vs. Non-Redundant Pro	oteins)
SEQ						
[D]	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human mitogen-				
		responsive				
		phosphoprotein DOC-				
Ì l	·	2 mRNA, complete			(AC004683) putative	
1659	U53446	cds.	6e-34	3395443	ammonium transporter. 3' partial	4.7
					PROTEIN-TYROSINE	
					PHOSPHATASE EPSILON	
					PRECURSOR (R-PTP-	
		Homo sapiens serine			EPSILON) >gi 1439605	
		protease mRNA,			(U62387) protein tyrosine	
1660	AF013988	complete cds	4e-34	· 2507226	phosphatase-e [Mus musculus]	3.2
1000	AF013988	Human mitogen-	40-34	2507220	phosphatase e [ivido masedido]	
1 1		responsive	٠.			
		phosphoprotein DOC-				
		2 mRNA, complete			LEP100 protein precursor -	
1661	U53446	cds.	2e-34	104757	chicken >gi 212254 gallus]	1.6
1991	030110	-				
1		Homo sapiens				
		endogenous retroviral				
1 1		sequence ERV-L pol				
		gene, clone ERV-L			(AJ233597) reverse	
1662	AJ233632	Human6	2e-34	3860513	transcriptase [Mus famulus]	4e-10
		Homo sapiens full			(AC002521) putative Ser/Thr	
		length insert cDNA	,		protein kinase [Arabidopsis	
1663	AF086310	clone ZD51F08	8e-35	2947070	thaliana] [40S RIBOSOMAL PROTEIN	2.3
					S2 (STRINGS OF PEARLS	
					PROTEIN)	
					>gi 1085158 pir \$50325	
1 1					ribosomal protein S2 - fruit fly	
					(Drosophila melanogaster)	
		Human mDNA for			melanogaster] >gi[515972	
166.1	V17206	Human mRNA for	3e-35	730652	(U01335) ribosomal protein S2	2e-10
1664	X17206	LLRep3	36-33	730032	(CO1555) (10050mar protein 32	
		Homo sapiens mRNA			j	
		for KIAA0565			(AB011137) KIAA0565 protein	
1665	AB011137	protein, complete cds	3e-35	3043654	[Homo sapiens]	2e-16
] [Human protease M		•	(AF091247) potassium channel	
1666	U62801	mRNA, complete cds	2e-35	3929231	[Rattus norvegicus]	1.0
					1	
		Homo sapiens serine				
		protease (Omi)			(AF020760) serine proteuse	
1667	AF020760	mRNA, complete cds	le-35	2738915	[Homo sapiens]	9e-14



	Nearest N	Neighbor (BlastN vs. G	enbank)	. Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEQ							
ΙĐ	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
		Human DNA					
		sequence from					
		cosmid U235H3 on			(M22333) unknown protein		
1668	Z93943	chromosome X	8e-36	1196432	[Homo sapiens]	3e-10	
					DEHYDRIN DHN3		
					>gi 100035 pir S18139 dehydrin		
					DHN3 - garden pea >gi 20709		
					(X63063) pea dehydrin DHN3		
1669	X06778	Rabbit 18S rRNA	7e-36	118588	[Pisum sativum]	0.011	
	İ				1		
		Homo sapiens					
		mRNA, chromosome		•			
	l'	1 specific transcript			(AE001350) hypothetical		
1670	AB007962	KIAA0493	3e-36	3329243	protein [Chlamydia trachomatis]	3.1	
	l	Human DNA					
	•	sequence from		•	<u> </u>		
		cosmid U65A4,					
		between markers			INDOTIFE CAL PROTESS		
		DXS366 and DXS87	, , ,	141100	HYPOTHETICAL PROTEIN	0.020	
1671	Z81014	on chromosome X *	3e-36	141103	ORF-1137 mouse	0.038	
		Human DNA					
		sequence from cosmid U65A4.			į		
ł							
] [between markers			(M29325) ORFI [Mus		
1672	701014	DXS366 and DXS87	3e-36	198651	musculusi	0.006	
10/2	Z81014	on chromosome X *	0.50	170031	musculusi	0.000	
		Human transporter					
• 		protein (g17) mRNA.			(U49082) transporter protein		
1673	U49082	complete cds	3e-36	1840045	[Homo sapiens]	2e-15	
****	0 4 7002	Human transcription		20.00,0	Control Supplierry		
 		factor SP1 mRNA. 3'			HF-1 regulatory element binding		
1674	J03133	end.	3e-36	477133	protein - rat	2e-31	
		Homo sapiens mRNA	•				
		for KIAA0465	1		(AB007934) KIAA0465 protein		
1675	AB007934	protein, partial cds	le-36	3413892	[Homo sapiens]	4e-37	
		Mouse Hox-2.5			homeotic protein Hox B9 -		
1676	M34857	mRNA.	9e-37	106296	human (fragment)	0.15	
·		Homo sapiens					
	,	(subclone H8 5_a10	į				
		from P1 35 H5 C8)					
1677	L35657	DNA sequence.	9e-37	2072960	(U93568) p40 [Homo sapiens]	3e-05	
		H.sapiens					
		endogenous					
		retrovirus HERV-	ļ		(Y17833) env protein [Human	j	
1678	X80240	KC4 DNA	8e-37	4185944	endogenous retrovirus K]	le-!5	



i	Nearest N	leighbor (BlastN vs. Ge	nbank)	Nearest Neight	oor (BlastX vs. Non-Redundant Pro	teins)
SEQ						
ID.	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human DNA				
-		sequence from				
		cosmid U235H3 on	Í	4	hypothetical protein (L1H 3'	
1679	Z93943	chromosome X	9e-38	106322	region) - human	4e-13
					HYPOTHETICAL ZINC FINGER PROTEIN ZK686.4	
					IN CHROMOSOME III	
			1		>gi 630780 pir S-14909 ZK686.4	
			i		protein - Caenorhabditis elegans	•
	,				>gi 304346 (L17337) coded for	
					by C. elegans cDNAs	
					GenBank:M88869 and T01933;	
				•	putative [Caenorhabditis	
		H.sapiens mRNA for	4n 70.	466044	elegans]	3e-37
1680	X97303	Ptg-12 protein	4e-38 ⁻	400044	Ciogania	
		H.sapiens mRNA for				
1681	Y08999	Sop2p-like protein	3e-38	3334339	SOP2-LIKE PROTEIN	5e-06
1001	108999	Sopzp-like protein	30 30			
		H.sapiens CpG DNA,			(U53181) F36D4.2 gene	1
		clone 74g6, forward			product [Caenorhabditis	
1682	Z62887	read cpg74g6.ftla.	2e-38	1245686	elegans]	0.19
		Human endogenous				
	ì	retrovirus clone				
•		c5.11, HERV-H				
	•	multiply spliced				
٠.		subgenomic leader.			(Z14310) tripartite fusion	
	}	protease and integrase	j		transcript PLA2L (Human	
		region mRNA, partial		59977	endogenous retrovirus	1e-06
1683	U35032	cds	1e-38	39911	(AC002544) Unknown gene	
		Human mRNA for	,		product splice form-2 [Homo	
	D0/07.	KIAA0220 gene,	1e-38	3337386	sapiens]	8e-11
1684	D86974	partial cds Human nonmuscle	10-50	223,300		
		myosin heavy chain	·			
		(NMHC) mRNA. 3'	l		(AB022023) nonmuscle myosin	
1685	M31013	end.	1e-38	4115748	heavy chain B	2e-11
1.005	1					1
1		Homo sapiens Arp2/3				
1		protein complex		1		
1	·	subunit p20-Arc				
		(ARC20) mRNA.			NO.TE-	<none></none>
1686	AF006087	complete cds	4e-39	<none></none>	<none> (AL009171) 62D9.a</none>	CINOINES
		D.melanogaster crn		2655000	[Drosophila melanogaster]	4e-42
1687	X58374	mRNA	4e-39	2655888	GTP-BINDING PROTEIN	<u> </u>
1	1	D		i	TC10 ras-like protein [Homo	
	50.50.5	Human DNA for	le-39	134080	sapiens}	3e-26
1688	D85815	rhoHP1, complete cds	16-22	134000	[suprens]	



VALU
VALU
5e-05
0 00
9e-08
le-30
0.61
0.01
2e-06
бе-23
5e-23
5e-23
5e-23
, U = 2 2 -
5e-31

SEQ ID ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE ACCESSION ATP-BINDING CASSETTE TRANSPORTER ABC1 human >gil495257 (X75926) abcl [Mus musculus] 3e-37 abcl [Mus musculus] 3e-37 abcl [Mus musculus] 3e-37 AF038200 Sequence 5e-41 3211975 abcl [Mus musculus] 3e-37 abcl [Musculus] 3e-37 abcl [Musculus] 3e-37 abcl [Musculus] 3e-37 abcl [Musculus] 3e-37 abcl [Musculus] 3e-37	·	Nearest	Neighbor (BlastN vs. C	Genbank)	Nearest Neigh	nbor (BlastX vs. Non-Redundant Pr	oteine)
D ACCESSION DESCRIPTION P VALUE ACCESSION ATP-BINDING CASSETTE TRANSPORTER ABC human >gil495257 (X75926) abc [Muman >gil495257 (X75926	SEC				T SEE CO. T VOIG	1001 (Diesare 13. : Voll-Redundant Fr	Otents)
1699 X75927 M.musculus abc2 1e-40 728773 TRANSPORTER ABC1 human sqil495257 (X75926) abc1 [Mus musculus] 3e-37	1	·	DESCRIPTION	PVALUE	ACCESSION .		P VALUE
M.musculus abc2 mRNA le-40 728773 abc1 (Mus musculus) 3e-37	—						
1700 AF038207 mRNA 1e-40 728773 abcl [Mus musculus] 3e-37	ı	1					
1700 AF038200 AF	1600	1/7500=		ĺ			
1700 AF038200 AF038200 Sequence Se-41 3211975 Sequence Se-41 3211975 Sequence Se-41 Sequence Se-41 Sequence Se-41 Sequence Se-41 Sequence Se-41 Sequence Se-41 Sequence Sequen	1095	X/3927	mRNA	1e-40	728773	abc1 [Mus musculus]	3e-37
1700 AF038200 Sequence 5c-41 3211975 Sequence Se-14 Sequence Se-14 Sequence Se-14 Sequence Se-14 Sequence Se-14 Sequence Se-14 Sequence Se-14 Sequence Se-14 Sequence			Homo sapiens clone			(AF068195) putative	
AF038200 Sequence Se-41 3211975 related protein [Homo sapiens] Se-14		1	23954 mRNA	i .			
Human estrogen sulforansferase (STE) gene, exon 8 and complete cds	1700	AF038200		5e-41	3211975		1
1701 U20521 and complete cds 4e-41 <none></none>			Human estrogen			Tiene sapiens	30-17
1701 U20521 and complete cds 4e-41 <none></none>	1					·	
Homo sapiens branched chain alphaketoacid dehydrogenase kinase precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds 2e-41 3182923 HYPOTHETICAL 66.5 KD PROTEIN F02A9.5 IN CHROMOSOME III > pil/280342 pir/ S28313 hypothetical protein F02A9.5 Caenorhabditis elegans Genefinder: similar to Propionyl-CoA carboxylase beta chain; cDNA EST EMBL: D28069 comes from this gene; cDNA EST EMBL: D28069 comes from th	l	ļ	(STE) gene, exon 8			1 .	
Homo sapiens branched chain alphaketoacid Gamethylu-2- OXOBUTANOATE DEHYDROGENASE (LIPOAMIDE)] KINASE PRECURSOR alphaketoacid dehydrogenase kinase PRECURSOR alphaketoacid dehydrogenase kinase PRECURSOR alphaketoacid dehydrogenase kinase PRECURSOR alphaketoacid dehydrogenase kinase precursor (Homo sapiens) 2e-09	1701	U20521	and complete cds	4e-41	· <none></none>	<none></none>	<none></none>
branched chain alphaketoacid [3-METHYL-2- OXOBUTANOATE DEHYDROGENASE (LIPOAMIDE)] KINASE PRECURSOR alpha-ketoacid dehydrogenase kinase precursor, mRNA, nuclear gene encoding mitochondrial mi		1					
Retoacid	ĺ	l		٠.		- 1	
dehydrogenase kinase precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds 2e-41 3182923 PRECURSOR alpha-ketoacid dehydrogenase kinase precursor [Homo sapiens] 2e-09	l	l	1			i	
DEHYDROGENASE (LIPOAMIDE) KINASE]	J		ł		[3-METHYL-2-	
1702 AF026548 National Nati	ĺ					1	
1702 AF026548 encoding mitochondrial protein, complete cds 2e-41 3182923 PRECURSOR alpha-ketoacid dehydrogenase kinase precursor (Homo sapiens) 2e-09		j	1-		•	DEHYDROGENASE	
Mituberculosis accBC 2e-41 465847 2e-60 465847 2e-60 46001237 9H11N46 1e-41 106322 1705 AB007934 KIAA0465 protein, partial cds 1e-41 1705 AB007934 Homo sapiens 1706 AB007934 Homo sapiens clone 24711 mRNA 1706 AB007934 Homo sapiens clone 24711 mRNA AB0078036 AB007934 AB0078036 AB00780	l]	_	Ī		(LIPOAMIDE)] KINASE	
1702 AF026548 protein, complete cds 2e-41 3182923 [Homo sapiens] 2e-09	1			ľ		PRECURSOR alpha-ketoacid	
HYPOTHETICAL 66.5 KD PROTEIN F02A9.5 IN CHROMOSOME III >gi 280542 pir S28313 hypothetical protein F02A9.5 - Caenorhabditis elegans Genefinder: similar to Propionyl-CoA carboxylase beta chain; cDNA EST EMBL:M89018 comes from this gene; cDNA EST EMBL:D28069 comes from this gene; cDNA EST EMBL:D28069 comes from this gene; cDNA EST EMBL:D28068 comes from this gene; cDNA EST EMBL:D28069 comes from this gene; cDNA EST EMBL:D28069 comes from this gene; cDNA EST EMBL:D28069 comes from this gene; cDNA EST EMBL:D28069 comes from this gene; cDNA EST EMBL:D28069 comes from this gene; cDNA EST EMBL:D28069 comes from this gene; cDNA EST EMBL:D28069 comes from this gene; cDNA EST EMBL:D28069 comes from this gene; cDNA EST EMBL:D28069 comes from this gene; cDNA EST EMBL:D28069 comes from this gene; cDNA EST EMBL:D28069 comes from this gene; cDNA EST EMBL:D28069 comes from this gene; cDNA EST EMBL:D28069 comes from this gene; cDNA EST EMBL:D28069 comes fro			1 '			dehydrogenase kinase precursor	- 1
PROTEIN F02A9.5 IN CHROMOSOME III >gi 280542 pir \$28313 hypothetical protein F02A9.5 - Caenorhabditis elegans Genefinder: similar to Propionyl-CoA carboxylase beta chain; cDNA EST EMBL:M89018 comes from this gene; cDNA EST EMBL:D28069 comes from this gene; cDNA EST EMBL:D28068 comes from this gene; cDNA EST EMBL:D28068 comes from this gene; cDNA EST EMBL:D28068 comes from this gene; cDNA EST EMBL:D28068 comes from this gene; cDNA EST 3e-38 Homo sapiens genomic DNA, 21q region, clone:	1702	AF026548	protein, complete cds	2e-41	3182923	[Homo sapiens]	2e-09
genomic DNA, 21q region. clone: 9H11N46 Homo sapiens mRNA for KIAA0465 protein, partial cds Homo sapiens clone 24711 mRNA hypothetical protein (L1H 3' region) - human (AB007934) KIAA0465 protein [Homo sapiens] 3e-12	1703	Y07660	gene	2e-41		PROTEIN F02A9.5 IN CHROMOSOME III >gi 280542 pir S28313 hypothetical protein F02A9.5 - Caenorhabditis elegans Genefinder: similar to Propionyl- CoA carboxylase beta chain; cDNA EST EMBL:M89018 comes from this gene; cDNA EST EMBL:D28069 comes from this gene; cDNA EST EMBL:D28068 comes from this	3e-38
genomic DNA, 21q region. clone: 9H11N46 Homo sapiens mRNA for KIAA0465 protein, partial cds Homo sapiens clone 24711 mRNA hypothetical protein (L1H 3' region) - human (AB007934) KIAA0465 protein [Homo sapiens] 3e-12			Homo sapiens		100017	gene, eDIVA EST	56-38
1704 AG001237 region, clone: 9H11N46 1e-41 106322 hypothetical protein (L1H 3' region) - human 5e-09	ı	The state of the s	•	j			
1704 AG001237 9H11N46 1e-41 106322 region) - human 5e-09 Homo sapiens mRNA for KIAA0465 protein, partial cds protein, partial cds Homo sapiens clone 24711 mRNA 1706 AF066000	ı			[hypothetical protein (LTH 3)	İ
Homo sapiens mRNA for KIAA0465 protein, partial cds le-41 3413892 [Homo sapiens] 3e-12 Homo sapiens clone 24711 mRNA	1704	1		le-41		• •	5e-09
Homo sapiens clone 24711 mRNA	1705	AB007934	Homo sapiens mRNA for KIAA0465 protein, partial cds			(AB007934) KIA.A0465 protein	
1706 A TOSSOOO	T	1	Homo sapiens clone			Citatio Supremo,	
1706 AF055029 sequence 5e-42 3250681 (AL024486) putative protein 2.7	i		24711 mRNA	j			i
	1706	AF055029 s	equence	5e-42	3250681	(AL024486) putative protein	2.2

	Nearest	Neighbor (BlastN vs. G	enbank)	Nearest Neigh	bor (BlastX vs. Non-Redundant Pr	roteins)
SEQ		Total Control of Control		. Total est Treate.	Del (Blasse vs. 1901) Recardaging	T
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		•			Į-	
1 .					PHOSPHATIDYLINOSITOL-	1
					4,5-BISPHOSPHATE	i
					PHOSPHODIESTERASE	ŀ
					DELTA I (PLC-DELTA-I)	1
1					(PHOSPHOLIPASE C-DELTA-	•}
					1) (PLC-III) >gi 163538	1
		O.cuniculus mRNA			(M20638) phospholipase C-III	
1707	Z49747	for phospholipase C	5e-42	130227	[Bos taurus]	5e-36
		Human set gene,				1
1708	M93651	complete cds.	2e-42	<none></none>	<none></none>	<none></none>
				•		,
		Sus scrofa mRNA for	·]		J	
		hypothetical protein			(U79010) delta 6 desaturase	
1709	AJ236940	(5': clone 7C4)	2e-42	2062403	[Borago officinalis]	8.5
		Human erythroid			NAME OF THE OWN DESCRIPTION OF THE OWN DESCRI	i
1710	102624	differentiation protein	2. 42	1709.177	INHIBIN BETA A CHAIN	2 10
1710	J03634	mRNA Mus musculus mRNA	2e-42	1708436	PRECURSOR STRIATIN	2e-10
1711	AJ223777	for striatin	6e-43	2494917		2e-32
1/11	AJ223111	Homo sapiens	06-43	2494917	>gi 1495773 gnl PID e254158	2e-32
l 1		potassium channel			(AF016411) KCNA3.1B [Homo	
1712	AF016411	subunit KCNA3.1B	2e-43	2708514	sapiens]	3e-13
	-4 010-11	Homo sapiens		2700314	Sapiens	30-13
		(subclone 2_f10 from	į		hypothetical protein 3 - rat	
1713	AC001443	BAC 2913	1e-43	111814	>gil565\$9	2e-06
					MAGUK P55 SUBFAMILY	
]	İ		MEMBER 2 (MPP2 PROTEIN)	
i 1		H.sapiens mRNA for			(DISCS, LARGE HOMOLOG	
1714	X82895	DLG2	6e-44	2497511	2)	6e-52
		Human BENE			(X57960) ribosomal protein L7	
1715	U17077	mRNA, partial cds.	3e-44	53912	[Mus musculus] >gi 55489	8c-30
		Homo sapiens mRNA	. 1		i i	
1716	AJ222700	for TSC-22 protein	2e-44	<none></none>	<none></none>	<none></none>
			ŀ		INHIBIN BETA A CHAIN	
			i		PRECURSOR PROTEIN)	
I		,			(EDF) >gi 87936 pir B24248	
ŀ	1		1		inhibin beta-A chain precursor -	
l			ł		human >gi 181947 (J03634)	
1		}	į		erythroid differentiation protein	į
	ľ	,,]		precursor [Homo sapiens]	ļ
		Human erythroid	į		sapiens)	
[1	differentiation protein	1		>gi 226850 prt] 1608260B	
1717	J03634	mRNA	2e-44	124279	inhibin beta.A [Homo sapiens]	0.73

J	Nearest	Neighbor (BlastN vs. C	Genhank)	Non	hha (Blasty as St. D.)	
-		Treighbol (Blastia Vs. C	Tenbank)	Nearest Neig	hbor (BlastX vs. Non-Redundant P	roteins)
SEC	ACCESSION	DESCRIPTION				į
	ACCESSION	DESCRIPTION	PVALUE	ACCESSION	DESCRIPTION	P VALUE
	 	Homo sapiens mRNA	-			
1.		for KIAA0618	1		(58086.1) 200-1	
1718	AB014518	protein, complete cds	7e-45	1911548	(S80864) cytochrome c-like polypeptide sapiens]	1
			75.3	1311340	polypeptide sapiens)	1.6
ł		H.sapiens genomic	1		(U29380) similar to adenylate	1
1719	X76808	DNA clone d2	7e-45	868201	cyclase (Caenorhabditis elegans	2e-09
1	ľ	Homo sapiens mRNA				
	ł	for beta 2-			(U95995) RNA-dependent RNA	
1720	AB021288	microglobulin,	2 45		polymerase [Cryptosporidium	
1/20	AB021288	complete cds H.sapiens mRNA for	2e-45	2465521	parvum]	0.15
1		transcription factor		••	j	
1721	X63468	TFIIE alpha	8e-46	<none></none>	<none></none>	-NONE.
		Homo sapiens D2-2	- 30 .9	41011E	Z.NONES	<none></none>
1722	AF019226	mRNA, 3'UTR	7e-46	<none></none>	<none></none>	<none></none>
		Human mRNA for				41.01.12
		KIAA0064 gene.	1		HYPOTHETICAL PROTEIN	
1723	D31764	complete cds Human MHC class II	2e-46	3123050	KIAA0064	le-15
f		HLA-DR-beta-psi	.			
į		(DW4/DR4)	I	•	1	
		pseudogene, exons			1	
		3,4, 5,6, clones cos II-			(Y17834) gag protein (Human	
1724	K02774	3301 and cosII-801.	le-46	4185946	endogenous retrovirus K]	2e-14
				13357	BRIDE OF SEVENLESS	26-14
			l		PROTEIN PRECURSOR	
					>gi 1079166 pir A47550 bride	
:		,			of sevenless precursor - fruit fly	
1725	V02100	.,			(Drosophila virilis) >gi 290216	j
1723	X92109	H.sapiens hcgIX gene	9e-47	2498185	virilis]	1.4
		H.sapiens	i		NADH-UBIQUINONE OXIDOREDUCTASE CHAIN	i
		mitochondrial DNA.			4 >gi 86696 pir A00435 NADH	.]
1726		complete genome	8e-47	128753	dehydrogenase (ubiquinone)	4e-15
		Human tumor				
ł		necrosis factor				1
1727		receptor, 3' flank.	3e-47	<none></none>	<none></none>	<none></none>
ı		H.sapiens	T			
ı		endogenous	1		l	ł
1728		retrovirus HERV- KC4 DNA	20.47	41050	(Y17833) env protein [Human	
	700240	INCH DINA	3e-47	4185944	endogenous retrovirus K)	7e-18
J	Į,	H.sapiens CpG DNA.	- 1			į
- 1	1	lone 87t9, forward	}		(AE001222) T. pallidum	j
1729	Z63594 r	ead cpg87f9.ft1a.	le-47	3322743	predicted coding region TP0454	2.4

(9,a,)	Nearest	Neighbor (BlastN vs. C	irnbank)	Nearner Maint	nbor (BlastX vs. Non-Redundant P	
		Treighbor (Bhash) vs. C)	Nearest Neigh	ibbr (Blascx vs. Non-Redundant Pr	roteins).
SEQ	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		R.rattus mRNA for		T		
		vascular type-1				
1	1	angiotensin U		į.	(U43629) integral membrane	}
1730	X62295	receptor	4e-48	1209756	protein (Beta vulgaris)	le-07
		Human tumor				1-100/
1		necrosis factor	1	-	i	ļ
1731	M85145	receptor, 3' flank.	3e-48	<none></none>	<none></none>	<none></none>
	l					
1	ł	Homo sapiens mRNA				i
1		for KIAA0905			(AB020712) KIAA0905 protein	1
1732	AB020712	protein, complete cds	4e-49	4240299	[Homo sapiens]	2e-20
1						
1	1	Homo sapiens mRNA			i	{
		for KIAA0905			(AB020712) KIAA0905 protein	
1733	AB020712	protein, complete cds	3e-49	4240299	[Homo sapiens]	2e-20
1	İ	R.rattus mRNA for				
	ł	vascular type-1			1	ĺ
	1	angiotensin II	1		(U43629) integral membrane	
1734	X62295	receptor	le-49	1209756	protein [Beta vulgaris]	7e-12
			1			
		Homo sapiens mRNA	1			
1722		for E1B-55kDa-			(AJ007509) E1B-55kDa-	
1735	AJ007509	associated protein	le-49	3319956	associated protein HYPOTHETICAL ZINC	4e-24
]			i		FINGER PROTEIN ZK686.4	
1 1			1		IN CHROMOSOME III	!
1 1			į.		>gi 630780 pir S44909 ZK686.4	
1			1		protein - Caenorhabditis elegans	i
			i		>gi 304346 (L17337) coded for	1
}	ļ		1		by C. elegans cDNAs	- 1
		H.sapiens mRNA for	- 1		GenBank:MS8869 and T01933;	l
1736		Ptg-12 protein	امنت	466044	putative [Caenorhabditis	
1,30		Homo sapiens	1e-49	466044	elegans]	8e-3!
		homolog of Nedd5	ł		1	
		(hNedd5) mRNA.	1		1	
1737		complete cds	4e-50	<none></none>	NONE	SION.
		Homo sapiens		MONES	<none></none>	< NON
		polycystic kidney	1		(L43619) polycystic kidney	
	1	disease (PKD1) gene,	Į		disease 1 protein [Homo	•
1738		exons 35-42	4e-50	903758	sapiens]	_3e-/
•				702.30	Jaupicita j	76-
1	Į.	Homo sapiens clone	1			!
- 1		22 mRNA, alternative	í		1	
- 1	The state of the s	splice variant alpha-1.	1		(AF009426) clone 22 [Homo	
1739	II.	complete cds	4e-50	2271473	sapiens]	5e

174	Nearest	Neighbor (BlastN vs. G	ienbank)	Nearest Neigh	nbor (BlastX vs. Non-Redundant Pr	roteins)
SEQ					The state of the s	1
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	PVALUE
ļ					monosaccharid transport protein	T T
	i	Homo sapiens			STP4 - Arabidopsis thaliana	
	l	(subclone 8_c11 from			>gi 16524 (X66857) sugar	
		P1 H22) DNA			transport protein (Arabidopsis	
1740	L77040	sequence.	2e-50	99758	thaliana]	6.4
1 1		Homo sapiens		•		
1 1		(subclone H8 5_a10				
	Y 2 7 4 7 7	from P1 35 H5 C8)				1
1741	L35657	DNA sequence.	2c-50	2072960	(U93568) p40 [Homo sapiens]	2e-05
		Hama anniana CTC7				
1742	1100716	Homo sapiens CTG7a	1- 50	MONTE		
1/42	U80745	mRNA, partial cds Bovine mRNA for	le-50	<none></none>	<none></none>	<none></none>
1743	D84514	p97, partial cds	1e-50	2070627	(AF103728) structural	
1.7.7.	D04314	p97, partial cus	16-30	3978527	polyprotein [Sindbis virus] LYSOSOMAL PROTECTIVE	9.9
			Ì		PROTEIN PRECURSOR	
			1		(CATHEPSIN A)	
		Human protective			(CARBOXYPEPTIDASE C)	
		protein mRNA.			human >gi 190283 (M22960)	
1744	M22960	complete cds.	1e-50	131081	protective protein precursor	le-12
					mufl protein - human	
		H.sapiens mRNA for	ł		>gi 762953 (X86018) muf1	
1745	X86018	MUF1 protein	le-50	1082610	[Homo sapiens]	le-21
			1			
		Human transcription				
1745		factor LSF-ID		_	transcription factor LSF - human	
1746	U03495	mRNA, complete cds.	7e-51	2136296	>gi 476099	1e-21
		Homo sapiens HRIHFB2157	·			- 1
1747		mRNA, partial cds	5e-51	2070974	(AB015344) HRIHFB2157	
1/4/		Human zinc finger	3e-31	3970874	[Homo sapiens] MYC-ASSOCIATED ZINC	2e-35
1748		protein mRNA.	4e-51	3024110	FINGER PROTEIN sapiens	2e-06
		Human zinc finger		3024110	PUVOER PROTEIN Supreils)	26.00
I	T C	protein zfp6 (ZF6)	1		(AC003682) F1S547_1 [Homo	1
1749		mRNA, partial eds	4e-51	2689441	[sapiens]	2e-11
					60S RIBOSOMAL PROTEIN	
- [1	i i		L13A (23 KD HIGHLY BASIC	
	}		1		PROTEIN)	1
- 1	ĺ		1		>gi 345897 pir S29539 basic	1
		H.sapiens mRNA for	1		protein. 23K - human >gi 23691	1
		23 kD highly basic			(X56932) 23 kD highly basic	1
1750		orotein	4e-51	730451	protein [Homo sapiens]	12-11
- 1		H.sapiens flow-sorted	j			
		chromosome 6		·		
1751		HindIII fragment.	3.5.	-NONT		.:01=
1/31	2/3034	SCOPA_ICII	2e-51	<none></none>	<none></none>	<none></none>

11.00	Nearest	Neighbor (BlastN vs. G	enhank)	No No. 1 d	La colonia de la	
	realest	reignoof (Blastit Vs. O	Cildalik)	Nearest Neigh	bor (BlastX vs. Non-Redundant P	roteins)
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens				
1		BAF60b gene, partial			·	
1752	AF068245	sequence	5e-52	<none></none>	<none></none>	<none></none>
1753	AJ236932	Sus scrofa mRNA for hypothetical protein (5'; clone 4B8)	5e-52	400927	RIBONUCLEOPROTEIN RB97D ribonucleoprotein [Drosophila melanogaster]	4.7
1754	AF003693	Mus musculus scaffold protein Pbp1 homolog mRNA, complete cds	6e-53	2197106	(AF003693) scaffold protein Pbp1 homolog [Mus musculus]	2e-54
1755	M27319	Human calmodulin mRNA, complete cds.	5e-53	115528	CALMODULIN >gi 102408 pir JC1309 calmodulin - Stylonychia lemnae (SGC5) >gi 161195	0.002
1756	M74555	Mouse house-keeping protein mRNA, complete cds.	5e-53	284775	house-keeping protein - mouse	5e-30
1757		H.sapiens mRNA for phosphoenolpyruvate carboxykinase	6e-54	2135915	phosphoenolpyruvate carboxykinase (GTP) (EC 4.1.1.32) precursor, mitochondrial - human carboxykinase (GTP) [Homo sapiens]	6e-21
1758	AF007872	Homo sapiens torsinB (DQI) mRNA, partial cds	2e-54	2760121	(AB002405) LAK-4p [Homo sapiens]	0.27
1759	U49507	Mus musculus B6CBA Lisch7 mRNA, partial cds. Human DNA	2e-54	1236083	(U49507) Lisch7 [Mus musculus]	3e-27
1760		sequence from cosmid 92M18, BRCA2 gene region chromosome 13q12-			(Y14657) hydrophobin [Pleurotus ostreatus] >gi 2982620 gnl PID e1283986 (AJ225061) POH2 hydrophobin	
1760	(Human cytochrome c oxidase subunit VIa gene, exon 3 and	le-55	2370371	[Pleurotus ostreatus] (AE000682) hypothetical	2.0
1761		complete cds	8e-56	2982994	protein [Aquifex aeolicus]	7.0
1762	I	Homo sapiens mRNA for transducin (beta) ike 1 protein	7e-56		(Y12781) transducin (beta) like	
		ike i piotetti	76-30	3021409	l protein [Homo sapiens]	7e-39

		Neighbor (BlastN vs. C	Genbank)	Nearest Neig	hbor (BlastX vs. Non-Redundant P	roteins)
SEQ			1			
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
-	╂──	Homo sapiens mRNA	 			
I	1	for KIAA0866	1		(AF001548) Myosin heavy	
1763	AB020673	protein, complete cds	8e-57	2104552	chain (MHY11) (5'partial)	
	112020075	protein, complete cas	86-37	2104553	[Homo sapiens]	4e-04
	1	Sus scrofa mRNA for			RIBONUCLEOPROTEIN	
1	İ	hypothetical protein			RB97D ribonucleoprotein	ł
1764	AJ236932	(5': clone 4B8)	3e-57	400927	[Drosophila melanogaster]	4.7
ł		Human dystrophin			(2-1000) into the land gaster (4.7
l .	ł	gene, intron 1				
		containing pseudo			(AC005724) unknown protein	l
1765	L06900	exon.	1e-58	. 4185129	[Arabidopsis thaliana] thaliana]	7.0
1 1		H.sapiens				
1766	V02224	mitochondrial DNA.			(U60315) MC107L [Molluscum	
1766	X93334	complete genome	9e-59	1492050	contagiosum virus subtype 1]	0.17
		Rattus sp. 7acomp protein mRNA,				
1767	AF064856	complete cds	3e-59	3169626	(AF064856) 7acomp protein	
	12 00 1030	complete cus	36-39	3109020	[Rattus sp.]	2e-31
		Homo sapiens alpha-	ŀ		1	
		tubulin isoform!	i		(X06956) alpha-tubulin [Homo	
1768	AF081484	mRNA, complete cds	2e-59	32015	[sapiens]	4e-22
					suprens	46
ı		Homo sapiens mRNA	j			
1760		for FUS-CHOP	1		(U23523) histidine-rich	i
1769	X71427	protein fusion	1e-60	746557	[Caenorhabditis elegans]	0.45
ł		Homo sapiens serine	1			
- 1		protease mRNA.	1		(AB006622) No similarities to	İ
1770	1	complete cds	1e-60	2564316	any reported proteins [Homo	
		Mus musculus	16-00	2304316	sapiens]	0.26
- 1	ŀ	lymphocyte specific	1		1	I
- 1		helicase mRNA.			lymphocyte specific helicase -	
1771	U25691	complete cds	7e-61	2137490	[mouse musculus]	3e-25
- 1					most mescales,	30 22
	1		j		ubiquitin / ribosomal protein	i
	1_		J		S27a - human extension protein,	1
j		I.sapiens	1		HUBCEP80 [human, Peptide,	I
1772		nitochondrial DNA,			156 aa] ubiquitin extention	j
'''- -		omplete genome Homo sapiens mRNA	4e-61	70656	protein [Cavia porcellus]	9e-08
		or CAB1, complete	1		-	
1773		ds CAB1, complete	4e-61	2125214		
		lus musculus	46.01	2135214	gene MLN 64 protein - human	4e-23
}		emphocyte specific	1		1	l
l		elicase mRNA.	1		lymphocyte specific helicase -	
774	_	omplete cds	8e-62		mouse musculus]	Se-26
					mouse museutus]	oc0

1:00	Nearest 1	Neighbor (BlastN vs. G	enbank)	Nearest Neigh	bor (BlastX vs. Non-Redundant Pr	oteins)
SEQ						
ΙD	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human lipocortin-V			Human Annexin V With Proline	
1775	M21731	mRNA, complete cds.	6e-62	3212603	Substitution By Thioproline	2e-20
1		Rattus norvegicus			1	
		myotonic dystrophy				
		kinase-related Cdc42-			1	
		binding kinase			(AF021936) myotonic	ļ
1 1		MRCK-beta (MRCK-			dystrophy kinase-related Cdc42-	
		beta) mRNA,			binding kinase MRCK-beta	
1776	AF021936	complete cds	2e-62	2736153	[Rattus norvegicus]	3e-27
		H.sapiens HUNKI	_		(AC004798) R31546_1 [Homo	
1777	Y12059	mRNA	le-62	3184498	sapiens]	3e-09
1		Human (clone E5.1)				
1 1		RNA-binding protein		•	sialidase - Actinomyces viscosus	
1778	L37368	mRNA, complete cds.	6e-63	477578	>gil141852	7.8
	20.000	interval complete seas	30 00	,,,,,,,	ZINC FINGER PROTEIN 83	7.0
		Figure 2. Nucleotide			(ZINC FINGER PROTEIN	
		and translated protein			HPF1) >gi 106023 pir A32891	
1 1		sequences of HPF1, -			finger protein 1, placental -	
1779		2, and -9.	5e-63	1731443	human	3e-33
		Homo sapiens putative G protein-			(AL023288) hypothetical	
1780		coupled receptor	2e-63	3116131	protein	4.6
1700	AI 075448	coupled receptor	20-05	3110131	protein	
		}	j		.	į
ļ [Human transaldolase				
1 1		mRNA containing]	ł
	•	transposable element.			(U63159) transaldolase [Mus	l
1781	L19437	complete cds	2e-63	1553119	musculus]	4e-18
		1			PROSTASIN PRECURSOR	ŀ
		Homo sapiens			precursor - human >gi 862305 (L41351) prostasin [Homo	ĺ
		prostasin mRNA,	1	•	[L41331) prostasin [Hollo [sapiens] >gi[1143194 (U33446)]	ļ
1782		complete cds	1e-63	2833277	prostasin [Homo sapiens]	6e-14
		Homo sapiens 10kD	j			ļ
		protein (BC10)			hypothetical protein K03H1.9 -	
1783	AF053470	mRNA, complete cds	6e-64	482237	Caenorhabditis elegans	0.029

	Nearest	Neighbor (BlastN vs. C	ienbank)	Nearest Neigh	bor (BlastX vs. Non-Redundant P	oteins)
SEQ			T .			T
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	DVALLE
	i cezooioi	DESCRIPTION .	I TALOL	ACCESSION	T DESCRIPTION	P VALUE
<u> </u>	 			··	(Z93390) Similar to FY VE zinc	
	ĺ				finger; cDNA EST yk265b4.5	
i		ł			comes from this gene; cDNA	ļ
ſ			i i		EST yk359g9.5 comes from this	
1	i				gene; cDNA EST yk319c2.5	
i					comes from this gene	i
ŀ	ł				[Caenorhabditis elegans] zinc	
i .			ĺ		finger; cDNA EST yk265b4.5	
					comes from this gene; cDNA	
					EST yk359g9.5 comes from this	
		Mouse mRNA for			gene; cDNA EST yk319c2.5	1
		beta-1,4-			comes from this gene	
1784	D37791	galactosyltransferase	6e-64	3880102	[Caenorhabditis elegans]	3e-16
		, , , , ,			·	
		Mus musculus radical				
1785	AF015770	fringe (radical-fringe)	6.61	2204255	(U94350) radical fringe	
1765	AF013770	mRNA, complete cds H.sapiens flow-sorted	6e-64	2204355	precursor [Mus musculus]	1e-36
	:	chromosome 6				
		HindIII fragment.			1	
1786	Z79054	SC6pA21E11	2e-64	<none></none>	<none></none>	<none></none>
		Homo sapiens	ł			
		cytosolic selenium-				
		dependent glutathione	1			
		peroxidase gene,	.			
1707		complete cds, and			(U42580) A565R [Paramecium	
1787	M83094	rhoh12 gene, 3' end.	le-64	2447063	bursaria Chlorella virus 11	8.8
Į		H.sapiens LAG-3			(VI II I2)	
1788		gene, promoter region	7e-65	1944540	(X14112) tegument protein	,, I
1700	110211	gene, promoter region	76-03	1344340	[human herpesvirus 1]	2.3
I		Human lysozyme				
1789	1	mRNA, complete cds.	2e-65	<none></none>	<none></none>	<none></none>
					LIPASE MODULATOR	
j	1		1		PRECURSOR (LIPASE	
		į			HELPER PROTEIN) .	[
		Homo sapiens SS-	ŀ		>gi 480045 pir S36249 lipB	l
ĺ	ľ	A/Ro autoantigen 52	Ī		protein - Pseudomonas glumae	1
		kda component gene.	ŀ		>gi 49207 (X70354) helper	1
1790	U01882	complete cds	2e-65	585401	protein	4.2
j		Homo sapiens RNA	i			
		binding protein DEF-]`	ļ		
1701		3 mRNA, complete	2- 65		(AF069517) RNA binding	
1791	AF069517	cds	2e-65	3212101	protein DEF-3 [Homo sapiens]	le-25

	Nearest	Neighbor (BlastN vs. C	ienbank)	Nearest Neigh	bor (BlastX vs. Non-Redundant Pr	ntaina\
SEQ					1001 (Diaset vs. 14011-Reduildant Fr	(leins)
ID	ACCESSION	DESCRIPTION	P VALUE	ACCECCION	DESCRIPTION	
<u> </u>	THECESSION	Homo sapiens jerky	FVALUE	ACCESSION	DESCRIPTION	P VALUE
	 	gene product	 	 	<u> </u>	
j		homolog mRNA.	İ	1	(AF004715) jerky gene product	
1792	AF004715	complete cds	2e-65	2314829	homolog [Homo sapiens]	2-45
				2311025	hypoxanthine (guanine)	2e-45
1	1				phosphoribosyltransferase - long	
1]	C. longicaudatus hprt		•	tailed hamster	l
		mRNA for			phosphoribosyltransferase	
1793	X59652	hypoxanthine	3e-66	631625	[Cricetulus longicaudatus]	6e-54
1		Mus museulus maliant		*		
		Mus musculus radical fringe precursor			(5:0.050)	
1794	U94350	mRNA, complete cds	3e-67	2204266	(U94350) radical fringe	
	074330	mixiva, complete cas	36-07	2204355	precursor [Mus musculus]	2e-33
1		Mus musculus			1	
1 .		putative	1			
1 .		lysophosphatidic acid			(AF015811) putative	
] .		acyltransferase	ĺ		lysophosphatidic acid	
1795	AF015811	mRNA, complete cds	3e-68	2317725	acyltransferase [Mus musculus]	7e-51
		Cow	į			
		phosphoinositide- specific	į			
1796	J03137	phospholipase C	3e-69	226008	phospholipuse C 154 (Bos	[
1	.03137	phosphoripase C	26-09	226908	taurus)	3e-25
1 1		Rattus norvegicus				
		putative peroxisomal	i			
] [2,4-dienoyl-CoA	i			
1		reductase (DCR-	į		(AF044574) putative	
	. =	AKL) mRNA,	ľ		peroxisomal 2,4-dienoyl-CoA	j
1797	AF044574	complete cds	1e-69	4105269	reductase (Rattus norvegicus)	2e-33
		Mus musculus				Ì
		putative				1
		lysophosphatidic acid	-	•	(AF015811) putative	
		acyltransferase			lysophosphatidic acid	J
1798	_	mRNA. complete cds	4e-70	2317725	acyltransferase [Mus musculus]	3e-19
. T	1	M.musculus mRNA			[
		for desmoyokin.		f	desmoyokin - mouse (fragment)	l
1799	X65157	partial	5e-74	109781	>gi 50675	9e-37
ļ	1.	Mus musculus mRNA	ľ			7
1800		for B-IND1 protein	2e-74		(Z97207) B-IND1 protein [Mus	
+		or a-man protein	26-14	2231019	musculus]	6e-21
	le	Gallus gallus zinc				1
- 1		inger protein (Fzf-1)		i,	(U27196) zine finger protein	- 1
1801		nRNA, complete cds.	6e-75	i i	[Gallus gallus] gallus]	2e-44

SEQ ID ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE ACCESSION ACCESSION P VALUE ACCESSION DESCRIPTION P VALUE ACCESSION ACCESSION P VALUE ACCESSION ACCESSION P VALUE ACCESSION ACCESSION P VALUE ACCESSION ACCESSION P VALUE ACCESSION ACCESSION P VALUE ACCESSION ACCESSION P VALUE ACCESSION ACCESSI		Nearest	Neighbor (BlastN vs. C	ienbank)	Nanaga M-1-	hhos (Blast V vs. Non Batharia	
D ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE P VALUE ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE ACCESSION TO ROW REPEAT TUMOR: SPECIFIC ANTIGEN P gi/2505957 gni PD e353992 (Y15054) 70 kD tumor-specific antigen, partial 3e-77 3123027 Accession	SEC			Jenoank,	incarest Neig	mbor (Blastix vs. :Non-Redundant Pr	oteins)
Rattus norvegicus mRNA for 70 kDa tumor specific atumor spec		·	DESCRIPTION	P VALUE	ACCESSION		P VALUE
1802 Y15054 antigen, partial 3e-77 3123027 antigen [Rattus norvegicus] 4e						70 KD WD-REPEAT TUMOR-	i -
1802 Y15054 tumor specific antigen, partial antigen, partial antigen, partial antigen, partial antigen, partial antigen (Pattus norvegicus) 4e	1		_				
1802 Y15054	[1		1		>gi 2505957 gn1 PID e353992	
M.musculus mRNA for desmoyokin. partial 3e-79 109781 desmoyokin - mouse (fragment) 9e	1	1	, .			(Y15054) 70 kD tumor-specific	
Rattus norvegicus cardiac adriamycin responsive protein mRNA. complete cds	1802	Y15054		3e-77	3123027	antigen [Rattus norvegicus]	4e-42
1803 X65157 partial 3e-79 109781 2gi 50675 9e	1						
Rattus norvegicus cardiac adriamycin responsive protein mRNA. complete cds 2e-84 1362781 protein [Homo sapiens] 7e- Rattus norvegicus thioredoxin reductase (TrxR2) mRNA. nuclear gene encoding mitochondrial protein complete cds 2e-84 3757888 reductase [Rattus norvegicus] 6e- Rattus norvegicus putative peroxisomal 2.4-dienoyl-CoA reductase (DCR-AKL) mRNA. complete cds 6e-85 4105269 reductase [Rattus norvegicus] 1e- Rattus norvegicus putative peroxisomal 2.4-dienoyl-CoA reductase (DCR-AKL) mRNA. (U19181) Rabin3 mRNA, (U19181) Rabin3 mRNA, (U19181) Rabin3 mRNA, (U19181) Rabin3 mRNA, (U19181) Rabin3 mRNA, (U19181) Rabin3 mRNA, (U19181) Rabin3 mRNA, (U19181) Rabin3 mRNA, (U19181) Rabin3 mRNA, (U19181) Rabin3 mRNA, (U19181) Rabin3 mRNA, (U19181) Rabin3 mRNA, (U19181) Rabin3 mRNA, (U19181) Rabin3 mRNA, (U19181) Rabin3 mRNA, (U19181) Rabin3 masculus ninein mRNA. complete cds. 1e-91 1113865 musculus TROPOMYOSIN BETA 3, FIBROBLAST chicken segisiferatoxin binding protein 4e-92 136077 tropomyosin (Gallus gallus) 0.5: Rattus norvegicus putative peroxisomal 2.4-dienoyl-CoA reductase (DCR-AGHON) Potative protein (AF044574) putative	1,000	V/5165	1				
1804 U50736 U50736 U50736 mRNA. complete cds 2e-84 1362781 protein [Homo sapiens] 7e-	1803	X63157	partial	3e-79	109781	>gi 50675	9e-33
1804 U50736 U50736 U50736 mRNA. complete cds 2e-84 1362781 protein [Homo sapiens] 7e-	l		Pattus nonvenious	l l			
1804 U50736 mRNA, complete cds 2e-84 1362781 mRNA (X3703) nuclear protein [Homo sapiens] 7e-	1		_				
Rattus norvegicus thioredoxin reductase (TrxR2) mRNA. nuclear gene encoding mitochondrial protein, complete cds 2e-84 3757888 (AF072865) thioredoxin reductase [Rattus norvegicus] 6e-	1	ļ					
Rattus norvegicus thioredoxin reductase (TrxR2) mRNA. nuclear gene encoding mitochondrial protein. complete cds 2e-84 3757888 reductase [Rattus norvegicus] 6e- Rattus norvegicus putative peroxisomal 2,4-dienoyl-CoA reductase (DCR-AKL) mRNA. complete cds 6e-85 4105269 reductase [Rattus norvegicus] le-Rattus norvegicus Rabin3 mRNA. complete cds Rabin3 mRNA. (U19181) Rabin3 [Rattus norvegicus] le-Rattus norvegicus] Rabin3 mRNA. (U19181) Rabin3 [Rattus norvegicus] Rabin3 mRNA. complete cds. 1e-91 1113865 musculus] 2e-Rattus norvegicus] Rabin3 mRNA for cytosolic resiniferatoxin-binding protein 4e-92 136077 tropomyosin [Gallus gallus] 0.5in Rattus norvegicus putative peroxisomal 2,4-dienoyl-CoA reductase (DCR- (AF044574) putative putative peroxisomal 2,4-dienoyl-CoA reductase (DCR- (AF044574) putative	1804	1150736		20.01	1262701		
thioredoxin reductase (TrxR2) mRNA, nuclear gene encoding mitochondrial protein, complete cds Rattus norvegicus putative peroxisomal 2.4-dienoyl-CoA reductase (DCR- AKL) mRNA. (aF044574) putative peroxisomal 2.4-dienoyl-CoA reductase (DCR- AKL) mRNA. (areductase (Rattus norvegicus) Rattus norvegicus Particularia (U40342) ninein [Mus musculus] Rattus norvegicus Particularia (U40342) ninein [Mus musculus] Rattus norvegicus Particularia (U40342) ninein [Mus musculus] Rattus norvegicus Particularia (U40342) ninein [Mus musculus] Rattus norvegicus Particularia (U40342) ninein [Mus musculus] Rattus norvegicus Particularia (U40342) ninein [Mus musculus] Rattus norvegicus Particularia (U40342) ninein [Mus musculus] Rattus norvegicus Particularia (U40342) ninein [Mus musculus] Rattus norvegicus Particularia (U40342) ninein [Mus musculus] Rattus norvegicus Particularia (U40342) ninein [Mus musculus] Rattus norvegicus Particularia (U40342) ninein [Mus musculus] Rattus norvegicus Particularia (U40342) ninein [Mus musculus] Rattus norvegicus Particularia (U40342) ninein [Mus musculus] Rattus norvegicus Particularia (U40342) ninein [Mus musculus] Rattus norvegicus Particularia (U40342) ninein [Mus musculus] Rattus norvegicus Particularia (U40342) ninein [Mus musculus] Rattus norvegicus Particularia (U40342) ninein [Mus musculus] Rattus norvegicus Particularia (U40342) ninein [Mus musculus] Rattus norvegicus Particularia (U40342) ninein [Mus musculus] Rattus norvegicus Particularia (U40342) ninein [Mus musculus]	1004	030730	mikiya, complete cus	26-84	1362/81	protein [Homo sapiens]	7e-30
thioredoxin reductase (TrxR2) mRNA. nuclear gene encoding mitochondrial protein. complete cds Rattus norvegicus putative peroxisomal 2.4-dienoyl-CoA reductase (DCR- AKL) mRNA. complete cds Rattus norvegicus mRNA for cytosolic resiniferatoxin- binding protein Rattus norvegicus putative peroxisomal 2.4-dienoyl-CoA reductase (Rattus norvegicus norvegicus] (U19181) Rabin3 [Rattus norvegicus] 2e-3 TROPOMYOSIN BETA 3, FIBROBLAST chicken >gi 515694 (M23082) tropomyosin [Gallus gallus] 0.50 Rattus norvegicus putative peroxisomal 2.4-dienoyl-CoA reductase (DCR-	1		Rattus norvegicus	·			
(TrxR2) mRNA, nuclear gene encoding mitochondrial protein, complete cds 2e-84 3757888 reductase [Rattus norvegicus] 6e- Rattus norvegicus putative peroxisomal 2,4-dienoyl-CoA reductase (DCR-AKL) mRNA. 1806 AF044574 complete cds 6e-85 4105269 reductase [Rattus norvegicus] 1e-Rattus norvegicus Rabin3 mRNA, complete cds. 2e-87 624225 (U19181) Rabin3 [Rattus norvegicus] 2e-Rattus norvegicus] 1e-Rattus norvegicus] 1e-Rattus norvegicus] 1e-Rattus norvegicus] 1e-Rattus norvegicus] 1e-Rattus norvegicus] 1e-Rattus norvegicus] 1e-Rattus norvegicus] 1e-Rattus norvegicus] 1e-Rattus norvegicus] 1e-Rattus norvegicus] 1e-Rattus norvegicus] 1e-Rattus norvegicus] 1e-Rattus norvegicus] 1e-Rattus norvegicus] 1e-Rattus norvegicus] 1113865 (U19181) Rabin3 [Rattus norvegicus] 1113865 (U40342) ninein [Mus musculus] 1113865 (U40342) ninein [Mus mu	1		, –			1 -	
nuclear gene encoding mitochondrial protein. complete cds Rattus norvegicus putative peroxisomal 2,4-dienoyl-CoA reductase (DCR- AKL) mRNA. 1806 AF044574 complete cds Rattus norvegicus Ratius norvegicus mRNA for cytosolic resiniferatoxin- binding protein Rattus norvegicus putative peroxisomal 2,4-dienoyl-CoA reductase (DCR- (AF044574) putative (AF044574) putative	ł .	Ī					
encoding mitochondrial protein. complete cds 2e-84 3757888 (AF072865) thioredoxin reductase [Rattus norvegicus] 6e- Rattus norvegicus putative peroxisomal 2,4-dienoyl-CoA reductase (DCR-AKL) mRNA. complete cds 6e-85 4105269 reductase [Rattus norvegicus] 1e-Rattus norvegicus Rabin3 mRNA. 1807 U19181 complete cds. 2e-87 624225 (U19181) Rabin3 [Rattus norvegicus] 2e-3 (U40342) ninein [Mus musculus ninein mRNA. complete cds. 1e-91 1113865 (U40342) ninein [Mus musculus] 2e-3 (U40342) ninein [Mus musculus] 2e-3 (Rattus norvegicus mRNA for cytosolic resiniferatoxin-binding protein 4e-92 136077 tropomyosin [Gallus gallus] 0.5 (AF044574) putative	1	ļ	l' '	•		j	
mitochondrial protein, complete cds 2e-84 3757888 (AF072865) thioredoxin reductase [Rattus norvegicus] 6e- Rattus norvegicus putative peroxisomal 2,4-dienoyl-CoA reductase (DCR-AKL) mRNA. complete cds 6e-85 4105269 (AF044574) putative peroxisomal 2,4-dienoyl-CoA reductase [Rattus norvegicus] 1e-Rattus norvegicus Rabin3 mRNA. complete cds. 2e-87 624225 (U19181) Rabin3 [Rattus norvegicus] 2e-Mus musculus ninein mRNA. complete cds. 1e-91 1113865 (U40342) ninein [Mus musculus] 1808 U40342 (Rattus norvegicus mRNA for cytosolic resiniferatoxin-binding protein 4e-92 136077 tropomyosin [Gallus gallus] 0.50 Rattus norvegicus putative peroxisomal 2,4-dienoyl-CoA reductase (DCR- (AF044574) putative	l	1		1		1	
Rattus norvegicus putative peroxisomal 2.4-dienoyl-CoA reductase (DCR-AKL) mRNA. complete cds de-85 4105269 reductase [Rattus norvegicus] le-880 U40342 mRNA. complete cds de-87 624225 (U19181) Rabin3 [Rattus norvegicus] le-91 1113865 musculus] Rattus norvegicus mRNA for cytosolic resiniferatoxin-binding protein de-92 136077 tropomyosin [Gallus gallus] 0.50 Rattus norvegicus putative peroxisomal 2.4-dienoyl-CoA reductase [Rattus norvegicus] 0.50 Rattus norvegicus mRNA (AF044574) putative peroxisomal 2.4-dienoyl-CoA reductase (DCR- (AF044574) putative (AF044574) putative	I					(AF072865) thioredoxin	
Rattus norvegicus putative peroxisomal 2,4-dienoyl-CoA reductase (DCR-AKL) mRNA. complete cds 6e-85 4105269 reductase (Rattus norvegicus) 1e-Rattus norvegicus Rabin3 mRNA, complete cds. 2e-87 624225 (U19181) Rabin3 (Rattus norvegicus) 2e-3 (U40342) ninein [Mus musculus] Ranorvegicus mRNA for cytosolic resiniferatoxin-binding protein 4e-92 136077 tropomyosin [Gallus gallus] 0.50 (AF044574) putative	1805	AF072865	protein, complete cds	2e-84	3757888		6e-43
Dutative peroxisomal 2,4-dienoyl-CoA reductase (DCR-AKL) mRNA. (AF044574) putative peroxisomal 2,4-dienoyl-CoA reductase (DCR-AKL) mRNA. (D19181) Rabin3 mRNA, complete cds. 2e-87 624225 (24094574) putative peroxisomal 2,4-dienoyl-CoA reductase (Rattus norvegicus) 1e-1808 U40342 Mus musculus ninein mRNA. complete cds. 1e-91 1113865 (U40342) ninein (Mus musculus) 2e-1809 Rattus norvegicus mRNA for cytosolic resiniferatoxin-binding protein 4e-92 136077 1					0.5.000	reductase (reducts norvegicus)	00-43
2,4-dienoyl-CoA reductase (DCR- AKL) mRNA. (AF044574) putative peroxisomal 2,4-dienoyl-CoA reductase (DCR- AKL) mRNA. (AF044574) putative peroxisomal 2,4-dienoyl-CoA reductase (Rattus norvegicus) 1e- AKL Rattus norvegicus Rabin3 mRNA, (U19181) Rabin3 (Rattus norvegicus) 2e- AKL Rattus norvegicus (U40342) ninein (Mus musculus ninein mRNA. complete cds. 1e-91 1113865 musculus 2e- AKL TROPOMYOSIN BETA 3, FIBROBLAST chicken resiniferatoxin- pinding protein 4e-92 136077 tropomyosin (Gallus gallus) 0.50 Rattus norvegicus putative peroxisomal 2,4-dienoyl-CoA reductase (DCR- (AF044574) putative AKL Putative Peroxisomal (AF044574) putative Peroxisomal 2,4-dienoyl-CoA reductase (DCR- (AF044574) putative Peroxisomal 2,4-dienoyl-CoA reductase (DCR- (AF044574) putative Peroxisomal 2,4-dienoyl-CoA reductase (DCR- (AF044574) putative Peroxisomal 2,4-dienoyl-CoA reductase (DCR- (AF044574) putative Peroxisomal 2,4-dienoyl-CoA reductase (DCR- (AF044574) putative Peroxisomal 2,4-dienoyl-CoA reductase (DCR- (AF044574) putative Peroxisomal 2,4-dienoyl-CoA reductase (DCR- (AF044574) putative Peroxisomal 2,4-dienoyl-CoA reductase (DCR- (AF044574) putative Peroxisomal 2,4-dienoyl-CoA reductase (DCR- (AF044574) putative Peroxisomal 2,4-dienoyl-CoA reductase (DCR- (AF044574) putative Peroxisomal 2,4-dienoyl-CoA Peroxisomal 2,4-dienoyl-CoA Peroxisomal 2,4-dienoyl-CoA Peroxisomal 2,4-dienoyl-CoA Peroxisomal 2,4-dienoyl-CoA Peroxisomal 2,4-dienoyl-CoA Peroxisomal 2,4-dienoyl-CoA Peroxisomal 2,4-dienoyl-CoA Peroxisomal 2,4-dienoyl-CoA Peroxisomal 2,4-dienoyl-CoA Peroxisomal 2,4-dienoyl-CoA Peroxisomal 2,4-dienoyl-CoA Peroxisomal 2,4-dienoyl-CoA Peroxisomal 2,4-dienoyl-CoA Peroxisomal 2,4-dienoyl-CoA Peroxisomal 2,4-dienoyl-CoA Peroxisomal 2,4-dienoyl-CoA Peroxisomal 2,4-dienoyl-CoA Peroxisomal 2,4-dienoyl-CoA				· j			
reductase (DCR-AKL) mRNA. complete cds 6e-85 4105269 reductase [Rattus norvegicus] 1e- Rattus norvegicus Rabin3 mRNA, complete cds. 2e-87 624225 (U19181) Rabin3 [Rattus norvegicus] 2e Mus musculus ninein mRNA. complete cds. 1e-91 1113865 musculus] R. norvegicus mRNA for cytosolic resiniferatoxin- binding protein 4e-92 136077 tropomyosin [Gallus gallus] 0.50 Rattus norvegicus putative peroxisomal 2.4-dienoyl-CoA reductase (DCR- (AF044574) putative peroxisomal 2.4-dienoyl-CoA reductase (DCR-			putative peroxisomal				i
AKL) mRNA. complete cds Rattus norvegicus Rabin3 mRNA, complete cds. Rattus norvegicus Rabin3 mRNA, complete cds. Rattus norvegicus Rabin3 mRNA, complete cds. Rattus norvegicus Rabin3 mRNA, complete cds. Rattus norvegicus Rabin3 mRNA, complete cds. Rattus norvegicus Rabin3 mRNA, complete cds. Rattus norvegicus mRNA for cytosolic resiniferatoxin- binding protein Rattus norvegicus putative peroxisomal 2,4-dienoyl-CoA reductase (DCR- AKL) mRNA. complete cds Rattus norvegicus peroxisomal 2,4-dienoyl-CoA reductase [Rattus norvegicus] (U19181) Rabin3 [Rattus norvegicus] (U40342) ninein [Mus musculus] TROPOMYOSIN BETA 3, FIBROBLAST chicken >gil515694 (M23082) tropomyosin [Gallus gallus] 0.5:				İ			ŀ
1806 AF044574 complete cds 6e-85 4105269 reductase [Rattus norvegicus] 1e-	l		' '	i		(AF044574) putative	1
Rattus norvegicus Rabin3 mRNA, complete cds. 1807 U19181 complete cds. 1808 U40342 Mus musculus ninein mRNA. complete cds. 1809 K67877 binding protein Rattus norvegicus putative peroxisomal 2.4-dienoyl-CoA reductase (DCR- Rabin3 mRNA, complete cds. 2e-87 624225 norvegicus] (U19181) Rabin3 [Rattus norvegicus] (U40342) ninein [Mus musculus] TROPOMYOSIN BETA 3, FIBROBLAST chicken >gi]515694 (M23082) tropomyosin [Gallus gallus] 0.50			· I	i		peroxisomal 2,4-dienoyl-CoA	ĺ
Rabin3 mRNA, complete cds. 2e-87 624225 (U19181) Rabin3 [Rattus norvegicus] 2e-1 Mus musculus ninein mRNA, complete cds. 1e-91 1113865 (U40342) ninein [Mus musculus] 2e-1 R.norvegicus mRNA for cytosolic resiniferatoxin- binding protein 4e-92 136077 tropomyosin [Gallus gallus] 0.50 Rattus norvegicus putative peroxisomal 2.4-dienoyl-CoA reductase (DCR- (AF044574) putative	1806			6e-85	4105269	reductase [Rattus norvegicus]	le-41
1807 U19181 complete cds. 2e-87 624225 norvegicus] 2e-37 Mus musculus ninein mRNA. complete cds. 1e-91 1113865 musculus] 2e-3 R.norvegicus mRNA for cytosolic resiniferatoxin- binding protein 4e-92 136077 tropomyosin [Gallus gallus] 0.50 Rattus norvegicus putative peroxisomal 2.4-dienoyl-CoA reductase (DCR- (AF044574) putative		·	-	l l			
Mus musculus ninein mRNA. complete cds. le-91 1113865 musculus] 2e-3 R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein 4e-92 136077 tropomyosin [Gallus gallus] 0.50 Rattus norvegicus putative peroxisomal 2.4-dienoyl-CoA reductase (DCR- (AF044574) putative	1007	*****				-	1
1808 U40342 mRNA. complete cds. 1e-91 1113865 musculus] R.norvegicus mRNA for cytosolic resiniferatoxin- binding protein 4e-92 136077 tropomyosin [Gallus gallus] 0.50 Rattus norvegicus putative peroxisomal 2.4-dienoyl-CoA reductase (DCR-	1907	019181	complete cds.	2e-87	624225	norvegicus]	2e-∔1
1808 U40342 mRNA. complete cds. 1e-91 1113865 musculus] R.norvegicus mRNA for cytosolic resiniferatoxin- binding protein 4e-92 136077 tropomyosin [Gallus gallus] 0.50 Rattus norvegicus putative peroxisomal 2.4-dienoyl-CoA reductase (DCR-	ļ		Mus = 1 = 1 = 1	į			
R.norvegicus mRNA for cytosolic resiniferatoxin- binding protein 4e-92 136077 tropomyosin [Gallus gallus] 0.5 Rattus norvegicus putative peroxisomal 2.4-dienoyl-CoA reductase (DCR- (AF044574) putative	1808			1.0.	11122	1	
for cytosolic resiniferatoxin-binding protein X67877 binding protein 4e-92 136077 tropomyosin [Gallus gallus] 0.50 Rattus norvegicus putative peroxisomal 2.4-dienoyl-CoA reductase (DCR- (AF044574) putative	1000			16-91	1113865		2e-36
resiniferatoxin-binding protein 4e-92 Rattus norvegicus putative peroxisomal 2.4-dienoyl-CoA reductase (DCR- resiniferatoxin-binding protein 4e-92 136077 >gi 515694 (M23082) tropomyosin [Gallus gallus] 0.50 (AF044574) putative	ı					1	
1809 X67877 binding protein 4e-92 136077 tropomyosin [Gallus gallus] 0.50 Rattus norvegicus putative peroxisomal 2.4-dienoyl-CoA reductase (DCR- (AF044574) putative			•	ŀ			1
Rattus norvegicus putative peroxisomal 2.4-dienoyl-CoA reductase (DCR- (AF044574) putative	1809	J.		40.02	136077	(= '	0.56
putative peroxisomal 2.4-dienoyl-CoA reductase (DCR- (AF044574) putative			- mania protetti	~~/-	130077	Inoponivosin (Ganus ganus)	0.36
putative peroxisomal 2.4-dienoyl-CoA reductase (DCR- (AF044574) putative	l		Rattus norvegicus	l l		4	l
2.4-dienoyl-CoA reductase (DCR- (AF044574) putative				1			
reductase (DCR- (AF044574) putative				1			
	ł	1	- I	1		(AF044574) putative	1
AKL) mRNA. peroxisomal 2,4-dienoyl-CoA				1			ļ
1910 AFOLISTI	1810	I.		5e-93	4105269		le-50
Mus musculus EHF							10-20
(Ehf) mRNA. (AF035527) EHF (Mus	ſ		Ehf) mRNA.	1		(AF035527) EHF (Mus	l
1911 AE035537 1 1 1 1 0 07 1	1811	AF035527 c	omplete cds	2e-95	3138930	1	2e-47

	Nearest	Neighbor (BlastN vs. C	ienbank)	Nearest Neig	hbor (BlastX vs. Non-Redundant P	
SEQ				· · · · · · · · · · · · · · · · · · ·	1001 (2.1352 V3. 140H-Redundant P	Toteins)
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
	 	<u> </u>	<u> </u>			
1812	AB016930	Cricetulus griseus mRNA for Phosphatidylglycerop hosphate synthase, complete cds	6e-96	. 4159682	(AB016930) Phosphatidylglycerophosphate synthase [Cricetulus griseus]	7e-41
		Rattus norvegicus mRNA for atypical PKC specific binding			(AB005549) atypical PKC specific binding protein [Rattus	
1813	AB005549	protein, complete cds	7e-97	3868778	norvegicus]	3e-41
1814	X90849	G.gallus PB l gene	 2e-97	2134381	polybromo 1 protein - chicken chicken >gi 951231 (X90849) polybromo 1 protein [Gallus	
	1336 9	h-lamp-2=lysosome- associated membrane protein-2 protein-2b (LAMP2) mRNA, alternatively spliced form h-lamp-2b,	26-97	2134361	gallus]	le-34
1815	S79873	complete cds.	3e-98	<none></none>	<none></none>	<none></none>
1816		Mus musculus ACF7 neural isoform 1 (mACF7) mRNA, partial cds	2e-98	1675224	(U67204) ACF7 neural isoform 2 [Mus musculus]	9e-39
1817	_	Rattus norvegicus nuclear-encoded mitochondrial elongation factor G mRNA, complete cds.	e-100	585084	ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G) >gi 543383 pir S40780 translation elongation factor G, mitochondrial - rat >gi 310102	2e-30
1818	1	M.musculus Spnr mRNA for RNA pinding protein	e-133		spermatid perinuclear RNA- binding protein Spnr - mouse >gi 673454 (X84692) spermatid perinuclear RNA binding	
	I c r	Rattus norvegicus cardiac adriamycin esponsive protein		1363238	cytokine inducible nuclear protein C193 - human >gi 793841 (X83703) nuclear	5e-35
1819	F	nRNA, complete cds HoxB9=Hox-2.5	e-113	1362781	protein [Homo sapiens]	2e-36
1820	ļn	mice, embryos, nRNA Partíal, 786	e-107	1708355	HOMEOBOX PROTEIN HOX- B9 (HOX-2.5)	Se-37

	Nea Nea	rest Neighbor (BlastN v	s. Genbank)	Nearest Nei	ighbor (BlastX vs. Non-Redundant P	
	EQ				2.1501-Redundant P	roteins)
-	ID ACCESS		PVALUE	ACCESSION	DESCRIPTION	D.,,,,
<u> </u>		HoxB9=Hox-2.5		†	- Joseph How	P VALU
		[mice, embryos, mRNA Partial, 786				
11	321 S6685	nt]	e-108	1708355	HOMEOBOX PROTEIN HOX- B9 (HOX-2.5)	4e-37
<u>ا</u>	200	Rattus norvegicus n tomosyn mRNA,	n-		(U92072) m-tomosyn [Rattus	40-37
1.0	22 U9207:	complete cds	e-102	3790389	norvegicus]	2e-38
18	23 D17577	Mouse mRNA for kinesin-like protein (Kiflb), complete co		2497524	KINESIN-LIKE PROTEIN KIF1B mouse >gi 407339 gn1 PID d1005029 (D17577) Kif1b [Mus musculus]	2e-39
181	24 AF06248	Mus musculus SDP8		3126981	(AF062484) SDP8 [Mus	26-39
		R.norvegicus mRNA		3120981	musculus] (H3.3Q) histone H3.3 - fruit fly (Drosophila melanogaster) histone H3.3B - chicken >gi 2119023 pir S61218 histone H3.3 - fruit fly (Drosophila hydei) 1-136) [Oryctolagus cuniculus] >gi 8046 (X53822) Histone H3.3Q gene product [Drosophila melanogaster] >gi 51198 gallus] >gi 161190 (M17876) histone H3 [Spisula solidissima] >gi 211853 (M11393) histone 3.3 [Gallus gallus] >gi 306848 (M11354) H3.3 histone [Homo sapiens] melanogaster] >gi 963031 (X81205) histone H3.3 H3.3A variant [Drosophila	5e-40
1825	X73683	for histone H3.3	e-109	122075	melanogaster] musculus]	2e-40
1826	U67203	Mus musculus ACF7 neural isoform 1 (mACF7) mRNA, partial cds	e-102	1675224	(U67204) ACF7 neural isoform 2 [Mus muscalus] KINESIN-LIKE PROTEIN	2e-40
1827	D17577	Mouse mRNA for kinesin-like protein (Kif1b), complete cds	e-131		KIFtB mouse >gi 407339 gn PID d1005029 (D17577) K::1b [Mus	7e-42

3 3	Neares	st Neighbor (BlastN vs. C	renbank)	None N. i.	the (DI)	
SE		1	1	ivemest ivers	zhbor (BlastX vs. Non-Redundant F	roteins)
П	· [N DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
-		Criscolius				
	1	Cricetulus griseus	}	1		
ł		Phosphatidylglycerop			LA BOLGORO	j
- 1		hosphate synthase,	1		(AB016930)	
182	8 AB016930		e-131	4159682	Phosphatidylglycerophosphate synthase [Cricetulus griseus]	3 40
					syndiase (Cricetulus griseus)	3e-43
182		Mus musculus SKD3	j		SKD3 PROTEIN SKD3 [Mus	1
102	9 U09874	mRNA, complete cds.	e-122	2493735	musculus]	7e-48
	ł	C.familiaris mRNA			(X99145) overexpressed in	
183	0 X99145	for C3VS protein	e-110	1420214	thyroid tissue after TSH	1
		P.walti mRNA for	- 6-110	1429314	stimulation [Canis familiaris]	2e-49
	1 .	rnp associated protein			(X99836) rap55 [Pleurodeles	
183	i X99836	55	e-106	4200286	waiti]	2e-50
.	1	24				20 30
İ	ı	Mus musculus SH3 domain-containing				! !
-	i	adapter protein			(AF077003) SH3 domain-	i i
1832	AF077003	mRNA. complete cds	e-121	3550240	containing adapter protein;	
			0 .2.	3330240	CD2AP	3c-51
1	1	Mus musculus strain	•			
-	ł	C57BL/6 zinc finger]
	I	protein 106 (Zfp106)	J			
1833	AF060246	mRNA, H3a-a allele, complete cds		22204	(AF060246) zinc finger protein	
	112 0002-10	complete cus	e-118	3372657	106 [Mus musculus] TRANSLOCON-	1e-52
			i		ASSOCIATED PROTEIN.	
1]			•	GAMMA SUBUNIT (TRAP-	
1			1		GAMMA) (SIGNAL	1
ļ	j ,		İ		SEQUENCE RECEPTOR	į
]			1		GAMMA SUBUNIT) (SSR-	
	i	R.norvegicus mRNA			GAMMA)	- 1
		for TRAP-complex	1		>gi 423185 pir S33294	
1834		gamma subunit.	e-120	1174453	translocon-associated protein gamma chain - rat norvegicus]	
				1174455	gattitia chain - rat norvegicus)	7e-54
		Mus musculus SH3	ļ		1	
]]		domain-containing	- 1	1	(AF077003) SH3 domain-	1
1835		adapter protein			containing adapter protein;	[
1033	71077003	mRNA, complete cds	e-132	3550240	CD2AP	5e-54
	lı	Rattus norvegicus			(L20427)	1
		lihydroxypolyprenylb			dihydroxypolyprenylbenzoate methyltransferase	j
	6	enzoate	ł		dihydroxypoiyprenylbenzoate	•
,,,,		nethyltransferase			methyltransferase [Rattus	
1836	L20427 r	nRNA, complete cds	e-116		norvegicus	4e-56

	Neare	st Neighbor (BlastN vs	. Genbank)	Nearest Vei	ghbor (BlastX vs. Non-Redundant	
SE					gliddi (Blastic Vs. 140n-Redundant	Proteins)
п	ACCESSIO	DN DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
-					PROTEIN TSG24 (MEIOTIC	1
- 1	į į		ł		CHECK POINT	
183	V90160	M.musculus mRNA	· ·		REGULATOR)	1
10.	7 X80169	for 200 kD protein	e-122	1717793	>gi 1083553 pir A55117 tsg24	2e-56
		Rattus norvegicus CTP:phosphoethano amine cytidylyltransferase	st .		(AF080568)	2030
183	8 AF080568	mRNA. complete cd	s e-119	3306103	CTP:phosphoethanolamine	1
			3 6-119	3396102	cytidylyltransferase	6e-58
1839	X99145	C.familiaris mRNA for C3VS protein	e-121	1429314	(X99145) overexpressed in thyroid tissue after TSH stimulation [Canis familiaris]	2e-58
1840	AF019075	Pan troglodytes breas and ovarian cancer susceptibility (BRCA1) gene, partial cds	e-145	2218154	(AF005068) breast and ovarian cancer susceptibility protein	20-30
		Bos taurus myosin X.	6145	2210134	splice variant [Homo sapiens]	1e-58
1841	U55042	complete cds	e-122	1755049	(U55042) myosin X [Bos taurus]	le-61
1842	AJ007780	Mus musculus mRNA for poly(ADP-ribose) polymerase-2 Rattus norvegicus		3283975	(AF072521) poly-(ADPribosyl)- transferase homolog PARP	4e-62
1843	AF072865	thioredoxin reductase (TrxR2) mRNA, nuclear gene encoding mitochondrial protein, complete cds	e-105	3757888	(AF072865) thioredoxin reductase [Rattus norvegicus]	3e-62
1844		Bos taurus myosin X,			(U55042) myosin X [Bos	30-02
1044	U55042	complete cds	e-121	1755049	taurus]	le-62
1845		Mouse E46 mRNA for E46 protein	e-139	114909	PRAIN PROTENTE	
1846	D90335	Bovine mRNA for GTP-binding protein alpha-subunit	e-148	585174	BRAIN PROTEIN E46 GUANINE NUCLEOTIDE- BINDING PROTEIN, ALPHA- 14 SUBUNIT (GL1) >gi 108711 pir A40891 GTP- binding protein GL1 alpha chain - bovine protein, alpha-subunit [Bos taurus]	9e-67.
- 1		Vius musculus			(= == remina)	2e-69
1847		B6CBA Lisch7 nRNA, partial cds.	e-140		(AC002128) Lisch7 [Homo sapiens]	2e-7 ∔

Table 4

	Nearest I	Neighbor (BlastN vs.	Genbank)	Nearest Neig	ghbor (BlastX vs. Non-Redundant F	Peneria :
SEQ			7		This is a second and the second and	roteins)
ΙD	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
<u> </u>	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>
2	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>
3	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>
4	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>
5	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>
6	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>
7	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>
8	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>
9	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>
10	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>
11	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>
12	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>
13	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>
14	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>	
15	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>
16	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>	
17	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>
_18	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>	
19	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>
20	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>
21	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>
_22	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>	<none></none>
					tMDC I protein - crab-eating	<none></none>
23	<none></none>	<none></none>	<none></none>	1079469	macaque	
				2077107	(AB011138) KIAA0566 protein	9.3
24	<none></none>	<none></none>	<none></none>	3043656	[Homo sapiens]	
				20 13030	[Tionio sapiens]	9.3
- 1	1				potassium channel protein RK5 -	
25	<none></none>	<none></none>	<none></none>	112175		0.6
			1.101.12	1121/3	rat protein [Rattus norvegicus] (AF091565) olfactory receptor	8.6
26	<none></none>	<none></none>	<none></none>	3769624		
			VA.O.N.E	3709024	[Rattus norvegicus] (Z81517) F28B1.6	7.2
27	<none></none>	<none></none>	<none></none>	3876443]
			- CANOLILES	3070443	[Caenorhabditis elegans]	7.1
28	<none></none>	<none></none>	<none></none>	2224464	(AB001684) ORF249 [Chlorella	
		2.02	VI TOTAL >	2224404	vulgaris] (U67940) ORFveg106; random	6.9
- 1	l		!			1
29	<none></none>	<none></none>	<none></none>	1510707	cDNA sequence [Dictyostelium	
		C. (OI)E	VIVOIVE)	1519707	[discoideum]	6.7
30	<none></none>	<none></none>	<none></none>	227101	protein kinase C II [Xenopus	
		- CITORIES	CHOINES	227491	laevis]	6.7
31	<none></none>	<none></none>	NONE	(20:25	C50C3.4 protein -	1
		CINOINE	<none></none>	630575	Caenorhabditis elegans	6.0
		J	1		35 KD PROTEIN IN RNA2	1
	1	ļ	1		clover necrotic mosaic virus	į
	1.	[}		>gi 61466 (X08021) ORF for 35	1
1	1		1		kDa polypeptide (AA-1-317)	i
32	<none></none>	NOMES	NONE		[Red clover necrotic mosaic	j
<u>1</u>	NIONE >	<none></none>	<none></none>	137290	virus]	6.0

		earest N	leighbor (BlastN v	s. Genbank)	Nearest N	leighbor (BlastX vs. Non-Redundant F	
- 1	EQ D ACCES		DESCRIPTION				Proteins) P VALU
3	3 <no< td=""><td>JE.</td><td>-NONE-</td><td></td><td></td><td>(X16711) pid:g30041 [Homo</td><td>IF VALU</td></no<>	JE.	-NONE-			(X16711) pid:g30041 [Homo	IF VALU
	1	'''' 	<none></none>	<none< td=""><td>> 30041</td><td>sapiens</td><td>5.9</td></none<>	> 30041	sapiens	5.9
.3	4 <non< td=""><td>πE></td><td><none></none></td><td><none< td=""><td></td><td>CELL DIVISION PROTEIN</td><td>1</td></none<></td></non<>	πE>	<none></none>	<none< td=""><td></td><td>CELL DIVISION PROTEIN</td><td>1</td></none<>		CELL DIVISION PROTEIN	1
3	5 <non< td=""><td>TE></td><td><none></none></td><td><none< td=""><td>2175505</td><td>FTSW</td><td>5.7</td></none<></td></non<>	TE>	<none></none>	<none< td=""><td>2175505</td><td>FTSW</td><td>5.7</td></none<>	2175505	FTSW	5.7
				KNONE	> 1001450	(D63999) hypothetical protein	5.7
30	6 <non< td=""><td>E></td><td> <none></none></td><td><none:< td=""><td>3182918</td><td>NITROGEN REGULATORY</td><td></td></none:<></td></non<>	E>	<none></none>	<none:< td=""><td>3182918</td><td>NITROGEN REGULATORY</td><td></td></none:<>	3182918	NITROGEN REGULATORY	
	i				3102918	PROTEIN AREA MITOCHONDRIAL	5.2
				İ		RIBOSOMAL PROTEIN S5	
		- 1		i		Emericella nidulans]
			•	1		mitochondrion (SGC3)	
37	NON	G.	MONT		· ·	>gi 12709 nidulans] >gi 472822	
	41014	-	<none></none>	<none></none>	140011	(J01390) unknown protein	4.3
				j		(AL034393) predicted using	7.3
	1			1		Genefinder; similar to WD	
	ł	1	•	I	1	domain, G-beta repeat; cDNA	
					1	EST yk362f7.5 comes from this	
	1	- 1		1		gene; cDNA EST yk362f7.3	
38	<none< td=""><td>></td><td><none></none></td><td><none></none></td><td>3979943</td><td>comes from this gene</td><td></td></none<>	>	<none></none>	<none></none>	3979943	comes from this gene	
39					37.7743	[Caenorhabditis elegans] (U31329) polyketide synthase	4.0
39	<none< td=""><td>> </td><td><none></none></td><td><none></none></td><td>950203</td><td>[Aspergillus terreus]</td><td> [</td></none<>	>	<none></none>	<none></none>	950203	[Aspergillus terreus]	[
		ĺ				it ispergritus terreus;	3.3
	Í	- 1		1		(AL031530) hypothetical zinc	l
40	<none:< td=""><td>. </td><td><none></none></td><td></td><td></td><td>finger protein</td><td></td></none:<>	.	<none></none>			finger protein	
		_	CIVOIVES	<none></none>	3560232	[Schizosaccharomyces pombe]	3.0
	ł	- 1			i	AXONEME-ASSOCIATED	
41	<none:< td=""><td></td><td><none></none></td><td><none></none></td><td>730071</td><td>PROTEIN MST101(1) product</td><td>1</td></none:<>		<none></none>	<none></none>	730071	PROTEIN MST101(1) product	1
					73007,1	[Drosophila hydei] HYPOTHETICAL 21.7 KD	2.6
ı		ł				PROTEIN IN INTE-PIN	
		- [INTERGENIC REGION	1
			,			>gi 1787402 (AE000214) orf,	- 1
12	<none></none>		NO. 77			hypothetical protein	
-	NONE>	+-	<none></none>	<none></none>	2506641	[Escherichia coli]	2.5
3	<none></none>		<none></none>	270275		(AF071556) anthranilate	
		+	CITORES	<none></none>	3511232	dioxygenase large subunit	2.4
- 1			į	1			
- 1		1				(U43139) envelope glycoprotein	İ
4	<none></none>		<none></none>	<none></none>	1150900	gp120 [Human	
					1120900	immunodeficiency virus type 1] (Z75536) similar to dynein	1.9
1			1	1		heavy chain; cDNA EST	1
1				i		EMBL:D27549 comes from this	- 1
1		1		ł		gene; cDNA EST	1
	<none></none>	l	NONE	1		EMBL:D34859 comes from this	
	SHORES		<none></none>	<none></none>	3876099	gene [Caenorhabditis elegans]	1

PCT/US00/18374

SEQ ID ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE Bkm-like sex-determining region hypothetical protein CS314 - fruit fly (Drosophila melanogaster) 2e-04 (AF038604) contains similarily to Drosophila ovarian tumor locus protein (GEX.13693) (Caenorhabditis segans) 6e-05 (AL033501) phox domain protein (Candida albicans) 3e-05 (CAENDA BINDING FACTOR GCF - human >gil179412 (M29204) (AF03386) FS9E12.5 gene product (Caenorhabditis) 2e-08 (CRICH SEQUENCE DNA-BINDING FACTOR GCF - human >gil179412 (M29204) DNA-binding factor (Homo sapiens) 2e-08 (CRICH SEQUENCE DNA-BINDING FACTOR GCF - human >gil179412 (M29204) DNA-binding factor (Homo sapiens) 2e-09 (CRICH SEQUENCE DNA-BINDING FACTOR GCF - human >gil179412 (M29204) DNA-binding factor (Homo sapiens) 2e-09 (CRICH SEQUENCE DNA-BINDING FACTOR GCF - human >gil179412 (M29204) DNA-binding factor (Homo sapiens) 2e-09 (CRICH SEQUENCE DNA-BINDING FACTOR GCF - human >gil179412 (M29204) 2e-09 (CRICH SEQUENCE DNA-BINDING FACTOR GCF - human >gil179412 (M29204) 2e-09 (CRICH SEQUENCE DNA-BINDING FACTOR GCF - human >gil179412 (M29204) 2e-09 (CRICH SEQUENCE DNA-BINDING FACTOR GCF - human >gil179412 (M29204) 2e-09 (CRICH SEQUENCE DNA-BINDING FACTOR GCF - human >gil179412 (M29204) 2e-09 (CRICH SEQUENCE DNA-BINDING FACTOR GCF - human >gil179412 (M29204) 2e-09 (CRICH SEQUENCE DNA-BINDING FACTOR GCF - human >gil179412 (M29204) 2e-09 (CRICH SEQUENCE DNA-BINDING FACTOR GCF - human >gil179412 (M29204) 2e-09 (CRICH SEQUENCE DNA-BINDING FACTOR GCF - human >gil179412 (M29204) 2e-09 (CRICH SEQUENCE DNA-BINDING FACTOR GCF - human >gil179412 (M29204) 2e-09 (CRICH SEQUENCE DNA-BINDING FACTOR GCF - human >gil179412 (M29204) 2e-09 (CRICH SEQUENCE DNA-BINDING FACTOR GCF - human >gil179412 (M29204) 2e-09 (CRICH SEQUENCE DNA-BINDING FACTOR GCF - human >gil179412 (M29204) 2e-09 (CRICH SEQUENCE DNA-BINDING FACTOR GCF - human >gil179412 (M29204) 2e-09 2e-09 2e-09 2e-09	×	Nearest	Neighbor (BlastN vs. (Genbank)	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
ID ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE Bkm-like sex-determining region hypothetical protein CS314 - fruit fly (Drosophila melanogaster) 2e-04 (AF038604) contains similarity to Drosophila ovarian tumor locus protein (GE:X16993) 6e-05 (AF038604) contains similarity to Drosophila ovarian tumor locus protein (GE:X16993) 6e-05 (AF038604) contains similarity to Drosophila ovarian tumor locus protein (GE:X16993) 6e-05 (AF033804) contains similarity to Drosophila ovarian tumor locus protein (GE:X16993) 6e-05 (AF033804) pox domain protein (GE:X16993) 6e-05 (AF033804) pox domain protein (GE:X16993) 700 70	SEQ							
S7	_	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
S7					1	Bkm-like sex-determining	1	
S7						region hypothetical protein	<u> </u>	
57				1	j		ļ	
S8	57	<none></none>	<none></none>	<none></none>	103076		2e-04	
S8						(AF038604) contains similarity		
58		•		ł		to Drosophila ovarian tumor	1	
Section Sect						locus protein (GB:X13693)	ļ	
SP	58	<none></none>	<none></none>	<none></none>	2702370		6e-05	
AFO03386) F59E12.5 gene product [Caenorhabditis elegans] 2e-08						(AL033501) phox domain		
Content Cont	59	<none></none>	<none></none>	<none></none>	3859713		3e-05	
Content Con	i					(AF003386) F59E12.5 gene		
GC-RICH SEQUENCE DNA-BINDING FACTOR GCF - human > gil 1794 2 (M2) 204				1	•	product [Caenorhabditis		
BINDING FACTOR GCF -	60	<none></none>	<none></none>	<none></none>	2088839		2e-08	
NONE NONE		-				-		
ONNE			,					
CNONE CNONE CNONE CNONE CASTANU Stapiens CASTANU Stapiens CASTANU Stapiens CASTANU Stapiens CASTANU Stapiens CASTANU Stapiens CASTANU Stapiens CASTANU CASTANU Stapiens CASTANU CAST	l			1 1				
(281490) similar to WD	1					DNA-binding factor [Homo		
domain, G-beta repeats (2 domains); cDNA EST EMBL:T00482 comes from this gene; cDNA EST EMBL:T00923 comes from this gene; cDNA EST EMBL:T00923 comes from this gene; cDNA EST yk449d4.3 comes from this gene; cDNA EST yk449d4.3 comes from this gene; cDNA EST yk449d4.5 comes from this gene; cDNA EST yk449d4.5 comes from this gene; cDNA EST yk49d4.5 comes from this gene; cDNA EST yk49d4.5 comes from this gene; cDNA EST yk49d4.5 comes from this gene; cDNA EST yk49d4.5 comes from this gene	61	<none></none>	<none></none>	<none></none>	121059	sapiens]	4e-09	
domains); cDNA EST				1 1				
EMBL:T00482 comes from this gene; cDNA EST EMBL:T00923 comes from this gene; cDNA EST EMBL:T00923 comes from this gene; cDNA EST yk449d4.3 comes from this gene; cDNA EST yk449d4.5 comes from this gene; cDNA EST yk449d4.5 comes from this gene; cDNA EST yk449d4.5 comes from this gen 9e-24				1				
gene; cDNA EST EMBL:T00923 comes from this gene; cDNA EST yk449d4.3 comes from this gene; cDNA EST yk449d4.3 comes from this gene; cDNA EST yk449d4.5 comes from this gene; cDNA EST yk449d4.5 comes from this gene; cDNA EST yk449d4.5 comes from this gene; cDNA EST yk449d4.5 comes from this gene; cDNA EST yk49d4.5 comes from this gene; cDNA EST yk49d4.5 comes from this gene; cDNA EST EMBL:CO917 kimilar to mitochondrial RNA splicing manual round in gene; cDNA EST EMBL:CO9217 comes from this gene [Caenorhabditis elegans] Rat annexin V gene; cNONE> NONE>	1			i l		1		
EMBL:T00923 comes from this gene; cDNA EST yk449d4.3 comes from this gene; cDNA EST yk449d4.3 comes from this gene; cDNA EST yk449d4.5 comes from this gene; cDNA EST yk449d4.5 comes from this gene; cDNA EST yk449d4.5 comes from this gene; cDNA EST yk449d4.5 comes from this gene; cDNA EST yk449d4.5 comes from this gene 9e-24 (U64857) No definition line found [Caenorhabditis elegans] 9e-28 (AB014561) K1AA0661 protein [Homo sapiens] 1e-29 (Z66521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:C09217 comes from this gene [Caenorhabditis elegans] 8e-31 Rat annexin V gene, exon7 and exon8 5.0 <none> (V41278) coded for by C. elegans cDNA yk79g8.5; coded for by C. elegans cDNA yk79g8.5; coded for by C. elegans cDNA yk79g8.3; similar to (subclone H8 2_d11 from P1 35 H5 C8)</none>	1						1	
gene; cDNA EST yk449d4.3 comes from this gene; cDNA EST yk449d4.5 comes from this gene; cDNA EST yk449d4.5 comes from this gene; cDNA EST yk449d4.5 comes from this gene 9e-24				İ		15		
Comes from this gene; cDNA EST yk449d4.5 comes from this gen 9e-24	ľ							
62 <none> <none> <none> 3875246 EST yk449d4.5 comes from this gen 9e-24 (U64857) No definition line found [Caenorhabditis elegans] 9e-28 (AB014561) KIAA0661 protein [Homo sapiens] 1e-29 (Z66521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:C09217 comes from this gene [Caenorhabditis elegans] 8e-31 Rat annexin V gene, exon7 and exon8 5.0 <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> CHegans cDNA yk79g8.5; coded for by C. elegans cDNA yk79g8.3; similar to leucine-rich repeats found in many proteins [Caenorhabditis</none></none></none></none></none></none></none></none></none></none></none></none></none>								
62								
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63 <none> <none> <none> <none> 1465834 found [Caenorhabditis elegans] 9e-28 (AB014561) KIAA0661 protein [Homo sapiens] 1e-29 (Z66521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:C09217 comes from this gene [Caenorhabditis elegans] 8e-31 Rat annexin V gene, exon7 and exon8 5.0 <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <no< td=""><td>62</td><td><none></none></td><td><none></none></td><td><none></none></td><td>3875246</td><td>gen</td><td>9e-24</td></no<></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none>	62	<none></none>	<none></none>	<none></none>	3875246	gen	9e-24	
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64 <none> <none> <none> 3327136</none></none></none>	<i>c</i> 2	NONTE	NONE:	1,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	1465004			
64 <none> <none> <none> 3327136 [Homo sapiens] 1e-29 (Z66521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:C09217 comes from this gene [Caenorhabditis elegans] 8e-31 Rat annexin V gene, exon7 and exon8 5.0 <none> <none> <none> <none> <none> <none> <none> <none> <none> <iu41278) [caenorhabditis]<="" by="" c.="" cdna="" coded="" elegans="" for="" found="" in="" leucine-rich="" many="" proteins="" repeats="" similar="" td="" to="" yk79g8.3;="" yk79g8.5;=""><td>0.5</td><td>CNOINE></td><td><nune></nune></td><td><nune></nune></td><td>1403834</td><td></td><td>9e-28</td></iu41278)></none></none></none></none></none></none></none></none></none></none></none></none>	0.5	CNOINE>	<nune></nune>	<nune></nune>	1403834		9e-28	
(Z66521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:C09217 comes from this gene [Caenorhabditis elegans] 8e-31 Rat annexin V gene, exon7 and exon8 5.0 <none> <none> <none> <none> <none> <none> <none> <none> <i [caenorhabditis]<="" by="" c.="" cdna="" cm10c8;="" coded="" elegans="" for="" found="" in="" leucine-rich="" many="" proteins="" repeats="" similar="" td="" to="" u41278)="" yk79g8.3;="" yk79g8.5;=""><td>64</td><td>NONE</td><td>-NONTS</td><td> NONE</td><td>2227126</td><td></td><td>120</td></i></none></none></none></none></none></none></none></none>	64	NONE	-NONTS	NONE	2227126		120	
mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:C09217 comes from this gene [Caenorhabditis elegans] Rat annexin V gene, exon7 and exon8 5.0 NONE> NONE> NONE> NONE> NONE> NONE> (U41278) coded for by C. elegans cDNA yk79g8.5; coded for by C. elegans cDNA cm10c8; coded for by C. elegans cDNA yk79g8.3; similar to (subclone H8 2_d11 from P1 35 H5 C8) mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:C09217 comes from this gene [Caenorhabditis elegans] 8e-31 (U41278) coded for by C. elegans cDNA cm10c8; coded for by C. elegans cDNA yk79g8.3; similar to leucine-rich repeats found in many proteins [Caenorhabditis]	-04	<none></none>	<inoine></inoine>	<nune></nune>	332/136	(766521) similar to	1e-29	
MSR4 like protein; cDNA EST EMBL:C09217 comes from this gene [Caenorhabditis elegans] 8e-31 Rat annexin V gene, exon7 and exon8 5.0 <none> <none> <none> <none> <none> <none> <none> Homo sapiens (subclone H8 2_dl l from P1 35 H5 C8) MSR4 like protein; cDNA EST EMBL:C09217 comes from this gene [Caenorhabditis elegans] 8e-31 NONE> <none> <none> <none> <none> </none> </none> </none> </none> <none> </none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none> <none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none></none>				! !				
EMBL:C09217 comes from this gene [Caenorhabditis elegans] Rat annexin V gene, exon7 and exon8 5.0 NONE> NONE NO	ſ	ļ						
65 <none> <none> <none> 3880433 gene [Caenorhabditis elegans] 8e-31 Rat annexin V gene, exon7 and exon8 5.0 <none> <none> <none> <none> <none> (U41278) coded for by C. elegans cDNA yk79g8.5; coded for by C. elegans cDNA cm10c8; coded for by C. elegans cDNA yk79g8.3; similar to (subclone H8 2_d11 from P1 35 H5 C8) Control of the c</none></none></none></none></none></none></none></none>	- 1					, .		
Rat annexin V gene, exon7 and exon8 5.0 <none> <none> <none> <none> <none> (U41278) coded for by C. elegans cDNA yk79g8.5; coded for by C. elegans cDNA cm10c8; coded for by C. elegans cDNA yk79g8.3; similar to (subclone H8 2_dl l from P1 35 H5 C8) leucine-rich repeats found in many proteins [Caenorhabditis]</none></none></none></none></none>	65	<none \<="" td=""><td><none></none></td><td>NONE</td><td>3880/133</td><td></td><td>80.31</td></none>	<none></none>	NONE	3880/133		80.31	
66 D42133 exon7 and exon8 5.0 <none> <none> <none> <none> <none> <none> (U41278) coded for by C. elegans cDNA yk79g8.5; coded for by C. elegans cDNA cm10c8; coded for by C. elegans cDNA yk79g8.3; similar to (subclone H8 2_d11 from P1 35 H5 C8) leucine-rich repeats found in many proteins [Caenorhabditis]</none></none></none></none></none></none>	 +			2110112	3000433	[gene [Caenomaudius elegans]	96-31	
(U41278) coded for by C. elegans cDNA yk79g8.5; coded for by C. elegans cDNA cm10c8; coded for by C. elegans cDNA yk79g8.3; similar to (subclone H8 2_d11 from P1 35 H5 C8) (U41278) coded for by C. elegans cDNA yk79g8.3; similar to leucine-rich repeats found in many proteins [Caenorhabditis	66			5.0	<nonf></nonf>	<nonf></nonf>	<none></none>	
elegans cDNA yk79g8.5; coded for by C. elegans cDNA cm10c8; coded for by C. elegans cDNA cm10c8; coded for by C. elegans cDNA yk79g8.3; similar to (subclone H8 2_dl l leucine-rich repeats found in from P1 35 H5 C8)			Chair and Chono		110112	(U41278) coded for by C.	31101127	
for by C. elegans cDNA cm10c8; coded for by C. elegans Homo sapiens cDNA yk79g8.3; similar to (subclone H8 2_dl1 from P1 35 H5 C8) leucine-rich repeats found in many proteins [Caenorhabditis	- 1	1		l l				
cm10c8; coded for by C. elegans Homo sapiens (subclone H8 2_dl1 from P1 35 H5 C8) cm10c8; coded for by C. elegans cDNA yk79g8.3; similar to leucine-rich repeats found in many proteins [Caenorhabditis]	- 1		•	ĺ				
Homo sapiens (subclone H8 2_dl l leucine-rich repeats found in from P1 35 H5 C8) CDNA yk79g8.3; similar to leucine-rich repeats found in many proteins [Caenorhabditis	-	ļ						
(subclone H8 2_dl l leucine-rich repeats found in from P1 35 H5 C8) leucine-rich repeats found in many proteins [Caenorhabditis	1	ŀ	Homo sapiens		•			
from P1 35 H5 C8) many proteins [Caenorhabditis	1							
67 L35679 DNA sequence. 5.0 1086902 elegans] 6.6	67		DNA sequence.	5.0	1086902	1	6.6	

	Nearest	Neighbor (BlastN vs. (Genbank)	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEC			1	- Tousest Iveig	1001 (Blasta Vs. Non-Redundant Pr	roteins)	
ID	- I		P VALUE	ACCESSION	DESCRIPTION	P VALUE	
<u> </u>	 	HIV-1 strain BX220					
1	1	from USA, envelope				 	
1	I	glycoprotein C2V3	1			!	
68	1100194	region (env) gene,	1		(Z71986) convicilin precursor		
100	U90184	partial cds Human myosin VIIa	5.0	1297070	[Vicia narbonensis]	6.6	
		(MYO7A) gene, 5'			(AE000535) L-lactate permease		
69	U61465	exon 37	5.0	2313225	(lctP) [Helicobacter pylori		
	1	exon 57	3.0	2313223	26695] (AF064869) brain-enriched	5.0	
1		Homo sapiens		1	guanylate kinase-associated		
		periplakin (PPL)	ļ ·		protein 2; BEGA2 [Rattus		
70	AF013717	mRNA, partial cds	5.0	3719238	norvegicus)	3.8	
1		Soybean mRNA for				3.6	
71	X58245	HMG-1 like protein	5.0	2995363	(AL022245) biotin synthase	0.99	
	1						
		Frasera paniculata					
		tRNA-Leu (tmL)		•	(AC004411) putative		
72	AF102425	gene, intron,			pectinesterase [Arabidopsis		
-/-	AF102423	chloroplast sequence	4.9	3522958	thaliana] (Z81494) CDINA EST	6.4	
					EMBL:D27474 comes from this		
					gene; cDNA EST		
			j		EMBL:D27473 comes from this		
					gene; cDNA EST		
					EMBL:T00471 comes from this		
					gene; cDNA EST		
]			EMBL:D34192 comes from this		
(H.sapiens	ł		gene; cDNA EST		
		PTP1C/HCP-variant	.1		EMBL:D37241 comes from this	Ì	
73	X82817	gene	4.9	3875514	gene;	2.8	
		j	- 1				
		}	ľ		(AL031765) 1-		
- 1	1	.	•	* 💉	evidence=predicted by content;	•	
	ĺ		ľ		1-method=genefinder;084; 1-		
					method_score=31.96; 1-	4	
					evidence_end; 2-	ł	
		1	[,	evidence=predicted by match; 2-	ļ	
I	1	1	į.		match_accession=SPTREMBL:	İ	
J		Mus musculus brain	j		Q93319; 2-		
		atty acid-binding			match_description=HYPOTHE		
74	U04827 p	protein	4.9	3676132	TICAL PROTEIN C33A11.2.;	2e-09_	
- 1	1.	Janana hustani					
-		Neospora hughesi train NE1 internal	1				
- 1		ranscribed spacer 1,	I				
75		omplete sequence	4.8	NONE.	No.		
	55057	opiete sequence	7.0	<none></none>	<none></none>	<none></none>	

		Near	est Neighbor (BlastN vs				
	-		est regindor (Blastia vs	. Genbank)	Nearest Nei	ghbor (BlastX vs. Non-Redundan	(Proteins)
•	SEQ	- 1		j			
		ACCESSI	ON DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	İ
			M.musculus MFH-		1	DESCRIPTION	P VALUE
	76	Y08222		4.8	<none></none>		
			Borrelia burgdorfer		TONES	<none></none>	<none></none>
i		1	left chromosomal		ľ		
		1	subtelomeric region	ĺ			1
ı	77	AJ22447		4.8	4210141	(AJ236702) HMR1 protein	j
			Mus musculus LAF	7.0	4218141	[Antimhinum majus]	8.3
ı			putative membrane	[
j		l	protein (KRAG)	1			i i
- 1			gene, exon 3 and			(AP000006) 367aa long	
	78	U02486	complete cds	4.8	2050100	hypothetical protein	
Γ			Rat mRNA for	4.0	3258103	[Pyrococcus horikoshii]	2.7
1			peptide/histidine	ŀ	ŀ		
-			transporter, complete	.]	j] }
-	79	AB000280	cds	4.8	9963.5	(M29067) unknown protein	1 1
Γ				+-0	806317	[Saccharomyces cerevisiae]	100.0
-1	ı		A.cepa mitochondria	1	I		
ĺ			gene for NADH	1	j	1	1 1
	ı		dehydrogenase'		ł		1 1
	- 1	•	subunit 3 and		ł	ļ	1
	ı		ribosomal protein				ľ
	80	Z49771	S12	4.5		1	1 1
			Mouse IgG receptor	4.5	<none></none>	<none></none>	<none></none>
	ı		(beta-Fc-gamma-RII)	ĺ			
	ł		gene, exons 6 and 7,			1:	1
1	ı		clones lambda-) [i	1 1
	81	M63494	Fc(3.2,93).	1 1			1 1
			1 0(3.2,73).	4.3	<none></none>	<none></none>	<none></none>
			1	1			
1 :	82	Z14035	S.pombe carl gene	20	200011	(AF099000) No definition line	1
			Rhodococcus	2.0	3790665	found [Caenorhabditis elegans]	1.2
l	- 1		erythropolis The A	1		(AL021687) putative protein	
1			(thcA) gene, complete	i		[Arabidopsis thaliana]	1 1
		-	cds; and unknown			>gi 2832633 gnl PID e1249651	j ·
8	33	U17129	genes	20	******	(AL021711) putative protein	J . 1
			Plasmodium	2.0	2828280	[Arabidopsis thaliana]	2e-26
	1		falciparum	- 1			7
ĺ			chromosome 2,	ŀ			
			section 23 of 73 of				
			the complete	}			
8	4 7	AE001386	sequence	20		(AL031177) dJ889M15.3 (novel	
	- -		Human clone 23734	2.0	4176500	protein)	9e-59
8:	5		mRNA sequence		[
	_		Chloroplast Euglena	1.9	<none></none>	<none></none>	<none></none>
			gracilis gene coding	1			
	- 1		for the 5S and 16S	- 1	1	.]	1
86	5 		rRNA.	1	1	,	I
		30.37	IMIA.	1.9	<none></none>	<none></none>	<none></none>

<u> </u>	Neare	st Neighbor (BlastN vs.	Genbank)	Nearest Ne	ighbor (BlackY up Now De L	
SEQ			T	1100.031710	ighbor (BlastX vs. Non-Redundant	Proteins)
ID	ACCESSIO		P VALUE	ACCESSION	N DESCRIPTION	P VAL
-	 	Xenopus laevis XL-				II VAL
ł	İ	INCENP (XL-				
87		INCENP) mRNA,		i		1
-8/	U95094	complete cds	1.9	<none></none>	<none></none>	
	•	H.salinarium TATA			CITONES	<non!< td=""></non!<>
88	Young	box-binding protein	`	j	-1.	Í
00	X93206	genes and ORFs	1.9	<none></none>	<none></none>	<non!< td=""></non!<>
		Carrie I I I II	1		1.0112	KNOM
•		Caenorhabditis	1	ĺ		1
		elegans programmed	l			
	•	cell death specifier	}		·	
89	1160070	(ces-2) gene,		•		1
~	U60979	complete cds	1.9	<none></none>	<none></none>	<none< td=""></none<>
90	X56272	C. tentans ORFs (A-]			TATOME
-~	X30272	E) for hemoglobin Homo sapiens DNA	1.9	<none></none>	<none></none>	<none< td=""></none<>
- 1			1		·	1
91	L22383	sequence, repeat region.				i
		Hirudo medicinalis	1.9	<none></none>	<none></none>	<none< td=""></none<>
ı		neuron-specific	ı I			
		protein mRNA,	ł		1	1
92	U82814	complete cds	1.9		(AF094531) immunoglobulin	1
		Haplomitrium	1.9	3822533	heavy chain precursor	2.0
1		hookeri 18S rRNA	i			
1		gene, partial	i		1	į
93	U18504	sequence.	1.9	1083969	hypothetical protein 6 - fowlpox	[
		Pseudomonas stutzeri		1003707	virus virus]	2.0
		nosDFY genes	ı			
.		involved in copper				
94	X53676	processing	1.9	2980781	(AL022198) putative protein	0.70
- 1		D			(2022196) putative protein	0.70
1		Dictyostelium	I			
- 1		discoideum multidrug	į.	•	1	
		resistance	1		(Z49130) cDNA EST	
ı		transporter/Ser	1		yk486b9.3 comes from this	
5		protease (tagC)			gene; cDNA EST yk486b9.5	
\dashv		mRNA, complete cds. Human purative G-	1.9	3879530	comes from this gene	6e-05
1		protein-coupled	1	- ·		
		receptor (GPR17)	I		(Z75550) similar to cell division	
5		gene. complete cds			control protein [Caenorhabditis	
		one. complete cus	1.9	3880034	elegans]	7e-1∔
1	İs	Sus scrofa lactoferrin	1			
ı		nRNA, complete cds.	ľ	•	1	
		:: gb I2\$421 I28421	l			ı
1		equence 5 from	I		1	ļ
1		atent US 5571691	1.8	NONE		ł
	•		4.0	<none></none>	<none></none>	NONE>

<u> </u>	Near	est Neighbor (BlastN vs.	Genbank)	Nearest Ne	eighbor (BlastX vs. Non-Redunda	
	EQ				Agricol (Blastix Vs. Non-Redunda	int Proteins)
	D ACCESS	ON DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION OF THE PROPERTY OF	1
		S.iniae lctP & lctO	1 VALUE	ACCESSION	N DESCRIPTION	P VALU
9	8 Y0762	genes and ORF1	1.8	ANONE		
			1.8	<none></none>	<none></none>	<none></none>
i	1		1	1 .		
	<u>I</u>	Mouse myristoylated	1	j		
-		alanine-rich C-kinase	e Í			1
1 .	.	substrate (MARCKS			1	İ
99	M60474	Tanada in Complete ed.	s. 1.8	<none></none>	<none></none>	
1		Homo sapiens FGFR			RIVONES	<none></none>
10	0 Y13901		1.8	<none></none>	<none></none>	4NOVE
i	- [Human Down	j		3,0,12	<none></none>
	ļ	Syndrome region of	1	• •		1 .
10	1 7744400	chromosome 21,				ĺ
10	U44400	clone A31D6-1D6.	1.8	<none></none>	<none></none>	<none></none>
1	I	Ruminococcus albus	! !			NATION LE
1		beta-glucosidase	. I			1 .
	1	(gluA) mRNA,]]		1	i i
102	U92808	complete cds			1	
	0>2000	Candida albicans	1.8	<none></none>	<none></none>	<none></none>
ł	1	argininosuccinate	!!!			
1	j.	lyase (ARG4) gene,	1 1		,	
103	L25051	complete cds.	1.8	<none></none>		1 1
		Helicobacter pylori		CHOINES	<none></none>	<none></none>
	1	26695 section 24 of			1	1 1
	1	134 of the complete	1			
104	AE000546	genome	1.8	<none></none>	<none></none>	
	İ	Xenopus laevis major			KINONES	<none></none>
		beta-globin gene,				1
105	J00978	complete cds.	1.8	<none></none>	<none></none>	<none></none>
	ł	Human	T		- THE STATE OF THE	KNONES
	j	immunodeficiency	I			
	ĺ	virus type 1 isolate	1.			1 1
106	U41716	JW95-5, vpr gene,	1		1	1 1
100	041716	complete cds.	1.8	<none></none>	<none></none>	<none></none>
107	X66286	G.gallus mRNA for tensin				1 1 1 1 1
	200200	Xenopus calbindin	1.8	<none></none>	<none></none>	<none></none>
		D28k mRNA,	l i			
108	U76636	complete cds	1.0	\10\1=		
		rabbit embryonic beta-	1.8	<none></none>	<none></none>	<none></none>
109	J00664	4-globin gene.	1.8	MONTE		
\neg			1.0	<none></none>	<none></none>	<none></none>
i		Human erg protein	1			1 1
ł		(ets-related gene)			(AE000602) L.]]
110	M21535	mRNA, complete cds.	1.8	2983160	(AE000693) hypothetical protein [Aquifex aeolicus]	1 1
				2703100	[Protein [Adultex acolicus]	7.7

		Neare	st Neighbor (BlastN vs.	Genbank)	Nearest Naid	hhor (Blact V N	
S	EQ				- Total Cat INC	hbor (BlastX vs. Non-Redundant Pr	oteins)
	D	ACCESSIO		P VALUE	ACCESSION	DESCRIPTION	P VALU
<u> </u>			Rat troponin T			(Z46595) incomplete interleukin	I VALU
- 1.	11	1400000	cardiac isoform gene	•		11 receptor isoform [Homo	
 `	* 	M80829	complete cds	1.8	999450	sapiens]	
112		D37887	Cyprinus carpio c- myc gene for c-Myc, complete cds Homo sapiens G protein-coupled receptor kinase 1 and G protein-coupled receptor kinase 1b (GRK1) gene, alternatively spliced, alternative exon 6,	1.8	3023408	BRANCHED-CHAIN AMINO ACID TRANSPORT SYSTEM CARRIER PROTEIN (BRANCHED-CHAIN AMINO ACID UPTAKE CARRIER) >gi 1075007 pir D64056 membrane-associated component, branched amino acid transport system (brnQ) homolog - Haemophilus influenzae (strain Rd KW20) system II carrier protein (brnQ) [Haemophilus influenzae Rd]	7.2
113		NF019765	exon 7, and partial			(U10270) G-box binding factor	
	╁	01//05	cus	1.8	498643	1 [Zea mays]	7.2
114	Δ		Helicobacter pylori J166 virulence regulon transcriptional activator homolog gene, partial cds, strain-specific genomic sequence B2	. 1.8	3850108	(AL033388) putative calcium- transporting atpase [Schizosaccharomyces pombe] PROBABLE	5.7
115	ַט	C	Kenopus laevis Xwnt-4) mRNA, omplete cds.	1.8		HYDROXYACYLGLUTATHI DNE HYDROLASE GLYOXALASE II) (GLX II) protein [Escherichia coli] pgi 1786406 (AE000130) probable ydroxyacylglutathione	5.5

┝──	Neares	t Neighbor (BlastN vs.	Genbank)	Nearest Nei	ghbor (BlastX vs. Non-Redundant P	
SEQ	- 1				Sites 13: 11011-Redundant P	roteins)
ID	ACCESSIO	N DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALU
	 	Na+/Cl(-)-dependen	. 			
	1	neurotransmitter	`			
116	S68944	transporter	1.8	2276216	(Z96810) GLYT-1 LIKE [Homo	×
		Rat calcium channel	1.0	2276316	sapiens]	5.5
	Ì	alpha-1 subunit (rbB	-1	ł		
	Ĭ	I) mRNA, complete	1	l	(AE067607) 8::1	j
117	M92905	cds.	1.8	3165522	(AF067607) Similar to cuticular collagen; C18H7.3	
	l	Xenopus laevis U1			(AF015685) reverse	5.5
118	X12429	70K gene exon 10	1.8	2735957		
					transcriptase domain protein	3.3
]	1	٠.	cyclin A/CDK2-associatd	· .
		İ	1		protein P19 (RNA polymerase	
		1			elongation factor)	
		1			(SW:SKP1_HUMAN); cDNA	
		i			EST EMBL:T00114 comes	
]		from this gene; cDNA EST	
- 1			i 1		yk390f1 1.5 comes from this	
- 1			1		gene; cDNA EST yk402e11.5	
ŀ					co	
- 1					>gi 3877216 gnl PID e1346850	
- 1		Mouse hepatitis virus			protein P19 (RNA polymerase	
- 1		genomic RNA for			elongation factor) gene; cDNA	ĺ
	j	spike protein, partial	ł		EST yk390f11.5 comes from	
19		cds	1.8	3876559	this gene; cDNA EST yk402e11.5 co	
- 1	1			3070337	(Z99942) similar to von	3.3
- 1		Cervus elaphus			Willebrand factor type A	
	1	REDDEER	ı		domain; cDNA EST yk412d4.5	
i		mitochondrial D-	i i		comes from this gene; cDNA	
20		oop, complete	1		EST yk412d4.3 comes from this	
 -	AF016972	equence	1.8	3878057	gene	3.2
- 1	-1				HYPOTHETICAL 21.0 KD	
i	ı		i	•	PROTEIN IN RPS3-PSD1	· j
- [1				INTERGENIC REGION	
		Į.	1		>gi 2132762 pir S63129	ļ
ı		j	1		probable membrane protein	i
	j		1		YNL174w - yeast	
- [lo	ncorhynchus mykiss	1		(Saccharomyces cerevisiae)	j
1	l m	RNA for rtSox24,	Į.	·	>gi 1302152 gnl PID e239548	l
1 4		omplete cds	1.8	1730805	(Z71451) ORF YNL174w	j
					[Saccharomyces cerevisiae] A-TYPE INCLUSION	2.5
1		aemophilus	[PROTEIN (ATI) camelpox	ĺ
ſ	in	fluenzae Rd section	- 1	ľ	virus >gi 62381 (X69774)	- 1
	115	9 of 163 of the	Ī		84kDa A-type inclusion protein	
2		mplete genome			OHKID A-IVDA INCLISIOS SESSE !	

<u> </u>	Neare	st Neighbor (BlastN vs.	Genbank)	Nearest Nei	ghbor (BlastX vs. Non-Redundant P	
SEQ	1				2000 (Diastit Vs. 1401)-Redundant P	roteins)
B	ACCESSIO	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALI
 	 	17	<u> </u>			I VALU
ł	l	Human ionizing	ł			
l	I	radiation resistance	1		1	ļ
123	111020	conferring protein	1		ribosomal protein YS7 homolog	i
	U18321	mRNA, complete cds	1.8	2133273	Emericella nidulans	1.4
	ŀ	Human cystic fibrosis	ł			1.4
		mRNA, encoding a	İ	l		l
		presumed		Ĭ	1	l
		transmembrane	1	ł	1	
		conductance regulator				
- 1		(CFTR). > ::				
		gb I11500 I11500		·		
ı		Sequence 1 from	٠.			
124	M28668	Patent US 5407796			filaggrin precursor - mouse	
		1 atent 03 3407790	1.8	90492	(fragment)	0.87
- 1		1	1	•	PROBABLE PROTEIN	
	•			•	DISULFIDE ISOMERASE P5	
- 1		Mus musculus NSD1	ŀ		PRECURSOR >gi 1065461	
1		protein mRNA.	1		(U40411) Similar to protein	
125	AF064553	complete cds	1.8	250100=	disulfide-isomerase.	
			1.6	2501207	[Caenorhabditis elegans]	0.87
		1	İ		REGULATORY PROTEIN	
- 1		1	1		BRLA (BRISTLE A PROTEIN)	
		Human mRNA for			>gi 83718 pir A28913 regulatory protein brlA -	
		KIAA0316 gene,	1		Emerically protein orlA	
126	AB002314	complete cds	1.8	115131	Emericella nidulans >gi 168029 (M20631) brlA protein	
- 1		Homo sapiens			(14120031) BriA protein	0.84
ł		(subclone 10_d2 from	I		1	
27		PI H21) DNA	Į		metalloproteinase I (EC 3.4.24	
/ 		sequence.	8.1	2135624) - human	0.65
28		R.norvegicus renin			(AF109907) S164 [Homo	0.65
-0	M37278	gene, exons 1-9.	1.8	4050087	[sapiens]	0.58
		Artificial sequences			(L13442) cysteine-rich extensin-	00
29 .	7000	DNA for ART 2			like protein-4 [Nicotiana	
	1020/9	consensus	1.8	310929	tabacum]	0.52
-	l,	Homo sapiens mRNA	ı			J.J.
1	1,	or CRM1 protein,	1			
0		omplete cds		_ · _ !	(AJ010792) Muc5AC protein	
	- 37,29	ombiere cas	1.8	3559944	[Mus musculus]	0.38
	1	fus musculus	1			
1		epiapterin reductase	1		(AE000766) enolase-	ı
1 1		ene. exons 1 and 2	,		phosphatase E-1 [Aquifex	- 1
	15	CAOIIS 1 allu 2	1.8	2984225	aeolicus] (0.095

	Near	est Neighbor (BlastN v	s. Genbank)	Nearest Nei	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEQ	!			33.710	(Blasta, vs. Non-Redundant P	roteins)		
ID	ACCESSI	ON DESCRIPTION	PVALUE	ACCESSION		P VAL		
	 				COLLAGEN ALPHA I(VIII)	1. 17.		
	ł	1	- 1		CHAIN PRECURSOR	 		
	1	Para - 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		1	(ENDOTHELIAL	1		
	l	Paramecium 168G	Í	1	COLLAGEN)	ł		
132	X52133	gene for 168G		1	>gi 105686 pir S15435 collagen			
	7.02133	surface protein	1.8	115316	Jalpha I(VIII) chain precursor	0.07		
	ĺ				(U61944) coded for by C.			
			j	1	elegans cDNA ykl 12f3.5; coded	1		
					for by C. elegans cDNA	j		
- 1			j	į	cm21d2; coded for by C.	1		
ı			l	I	elegans cDNA CEESR07F;			
Į				l '	coded for by C. elegans cDNA			
ı		77	1 .	Ī	ykl12f3.3; coded for by C.			
133	M77020	Human desmoplakin	ı II		elegans cDNA CEESR29F			
133	M77830	mRNA, complete cd	s. 1.8	1397246	[Caenorhabditis elegans]			
134	AJ224150	Plasmodium berghei			(U43192) myosin II heavy chain	le-04		
	AJ224150	EF-1alpha A-gene	1.8	1353761	[Naegleria fowleri]	2 22		
- 1		M			- Servicing	2e-05		
		Mus musculus	1 1		(U58748) similar to potential			
- 1		somatostatin receptor	r)		transmembrane domains in S.			
35	A 10055 to	2 gene, exon 1 and 5			cerevisiae nulcear division			
-	AJ005518	flanking region	1.8	1326350	RFT1 protein (SP:P38206)	2. 00		
		Ralstonia eutropha			pretent (61:1 38200)	2e-08		
ı		megaplasmid pHG1	1 1		1 1			
		nitric oxide reductase	1 1					
36	AF002217	(norB) gene,	1		(AL031174) hypothetical			
~	AP-002217	complete cds	1.8	3393018	protein	2-00		
-		Caenorhabditis	1			2e-08		
7	AF039035	elegans cosmid	1		(AL033388) 3-oxoacyl-[acyl-			
-	AT 039033	C53A3	1.8	3850109	carrier-protein]-synthase	20.11		
- 1		S.domesticus			protein synthase	3e-11		
- 1	į		1		1			
1		immunoglobulin		. ,				
		rearranged gamma	1		(AL022600) putative mannose-1			
8		chain mRNA, VJC	j		phosphate gaunyl transferase			
+-	1.101709	region, complete cds.	1.8	3080527	[Schizosaccharomyces nombel	3e-14		
1	1	j	Γ		HYPOTHETICAL 24.2 KD	JC-14		
j	1	1	1		PROTEIN C13A11.03 IN			
, -	Y11106	P mastaria BVC		i i	CHROMOSOME 1 >gi 984224			
 	-11100	P.pastoris PYC1 gene Human putative	1.8	11754[2	/754000	le-15		
J	12	Ca2+/calmodulin-	ł	i		10-12'		
1		lependent protein	J	lo	(AL021687) putative protein			
1			1	I	[Arabidopsis thaliana]			
		inase kinase gene. 3'	i	>	>gi 2832633 gn PID e1249651			
1		lanking region,	J	1/	AL021711) putative protein	1		
ι	J87803 p	artial sequence	8.1					

\vdash	N	earest Neighb	or (BlastN vs.	Genbank)	Nearest Mai	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
S	EQ			1	rical car i tel	endor (BlastX vs. Non-Redundani	Proteins)		
	D ACCES	SION DE	SCRIPTION	P VALU	I				
L		Plasm	odium	1 1/40	E ACCESSION	DESCRIPTION	P VAL		
1	1	falcipa	ırum	+					
l	1		osome 2,	1	1				
	j		n 67 of 73 of	i			J		
1	- 1	the co		ł ·		1	- J		
14	1 AE001	430 sequen	-	1.8		(U95973) endomembrane	1		
				1.0	1931647	- protein EMP70 precusor isolo	g 2e-20		
	J	ļ		1	1	HAYPOTHETICAL 75.5 KD			
	1	- 1			I	PROTEIN C14A4.3 IN	1		
	1	i		ı		CHROMOSOME II	1		
	j	Rat N-1	nethyl-D-	1	1	>gi 3874230 gnl PID e1351618			
		asparta	te receptor	1] •.	protein (Swiss Prot accession	1.		
	. 1	(NMD)	AR1) gene,	1]	number P38376); cDNA EST	1		
142	2 L1970	8 first exc		1.8	1731181	yk220e10.5 comes from this	1		
	1				1/31101	gene [Caenorhabditis elegans]	3e-21		
·	1			Į	İ	(Z81103) predicted using			
	1	ļ				Genefinder; cDNA EST			
	ł	P.schwa			i	yk303g11.5 comes from this	1		
147			ndrial cytb			gene; cDNA EST yk303g11.3 comes from this gene	1		
143	Y1072	gene, pa	rtial	1.8	3878644	[Caenorhabditis elegans]			
	ł	1	T			[Caenomabdins elegans]	le-28		
	1	Homo sa	piens mRNA				İ		
144	AB0066	for KIAA	A0293 gene,	1		(AL031177) dJ889M15.3 (novel	,[
	ADUUGO.			1.8	4176500	protein)	I		
	j	Mus mus protein m		ſ			7e-45		
45	AF10696	- 1					1		
	112 10050	7 complete Archaeog	lobus	1.7	<none></none>	<none></none>	<none></none>		
	ł	fulgidue	section 34 of	1			KNONES		
	i	172 of the	complete	- 1					
46	AE00107.	genome	Complete						
		Pseudomo	onas	1.7	<none></none>	<none></none>	<none></none>		
		lemoignei	poly(3-	ł	j				
- 1	·	hydroxybi	ityrate)	. 1					
- 1		depolyme	rase A	j		i			
- 1		precursor				1	i		
- 1		gene, com		- 1	1	,	j		
- [and glycer		1	1	, l	ľ		
-		phosphate-		ı	į		1		
	•	dehydroge		i i		}	ı		
., [••••	homolog, c	omplete	1			j		
7	U12977	cds.		1.7	<none></none>		i		
1		Mus muscu			1101165	<none></none>	NONE>		
•		(SK/CamR	k)	I					
	M27038	germline Ig gene. J1-5 r	K chain	- 1		1	I		

25.50	Nearest	Neighbor (BlastN vs. C	enbank)	Nearest Neighbor (BlastX vs. Non-Redundant Protein		
SEQ		l signoon (Brasen vo. e	T T	riemest rieign	ibor (Blasta Vs. Non-Redundant F	roteins)
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
<u> </u>		H.sapiens HBF-1				
1		mRNA for				
149	X74142	transcription factor Streptococcus	1.7	<none></none>	<none></none>	<none></none>
		thermophilus DeoD	}			
i	1	gene, partial cds and				
1		EpsA, EpsB, EpsC,			İ	1
1		EpsD, EpsE, EpsF,				
1	1	EpsG, EpsH, EpsI,				1
İ	ļ	EpsJ, EpsK, EpsL,				Ì
İ	1	EpsM, Orf14.9	İ	,		
150	1140920	protein genes,			1	1
130	U40830	complete cds Rabbit Ig germline	1.7	<none></none>	<none></none>	<none></none>
l i		gamma H-chain				j
		(allotype d12,e15) C-	·		·	
151	L29172	region gene, 3' end.	1.7	<none></none>	<none></none>	<none></none>
				4101122	CHOILE	CHONES
		Human lysozyme				1 1
152	M19045	mRNA, complete cds.	1.7	<none></none>	<none></none>	<none></none>
		, , , , , ,	j			
	-	Borrelia burgdorferi	ľ			1
153	AE001159	(section 45 of 70) of the complete genome	1.7	-NONE-		
133		Plasmid pFdA (from	1./	<none></none>	<none></none>	<none></none>
		Fremyella				1
		diplosiphon) DNA	I			
l		sequence, including	[
		unidentified cds and	1			i i
154	L17027	stem loop.	1.7	<none></none>	<none></none>	<none></none>
- 1	1					
ſ		Arabidopsis thaliana Columbia GTP	. [
ĺ		binding protein beta				l • }
- 1		subunit (AGB1)		·	·	i i
155		mRNA, complete cds.	1.7	<none></none>	<none></none>	<none></none>
ľ		Arabidopsis thaliana	j			
- 1		ATPK6 mRNA for	ì			
- 1		ribosomal-protein S6		. [
156		cinase homolog.	1.7	NONE		
	D-72030	ompiete cus	1./	<none></none>	<none></none>	<none></none>
	Ìs	Rhizobium				
	h	eguminosarum prsD.	1			j
157		orsE, ORF3 genes	1.7	<none></none>	. <none></none>	<none></none>

	Nearest	Neighbor (BlastN vs. C	Genbank)	Nearest Neig	hbor (BlastX vs. Non-Redundant l	Page 1 - 1
SEC					Tool (Blaset Vs. Ivon-Redundant)	Proteins)
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
-						1
	1	Spinacia oleracea				
1	1	heat shock 70 protein	j ·			1
158	AF039084	protein, complete cds	1.7	<none></none>	<none></none>	<none></none>
1	1	R.norvegicus gene for				- TANOLINE
1.50		catechol	ļ			-
159	Z12651	methyltransferase	1.7	<none></none>	<none></none>	<none></none>
1	1	Fringilla coelebs				
l	Ì	mitochondrial control			ľ	İ
160	A F0000 60	region, partial			1	ł
160	AF002968	sequence	1.7	<none></none>	<none></none>	<none></none>
l		<u></u>				
		Borrelia burgdorferi	·			j i
161	AE001160	(section 46 of 70) of	·			
101	AE001160	the complete genome Methanococcus	1.7	<none></none>	<none></none>	<none></none>
				÷		
l		jannaschii section 95 of 150 of the			,	
162	U67553	complete genome				i
102	00/333	S.ruminantium	1.7	<none></none>	<none></none>	<none></none>
163	M86247			NONE	1	
	14100247	plasmid pS23 DNA. oIL-8=interleukin-8	1.7	<none></none>	<none></none>	<none></none>
		[sheep, spleen ceils,]
164	S74436	mRNA, 1435 nt]	1.7	«NONTE»		
		Candida maltosa	1.7	<none></none>	<none></none>	<none></none>
		ALK7 (CYP52A10)			1	i i
		and ALK8 complete	1			1 1
165		cds	1.7	<none></none>	NONE	NONT
		Geotrichum		11.01112	<none></none>	<none></none>
	[candidum NRRL Y-	[]	[
	1	553 lipase gene,			230k bullous pemphigoid	{
166	_	partial cds.	1.7	321245	antigen BPM1 - mouse	9.3
1					gon Di Mi - mouse	9.3
ı		H.sapiens CpG DNA,	1			
		lone 114a4, reverse			(U66298) bone morphogenetic	1 1
167	Z58881 1	ead cpgll4a4.rtla.	1.7	1854675	protein-6 [Rattus norvegicus]	9.1
					LARGE PROLINE-RICH	
ļ		İ	1		PROTEIN BAT2 MHC class III	
- 1	1		1		histocompatibility antigen HLA-	· · · · · · · · · · · · · · · · · · ·
- 1	1		1	•	B-associated transcript 2 -	ł
1	1		1		human >gi 179339 (M33509)	
- 1	- 1.		[HLA-B-associated transcript 2	
- 1		Agrobacterium	l		(BAT2) [Homo sapiens]	ı
- 1		ımefaciens conjugal	1	İ	>gi 179345 (M33518) HLA-B-	ł
ا ،،،		ansfer region 1	1		associated transcript 2 (BAT2)	
168	U43674 g	enes	1.7	1352066	[Homo sapiens]	9.1

1.50	Neare	st Neighbor (BlastN vs.	Genbank)	Nearest Neig	hbor (BlastX vs. Non-Redundant P	
SEC	2				Tool (Blastix Vs. Non-Redundant P	roteins)
ID	ACCESSIO	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
—		<u></u>			PROTOPORPHYRINOGEN	1
	1		1		OXIDASE (PPO) yeast	
-	1	1			(Saccharomyces cerevisiae)	l
1	İ	Caenorhabditis	1	1	>gi 603606 (U18778) Hem14p:	1
1	İ	_			protoporphyrinogen oxidase	
	1	elegans cosmid	ł		[Saccharomyces cerevisiae]	ĺ
j	1	Y12A6A, complete			>gi 1403536 gn1 PID e249333	
1	Į	sequence [Caenorhabditis	1		(Z71381) protoporphyrinogen	1
169	AL023827		1 1		oxidase [Saccharomyces	
100	7 LL023627	X.laevis mRNA for	1.7	731440	cerevisiae]	8.9
ł	i	glutathione	1			
1	J	synthetase, large			1	
170	X69662	subunit	1.7	40000	(AC005897) hypothetical	
		S.cerevisiae	1./	4038057	protein [Arabidopsis thaliana]	8.8
1		chromosome II	1 1			
1 .		reading frame ORF	1 1		121.55.5	ļ
171	Z35824	YBL063w	1.7	3021450	(Y15515) prdl-a [Hydra	
			- 	3021430	vulgaris] COLLAGEN ALPHA I(XII)	7.0
			1		CHAIN PRECURSOR I(XII)	
					chain - chicken	1
					>gi 222811 gnl PID d1001160	
		Cowpea chlorotic			[gallus]	ŀ
ı		mottle virus (CCMV)	1		>gi 2326442 gn1 PID e39435	ſ
		la protein gene.			(X61024) collagen type XII	1
172	M65139	complete cds.	1.7	2506307	alpha 1 chain [Gallus gallus]	7.0
. !					HYPOTHETICAL 10.0 KD	7.0
ı		l	i		PROTEIN IN ALPA-GABD	. [
			- 1	i	INTERGENIC REGION (F87)	j
		Drosophila distal BX-	1		>gi 1033124 (U36840)	ļ
ĺ		C region (bithorax	ł		ORF_f87 [Escherichia coli]	
173	I	complex) pH189 5	- 1		>gi 1788982 (AE000348) orf,	
1/3	X15065	region;	.1.7		hypothetical protein	6.9

<u> </u>	Nearest Neighbor (BlastN vs. Genbank)			Nearest	Nearest Neighbor (DL W. N. D.			
SEQ	2		T	. vourest	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
ID	ACCESS	ION DESCRIPTION	BVAL					
			P VALI	JE ACCESSI	ON DESCRIPTION	P VAL		
								
	i	·	1	- 1	(Z46792) similar to lethal(1)			
l	l			1	discs large-1 tumor suppresso			
		}	1	<u> </u>	protein-like repeats; cDNA E	or		
	ĺ		1	l l	EMBL D33495 comes from t	ST		
	ĺ		İ	ļ	gene; cDNA EST	his		
	ľ		1	1	EMBL:D35117 comes from t			
			1	ı	gene; cDNA EST	his		
		j	1		EMBL:D36356 comes from the			
		· .		1	gene; cDNA EST EMB	nis		
J		1		1.	>gi 3879984 gnl PID e135176	_		
		Í			suppressor protein-like repeats	′ I .		
ı			1	1	cDNA EST EMBL:D33495	·		
- 1		*	l	-	comes from this gene; cDNA	1		
- 1			ļ	1	EST EMBL: D35117 comes	İ		
- 1		S.cerevisiae]		from this gene; cDNA EST	İ		
174	Z46255	chromosome VI			EMBL:D36356 comes from th	: .		
	240233	lambda clone. Human CD4	1.7	3875228	gene; cDNA EST EMB	6.7		
					THYMIDINE KINASE			
175	U01066	promoter, partial sequence.		ł	saimiriine herpesvirus 1 (strain	1		
		sequence.	1.7	125448	11[Onc]) >gi 60341	6.7		
- 1		Phalaenopsis sp.		1				
- 1		'hybrid SM9108'		ſ		İ		
		homeobox protein			(7/20.0.1	1 .		
76	U34743	mRNA, complete cds	1.7	1022010	(U38184) ATPase subunit 6	i i		
- 1		Baboon herpesvirus		1022918	[Trypanosoma cruzi]	6.7		
- 1		HVP2 gB		İ	(AI 023862) books			
,,	***	glycoprotein (UL27)		l	(AL023862) hypothetical)		
77	U14662	gene, complete cds.	1.7	3218378	protein SC3F9.07 [Streptomyces			
- 1		Homo sapiens			- Cocheolof	6.7		
78 /	A DOLTOC	PMS2L15 mRNA,		. ·	(U64859) glutamine-rich protein	 		
	AB017006	partial cds	1.7	1465855	[Caenorhabditis elegans]			
		Brassica oleracea var.			- Cicgans	6.7		
- 1		botrytis tonoplast	i			ľ		
		intrinsic protein	I		DYNEIN HEAVY CHAIN,			
ľ		bobTIP26-1 mRNA,			CYTOSOLIC (DYHC) dynein			
9	U92651	complete cds	,, 1		heavy chain	1		
$\neg \vdash$		-ompiete eus	1.7	3023675	[Schizosaccharomyces pombe]	6.6		
1]	Lytechinus variegatus	I					
1		notch homolog	j		(M58520) endo-1,4-beta-	ł		
) A		mRNA, complete cds	1.7	14057	glucanase [Fibrobacter			
		, samplete eds	1./	148574	succinogenes]	6.6		

	Near	est Neighbor (BlastN vs.	Ganhank)	Name N		
S	EQ	Jest Tolghoot (Blast 1 Vs.	Genbank)	Nearest Nei	ghbor (BlastX vs. Non-Redundant Pr	oteins)
	D ACCESSI	ON DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	
			1	T ACCESSION	DESCRIPTION	P VALUE
		Arabidopsis thaliana	1	 		
		anthranilate synthase		f		
j	ł	alpha subunit gene,	J	· ·	blue lieba et e	1
	81 M92354		1.7	738308	blue light photoreceptor	ļ
- 1		Hordeum vulgare		750500	[Arabidopsis thaliana] (AC002411) Strong similarity to	6.5
	1	genomic DNA	1	l	myosin heavy chain gb/Z34293	
	I	fragment; clone	ł]	from A. thaliana. [Arabidopsis	
18	32 AJ234856	MWG2234.rev	1.7	3142302	thaliana]	
		Stercorarius			(danata)	6.5
	1	parasiticus bird J33	1 .		1	
١.,		cytochrome b protein	1,	•	(Y17034) Bassoon [Mus	
18	3 U76827	partial cds	1.7	3413810	musculus]	5.4
		Saccharomyces				<u></u>
1	ŀ	cerevisiae Ttp1p				
18	4 U05211	(TTP1) gene,	1		(L24492) lipoprotein	
10	+ 003211	complete cds.	1.7	403173	[Rhodococcus ervitiropolis]	4.9
1		Homo sapiens		_	PUTATIVE	
		TRRAP protein	i 1		ENDOGLUCANASE TYPE K	į
	Į.	(TRRAP) mRNA,	i 1		PRECURSOR (ENDO-1,4-	
185	AF076974	complete cds	1 , , 1		BETA-GLUCANASE)	- 1
		complete eds	1.7	1170140	(CELLULASE)	4.1
		1	1 1		DNA ADENDE ACTIVA	
ĺ	1	1	1		DNA ADENINE METHYLASE site-specific DNA-	Ī
	ł	Aquifex aeolicus			methyltransferase (adenine-	i
1		section 85 of 109 of	Ì		specific) dam methylase gene	1
186	AE000753	the complete genome	1.7	1169357	product [Vibrio cholerae]	
ł	1				product (violio cholerae)	4.0
1		Tupaia glis	ľ		1	j
ł		apolipoprotein AI	ł			1
107		prepropeptide	ł		(AL031124) putative secreted	
. 187	AF005638	mRNA, complete cds	1.7	3355682	lyase	4.0
1	l					-7.0
1	i	Human germline IgK	1		1 .	
188	M23090	chain gene V3-region,			(AB004534) pi003	į
-00	14123090	clone Humkv328h5	1.7	2257483	[Schizosaccharomyces pombe]	4.0
l	1		1			
	}	Mink enteritis virus	1		myotonic dystrophy kinase -	1
		antigenic type 2	1		mouse (fragment) kinase, DM-	
ļ		capsid protein genes	1		kinase (C-terminal, alternatively	
		VP1 and VP2,	1	1	spliced, clone delta II,III,IV,V)	- [
189		complete cds.	1.7	214350 :	[mice, brain, Peptide Partial,	
		H.sapiens CST4 gene		2143504	474 aa] [Mus sp.]	3.9
190		for Cystatin D	1.7		(U37273) winged helix protein	, I
					CWH-2 [Gallus gallus]	3.1

- 77	Nancas	Majohhar (Disease				
SEC	iveares	t Neighbor (BlastN vs. C	Jenbank)	Nearest Neig	hbor (BlastX vs. Non-Redundant P	roteins)
ID	-	N DESCRIPTION	P VALUE	j	DESCRIPTION	P VALUE
	 				HYPOTHETICAL 11.7 KD	I VALUE
1		P.falciparum	j		PROTEIN C6B12.13 IN	
1	İ	complete gene map of			CHROMOSOME I	1
191	X95276	plastid-like DNA (IR-B)		i	>gi 2330843 gn1 PID e334047	1
1	A93276	Rat PMSG-induced	1.7	3219951	pombe]	3.0
ł	1	ovarian mRNA.	f			
192	D84487	3'sequence, N10	,,		(J02719) valyl-tRNA synthetase	
	337.07	Rattus norvegicus	1.7	173164	[Saccharomyces cerevisiae]	2.3
1	Ĭ	neurexin III-alpha			(AF060869) single-strand	
193	L14851	gene, complete cds.	1.7	3222504	binding protein [Salmonella	
		Beiner complete cas.	1.7	3323586	typhimurium]	2.3 .
1	1	Xenopus laevis/gilli			1	
1	·	hybrid pseudo-IgH	· ·			
1	Í	chain gene, V region,			MUC and the in-	
194	M97002	clone LG7G342A.	1.7	2118407	MHC sex-limited protein -	
				2110407	mouse (fragment) musculus]	2.3
		delta-endotoxin			1	
1 1	,	(CryA(a)) gene, 5'				ļ
1 1		end. > ::			1	ŀ
1 1		gb I34520 I34520	ı			1
		Sequence 1 from	- 1			
		patent US 5596071 >			j	
		:: gb I39790 I39790			1	
		Sequence 1 from	ı		1	ı
	Į	patent US 5616495 >			1	
ı		::	ł		HYPOTHETICAL 53.4 KD	i
]		gb AR008487 AR008	- 1		PROTEIN D1054.13 IN	
195		487 Sequence 1 from	ł		CHROMOSOME V	1
193	L07025	patent US 5753492	1.7	2496940	>gi 3875316 gnl PID e1344967	1.8
ı		insulin-like growth	ı			
- [factor II {intron 7}	i		1	1
196		human, Genomic,			(AB014512) KIAA0612 protein	ı
	373149	[702 nt]	1.7	3327038	[Homo sapiens]	1.8
ı			i			
- 1			i		Fv Fragment (Murine Se155-4)]
	1		Į.		Complex With The	j
i	ſ		1		Trisaccharide: Alpha-D-	,
[ĺF	Iuman (lambda)	i		Galactose(1-2)[alpha-D-	İ
ſ		NA for	ľ		Abequose(1-3)]alpha- D-	- 1
i		nmunoglobulin light	1		Mannose (P1-Ome) (Part Of	
197		hain	1.7	101367	The Cell-Surface Carbohydrate	_
			1./	494367	Of Pathogenic Salmonella)	1.8

	Nearest	Neighbor (BlastN vs. C	ienbank)	Nearest Neighbor (BlastX vs. Non-Redundant Prote		
SEQ			1	33.1.3.21	(Diame 13. 11011-Reduilddill Fl	J. Cilis)
B	ACCESSION	DESCRIPTION	PVALUE	ACCECCION	DESCRIPTION.	1
	ACCESSION	Plasmid pFdA (from	FVALUE	ACCESSION	DESCRIPTION	P VALUE
 	 	Fremyella	 			
		diplosiphon) DNA	1			
Ì		sequence, including	<u> </u>			
		unidentified cds and		·		l
198	L17027	stem loop.	1.7	1082702	poliovirus receptor-related	
	217027	Caenorhabditis	1.7	1082702	protein - human	1.4
		elegans cosmid			•	
		H22D14, complete				
		sequence			(AF069442) putative inhibitor	ŀ
		[Caenorhabditis			of apoptosis [Arabidopsis	
199	AL022273	elegans]	1.7	3924605	thaliana]	1.4
					(Ciuntaria)	1.4
		Drosophila	•			
		melanogaster cut			(Z97343) DNA-binding protein	
200	U89926	gene, partial sequence	1.7	2245100	homolog	1.3
					PROTEIN KINASE C	
1					SUBSTRATE, 60.1 KD	
					PROTEIN, HEAVY CHAIN	
		H.sapiens gene for			(PKCSH) (80K-H PROTEIN)	
201	Z25749	ribosomal protein S7	1.7	2493459	>gi 1215746	1.1
	1	Fundulus heteroclitus			(AF048977) Ser/Arg-related	
202		lactate dehydrogenase			nuclear matrix protein [Homo	
202	U59841	B Rabbit mRNA for	1.7	3005587	sapiens	0.82
- 1	1	smooth muscle	l		ļ	
J		calcium channel	i			
- 1		blocker (CaCB)	ŀ		(A E082202)	
203		receptor	1.7	3883128	(AF082302) arabinogalactan-	. 0.00
		Caenorhabditis	- '-' -	3003128	protein [Arabidopsis thaliana]	0.82
- 1	1,	elegans cosmid	i			
		C18B12A, complete				
ľ	1	sequence			1	1
ł	- 1	[Caenorhabditis	I	•	(D10123) core [Hepatitis C	·
204	Z75528	elegans]	1.7	940397	virus	0.80
		Human XIST gene,				
ļ		poly purine-	ł		(AF005370) large tegument]
1	1-	pyrimidine repeat	J		protein [Alcelaphine herpesvirus	ľ
205		region	1.7	2338027	1]	0.59
		Ovis aries beta-			(X65335) lacZ gene product	
206		actoglobulin gene	1.7	987050	[unidentified cloning vector]	0.45
- 1		Homo sapiens	1			
207		roponin T (TNNT2)	[(AF053947) unknown [Yersinia	
207	AF004419 g	gene, exon 13	1.7	2996364	pestis] >gi 3883090	0.22
- 1	l,	Collus domesticus	1		TRANSDUCIN-LIKE	
J		Gallus domesticus ONA microsatellite	į		ENHANCER PROTEIN I	
208		narker MCW119	,, [46 1006	enhancer-of-split homolog TLE-	
200	L43643 r	Harket MIC WITS	1.7	464896	1 - human >gi 307510	0.20

<u> </u>		st Neighbor (BlastN vs.	Genbank)	Nearest Nei	ghbor (BlastX vs. Non-Redundant I	Procein-
SE	- 1				(Diaset vs. Non-Redundant)	roteins)
П	ACCESSIO	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
\vdash						II VALUE
	!		ļ		HYPOTHETICAL 123.9 KD	
	1	İ	ł	j	PROTEIN C30D11.04C IN	
-1	1	1			CHROMOSOME I	
	İ	S.cerevisiae			>gi 2130411 pir \$62562	1
	Į.	chromosome XII	1		hypothetical protein	1
1	l l	reading frame ORF			SPAC30D11.4c - fission yeast	1
209	273278	YLR 106c	1.7	1251757	nuclear pore complex protein	1 .
			1./	1351657	[Schizosaccharomyces pombe]	0.20
	1	Mouse endogenous				1 7
1	1	provirus gag, pol, and		· .	(AF020766) h	1 1
210	M22345	env region DNA.	1.7	2444455	(AF020765) hypothetical	1 1
1		Escherichia coli K-12		2111133	protein [Myxococcus xanthus]	0.12
1		MG1655 section 250	1			1 1
1	1	of 400 of the	1		(AF039038) No definition line	i i
211	AE000360	complete genome	1.7	2736361	found [Caenorhabditis elegans]	0.12
1	1					0.12
1		Homo sapiens mRNA for KIAA0885	1 1			j l
212	AB020692				(AF029726) histidine kinase C	
	AD020092	protein, complete cds testis-determining	1.7	2605924	[Dictyostelium discoideum]	0.094
1	ł	gene/SRY homolog	1			
1	j	[Sminthopsis				
l	ł	macroura=striped-	i		TONE PROTEIN. 11444	
1	l	faced dunnarts,			TONB PROTEIN >gi 1666536 (U23764) TonB [Pseudomonas	-
213	S69429	Genomic, 855 nt]	1.7	2499016	aeruginosa)	
	1	testis-determining		2.55010	acruginosaj	0.092
	1	gene/SRY homolog	1		i i	i
	ł	[Sminthopsis	j			ſ
	[macroura=striped-			TONB PROTEIN >gi 1666536	ı
214	S69429	faced dunnarts,	i		(U23764) TonB [Pseudomonas	1
217		Genomic, 855 nt] Mus musculus ACF7	1.7	2499016	aeruginosa]	0.088
j		neural isoform 3	1			
1		(mACF7) mRNA,	1		1	1
215		partial cds	1.7	20.120.:-	(AF000198) weak similarity to	
		partial cus		2047349	HSP90 [Caenorhabditis elegans]	0.052
- 1	1	Artificial DNA	ł		PUTATIVE CUTICLE	1
ł	1:	sequence for	1		COLLAGEN C09G5.6	ļ
	ŀ	mammalian lambda-	ļ		collagen; cDNA EST yk244c3.5 comes from this gene; cDNA	
	ļ:	neo minichromosome,	į		EST yk244c3.3 comes from this	j
216		1400 bp	1.7		gene [Caenorhabditis elegans]	0.042
- 1		Mus musculus			e (Cachol habdins elegans)	0.042
- 1		outative CCR4	j		· ·	İ
217		protein mRNA,	İ	ļ	(U95973) hypothetical protein	ł
	11/11/11/11	partial cds	1.7		[Arabidopsis thaliana]	

	Near	est Neighbor (BlastN vs.	Genbank)	Nearest Ne	ghhor (BlassY N. B.	
- 1	EQ D ACCESSI		P VALUE	1	ghbor (BlastX vs. Non-Redundant	Proteins)
				I ACCESSION	DESCRIPTION	P VALUE
	1	Homo sapiens alpha-		 	(AF045246) universal minicirc	
	ł	l type V collagen	1	1	sequence binding protein	le
12	8 1.38808	(COL5A1) gene, 5'	j	Į	minicircle sequence binding	j
 _	8 L38808	flank and exon 1.	1.7	2895760	protein [Crithidia fasciculata]	0.000
- 1	- {	B.napus mRNA for	1		(a fortancia fasciculata)	. 0.039
21	9 Z72151	AMP-binding protein	1		(K02576) salivary proline-rich	1 1
	= 131	Advir-binding protein	1.7	190475	protein 1 [Homo sapiens]	0.011
- 1	j	R.norvegicus mRNA	Į.			1
1	ľ	for cysteine sulfinate	1		synapsin IIb - human	1 1
22	0 X94152	decarboxylase	1.7	2136212	>gi 1594277 (U40215) synapsin	1
İ		Mouse stathmin gene		2130212	IIb [Homo sapiens]	0.008
22	L20255	sequence.	1.7	2317934	(U97553) unknown [murine	
ł				2317934	herpesvirus 68]	0.006
- 1	i	Rattus norvegicus			(U23175) similar to anion]].
222		glycine transporter	Í		exchange protein	! !
222	L13600	mRNA, complete cds.	1.7	726403	[Caenorhabditis elegans]	
223	4 1004150	Plasmodium berghei			(U95094) XL-INCENP	0.003
-223	AJ224150	EF-lalpha A-gene	1.7	2072290	[Xenopus laevis]	0.001
ł	I	butyrophilin [mice,	J			0.001
ſ	1	lactating mammary gland, mRNA Partial,	i			1
224	S80642	3193 ntl			(AJ223010) Pmt2	į
	200072	C.elegans unc-86	1.7	2695746	[Schizosaccharomyces pombe]	9e-04
	j	gene encoding two	1			
1	J	alternative proteins.	ļ			ł
225	M22363	complete cds.	1.7	2224602	(AB002369) KIAA0371 [Homo	I
į.	l			2224683	sapiens]	le-04
	j	M.musculus cgt gene			(Z49909) similar to Prokaryotic	
226	X92123	exon I	1.7	3874232	ribonuclease PH	
				00.1002	[Caenorhabditis elegans]	3e-05
		Ipomoea nil PKn2	1			1
227	ABOLOOO	(knotted-like gene)		·	(AF000422) TTF-I interacting	
221	AB016000	mRNA, complete cds	1.7	2183083	peptide 5 [Homo sapiens]	le-05
					peptide 5 [Homo sapiens] (AL032643) similar to	16-03
1 1		ŀ	1		Uncharacterized protein family	1
] i	l l	ļ	J		UPF0034, Double-stranded	i i
¦	ı		J	Į.	RNA binding motif; cDNA EST	ľ
	l		į	[:	yk489b3.5 comes from this	- 1
	h	Bovine mRNA for	ł	[8	gene; cDNA EST yk439g7.5	1
228	D 4 4 4 4 4 - 1	Synaptocanalin I	1.7	392527.7	comes from this gene	
				392321.1	Caenorhabditis elegans]	2e-06

	Neares	t Neighbor (BlastN vs. (Genbarik)	Nearest Nei	ghbor (BlastX vs. Non-Redundant F	
SEQ			1		(Biasix vs. Non-Redundant F	roteins)
ID	ACCESSIO	N DESCRIPTION	DVALLE			
-	Tiecessio	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUI
	 	 				
j	l ·	Mus musculus TAFG		ł		
ŀ	1	1-like neuronal	1		1	1
ł		glycoprotein (PCS)	1		(47 000000)	ł
229	L01991	mRNA, complete cds	. 1.7	3006130	(AL022299) hypothetical	
		Tomato yellow leaf	1.7	3006139	protein	4e-07
i	İ	curl virus Thailand	ļ	ł		İ
	l	isolate complete]
i i		genome (TYLCV-TH	ł		(AC005305) have above t	1
230	X63016	B-DNA)	1.7	3643608	(AC005395) hypothetical	l
		H.sapiens		3043008	protein [Arabidopsis thaliana]	1e-07
		microsatellite repeat.		٠,		· ·
		> ::	٠. ا		1	
		gb G34562 G34562		,		
		human STS SHGC-			extensin precursor (clone Tom L	
231	Z22802	51834	1.7	100210	4) - tomato esculentum]	
ı		Human complement		100210	4) - tomato esculentum	4e-09
- 1		component C3		•		
		mRNA, alpha and				
		beta subunits,			(AE000773) acetoin utilization	
232	K02765	complete cds.	1.7	2984320	protein [Aquifex aeolicus]	1e-09
f	·				(Z/3102) predicted using	16-09
1			1	•	Genefinder; Similarity to	
ł		1			Bacillus subtilis DNAJ protein	
- 1			• 1		gene; cDNA EST	i
		S.cerevisiae			EMBL:C12520 comes from this	
- 1		chromosome XV			gene; cDNA EST	1
233	_	reading frame ORF	ł		EMBL:D71409 comes from this	· [
233	Z74818	YOL076w	1.7	3873700	ge	7e-11
	l.	Dia mandala da anta	ł			
234		Pig mRNA for thimet			(Y15513) Prodos protein	l
 +	D210/1	oligopeptidase	1.7	2632098	[Drosophila melanogaster]	8e-13
]		. 1			(Z81070) cDNA EST	
	1	İ	1		EMBL:C12730 comes from this	
	- 1	1	i		gene; cDNA EST yk200b6.5	
	1,	Gallus gallus gene	ļ		comes from this gene; cDNA	1
		ncoding neurofascin.	<u>[</u>		EST yk349a12.5 comes from	
235		xons 9,10,11 & 12	1.7		this gene [Caenorhabditis	1
		cerevisiae	1./	3876421	elegans]	3e-14
	1	hromosome XVI	- 1		(164605) (0500 (1
1		ading frame ORF	1		(U64605) C05D9.6 gene	j
236		PL252c	1.7		product (Caenorhabditis	
				1437003	elegans]	6e-18

1,.,	Nearest I	Neighbor (BlastN vs. G	enbank)	Nearest Neigh	bor (BlastX vs. Non-Redundant P	roteins)
SEQ						1
Б	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					OLIGOSACCHARYL	1. 17202
					TRANSFERASE STT3	-
		Homo sapiens		•	SUBUNIT HOMOLOG	1
		genomic DNA, 21q			>gi 529357 (U13019) No	
		region, clone:			definition line found	1
237	AG000518	T171N23	1.7	1174468	[Caenorhabditis elegans]	6e-18
		Human mRNA for N-				1
		acetylglucosaminyltra			1	ŀ
		nsferase V, complete			(D63877) KIAA0157 gene	
238	D17716	cds	1.7	961446	product is novel.	5e-19
		Cheilodactylus	-			
i i		vittatus country USA:		· •	1	
1		Midway Island	• .		İ	Í
		cytochrome c oxidase	·			1 1
		subunit I gene,				1
		mitochondrial gene				4
		encoding			(U70848) C43G2.1 gene	1
220		mitochondrial			product [Caenorhabditis	1 1
239		protein, partial cds	1.7	1572756	elegans]	5e-40
1		Rattus norvegicus				
		liver-specific				1
240		transporter gene, promoter region.	1	4176142	(AL022238) dJ1042K10.4	2 40
240	L30107	promoter region.	1.7	4176443	(novel protein)	3e-49
	1	H.sapiens mRNA for				
		Na-Cl electroneutral	ı			
	i i	thiazide-sensitive			(AC005546) R29425_1 [Homo	l
241		cotransporter	1.7	3478637	sapiens]	6e-54
						
- 1			ľ		1	!
1		Rattus norvegicus	l			[]
1		calcium-independent	·		1 .	j i
		phospholipase A2	ŀ	•	<u>.</u>	
242		mRNA, complete cds	1.6	<none></none>	<none></none>	<none></none>
1	I	Pea seed-borne	T			
1		nosaic virus RNA for			1	ļ !
242		coat protein and	1			
243	Z48508	polymerase (partial) Rat leukocyte	1.6	<none></none>	<none></none>	<none></none>
- 1			1		j	
- 1		common antigen (L- CA) gene, exons I]			ľ
244		hrough 5.	1.6	ANONE-	NONE	NONE
		Yeast (S.pombe)	1.0	<none></none>	<none></none>	<none></none>
j		dc25+ gene (mitosis		•		
ł		nitiation), complete	1			
245		eds.	1.6	<none></none>	. <none></none>	<none></none>
				1101127	110112	11.01.12

	Neares	t Neighbor (BlastN vs. (Genhank)	Nagrasi N.:		
SE		Tronginor (Blastit Vs. (T T	inearest neig	hbor (BlastX vs. Non-Redundant P	roteins)
П		N DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
<u> </u>		Mycoplasma				I VALUE
1	1	genitalium section 34				
	.	of 51 of the complete	}		ļ	1
24	U39712	genome	1.6	<none></none>	<none></none>	<none></none>
ı	j				(Z81499) predicted using	110112
1		Mouse Murine			Genefinder; cDNA EST	
1	1	urokinase-type		,	yk410e3.3 comes from this	
1		plasminogen activator	i i		gene; cDNA EST yk410e3.5	.]
1 242	1,517000	protein gene,			comes from this gene	
247	M17922	complete cds.	1.6	3875750	[Caenorhabditis elegans]	8.0
248	140000	Human polymorphic		٠.	(Z84724) psd [Mycobacterium	
240	M89986	loci in Xq28.	1.6	3261710	tuberculosis]	6.4
249	M89986	Human polymorphic			inositol-polyphosphate 4-	
1 247	14193380	loci in Xq28. Rattus norvegicus	1.6	2143805	phosphatase - rat	6.2
		Deleted in colorectal				
250	U68725	Cancer	!	.3	(U51449) RING3 protein	
1250	008723	Cancer	1.6	1256804	[Xenopus laevis]	5.8
					MALEYLACETATE	1
	j	P.platessa GSTA,	į.		REDUCTASE Pseudomonas	
	ľ	GSTA1, GSTA2, and			cepacia >gi 643636 (U19883)	
251	X95199	PPTN genes	1.6	2015112	maleylacetate reductase	
	,	51 51 SULLO		3915113	[Burkholderia cepacia] HYPOTHETICAL 91 KD	4.9
			i		PROTEIN IN COB INTRON	ľ
}			1		>gi 2654230 gnl PID e1192341	
1			1		(X02819) unidentified reading	
	j	D.melanogaster	1		frame [Schizosaccharomyces	Ī
252	Y09103	RPA1 gene	1.6	3916021	pombel	4.8
}		T.aestivum			periodi	4.0
l		mitochondrion fMet,				ı
		18S, 5S repeat unit	ŀ		DYSTROPHIN-RELATED	
253	214078	DNA	1.6	2501668	PROTEIN 2 sapiens]	3.6
		İ	- 1		REPETITIVE PROLINE-RICH	1
			1		CELL WALL PROTEIN I	1
			•		PRECURSOR	J
	<u>,</u>		1		>gi 81809 pir A29324 proline-	
		Human mRNA for	Ī		rich protein precursor - soybean	i
254		KIAA0316 gene,	1		>gi 170049 (J02746) proline-	
	AB002314 (complete cds	1.6	130997	rich protein [Glycine max]	2.8
ľ		1	Į.		ENV POLYPROTEIN	
ł	ĺ,	luman muscle	l		PRECURSOR (COAT	<u> </u>
- 1		reatine kinase gene	1		POLYPROTEIN) [CONTAINS:	J
255	- 1	CKMM), exon 2.	16	110200	COAT PROTEIN GP62; COAT	j
	-121700 (CIXIMITI), CXUII 2.	1.6	119399	PROTEIN GP40]	2.2

	Neares	t Neighbor (BlastN vs. (Genhank)	Nearest Mais	ht- (DI W N D	
SE		1	T	1,001,031,1461	ghbor (BlastX vs. Non-Redundant	Proteins)
II	- 1	N DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUI
-	-}	D-1: 1	<u> </u>			
ı	1	Borrelia burgdorferi	1			
256	AE001164	(section 50 of 70) of the complete genome			(AF109907) hypothetical	1
	1.001104	the complete genome	1.6	4050089	protein [Homo sapiens]	1.5
	1	M.musculus	1			
1	1	rearranged T-cell	ł	I	1	1
	J	receptor beta variable	1		(AF080090) semaphorin IV	
257	X61757	region (Vb17a)	1.6	3377766	isoform b [Mus musculus]	1 , 2
1		T.cruzi tandemly		3077700	isotom o (isius musculus)	1.2
1	· ·	repeated gene	ļ			1 .
1	1	encoding an 85 kDa		j	(AF043695) similar to zinc	
1]	antigen with			metalloprotease family of	
258	M15346	homology to heat			peptidases [Caenorhabditis	1
238	M13346	shock proteins.	1.6	2804437	elegans]	0.41
1		Rattus norvegicus	·			
1		sodium channel				1
	1 .	protein 6 (SCP6)		,	(AE018081) **** - 3/1/1/1	
259	L39018	mRNA, complete cds	1.6	2920535	(AF018081) type XVIII collagen [Homo sapiens]	0.000
				2720333	conagen (Homo Sapiens)	0.037
1	[Human leukocyte	1]
	ſ	adhesion protein	ı		1	
260	M29483	p150,95 alpha subunit			(U49082) transporter protein	
200	W129483	gene, exons 7 - 15.	1.6	1840045	[Homo sapiens]	2e-09
I	j	Aspergillus niger beta	1		·	
1		D-fructofuranosidase	ľ		j	1
1		(suc1) gene, one			(AF071527) putative calcium	•
261	L06844	exon.	1.6	4206210	channel [Arabidopsis thaliana]	0. 10
					chamer [Arabidopsis manana]	9e-10
1 1		Chicken aldolase B			(AF040640) similar to peptidase	
		gene, complete cds,	- 1	•	family C19 (ubiquitin carboxyl-	
262		clones lambda-			terminal hydrolase)	
202		C(11.1.4). Human gene PRB3L	1.6	2746775	[Caenorhabditis elegans]	1e-31
		for proline-rich				
263		protein G1	1.5	<none></none>	3705	
				CHOINES	<none></none>	<none></none>
J	1	Vicotiana tabacum	i i		(Z99271) similar to Reverse	
_		JMP synthase (pyr5-		•	transcriptuse comes from this	i
264) mRNA, partial cds	1.5	3880923	gene [Caenorhabditis elegans]	0.50
Ì	I.	lus musculus				_ 0.50
j		iuclear protein	j		1	ļ
265		VIP45 mRNA.	,,		(U58761) C01F1.6 gene product	1
	070739 [0	omplete cds	1.4	1330394	[Caenorhabditis elegans]	8.9

· -	Nearest	Neighbor (BlastN vs.	Genbank)	Nearest Neig	hbor (BlastX vs. Non-Redundant F	
SEQ)	Treatest Inerg	noor (Blastx vs. Non-Redundant F	roteins)
I ID	ACCESSION	DESCRIPTION		Í		j
110	ACCE2210	DESCRIPTION	PVALUE	ACCESSION	DESCRIPTION	P VALUE
<u> </u>			<u> </u>		POTASSIUM-	
1	ĺ		1		TRANSPORTING ATPASE	
1	1		i	j	BETA CHAIN (PROTON	1
1		j	Í		PUMP) (GASTRIC H+/K+	
	1	L.	1		ATPASE BETA SUBUNIT)	j
		Rice tungro	ł	ľ	3.6.1.36) beta chain - human	1
		bacilliform virus	1		>gi 184105 (M75110) H,K-	1
244		Serdang strain,	1	i	ATPase beta subunit [Homo	
266	AF076470	complete genome	1.4	1703461	sapiens]	8.9
		C.jacchus interferon	1			
047	****	gene for interferon		l .	(U28832) US10 [Gallid	ł
267	X64659	gamma	1.4	1486485	herpesvirus 1] >gi 1486497	6.8
		Schistosoma				
li		japonicum structural	i i			
		muscle protein	ł			1
268	*****	paramyosin mRNA,				
208	U11825	complete cds.	0.88	<none></none>	<none></none>	<none></none>
		III DNA 6	j j		(AL031907) hypothetical serine	1
269	D04370	Human DNA for			rich protein	ì
209	D84278	CD38, exon 1 Boyine lens aldose	0.68	3766363	[Schizosaccharomyces pombe]	3.0
ł		reductase	1 . 1		1	
270	M59755			\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\		}
-270	14139733	pseudogene, 3' end.	0.67	<none></none>	<none></none>	<none></none>
		Homo sapiens				ĺ
ı		skeletal muscle				
J	i i	voltage-dependent				
ſ		sodium channel alpha				ľ
ı		subunit (SkM1)	ľ		(796105) 1 4 1	
271		mRNA, complete cds.	0.65	2437819	(Z86105) 1,4-beta-glucanase	
		Human type IV	0.03	473/017	[Anaerocellum thermophilum]	3.6
1		sodium channel alpha			(Z86105) 1,4-beta-glucanase	}
272	1	polypeptide	0.64	2437819		١ , .
		Danio rerio bone	- 0.07	243/017	[Anaerocellum thermophilum]	3.5
- 1		morphogenetic	1		(AE000720) formate	
		protein-4 (bmp4)			dehydrogenase alpha subunit	
273	The state of the s	mRNA, partial cds	0.63	2983532	[Aquifex aeolicus]	70
		Hylobates lar mucin	- 5.05	2703332	[[Aquitex acolicus]	7.9
		(MUC1) gene, exons	I		(D79215) FGF-10 [Rattus	1
274		1-6.	0.63	1517808	norvegicus]	0.91
				171,000	inoi regicus)	0.91

21.50	Nea	rest Neighbor (BlastN v	s. Genbank)	Nearest N	Jaiobhos (Blank)	
SE	Q.		June,	realest N	leighbor (BlastX vs. Non-Redundant F	roteins)
III.	ACCESS	ION DESCRIPTION	N P VALU	E ACCESSIO		P VALI
					(U67936) coded for by C.	
		Fugu rubripes sush	g l		elegans cDNA ykl26i9.5; coder for by C. elegans cDNA ykl59h6.3; coded for by C. elegans cDNA ykl26f9.3; codec	1
275	AF03088	polyprotein (gag) a pol polyprotein (po	01)		for by C. elegans cDNA ykl59h6.5 [Caenorhabditis	
	74 03088	I genes, complete cd. Arabidopsis thalian	s 0.63	1519696	elegans]	0.38
276	U52909	U1 snRNP 70K protein gene,	0.62	AIONIT		. 0.38
			0.02	<none></none>	<none></none>	<none:< td=""></none:<>
277	AF008192	Homo sapiens putative GR6 protein (GR6) mRNA, complete cds			(AF100655) contains similarity to ser/thr protein kinases	
	1	Human fatty acid	0.62	3800934	[Caenorhabditis elegans]	9.7
278	U17081	binding protein (FABP3) gene, complete cds	0.62	3617848	(AF049709) tyrosylprotein sulfotransferase-A; TPST-A	
279	AB018340	Homo sapiens mRNA for KIAA0797 protein, partial cds	0.62	424044	VP5 protein - porcine rotavirus	7.7
80	Y00093	H.sapiens mRNA for leukocyte adhesion glycoprotein p150,95	0.62	1054945	(U38621) polyprotein [Tobacco vein mottling virus]	
		Human cathepsin D			GLYCOPROTEIN M >gi 73791 pir WMBE51 UL10 protein - human herpesvirus 1 1-	4.5
81	M63138	(catD) gene, exons 7, 8, and 9.	0.62	136810	473) [Human herpesvirus 1] >gi 221732 gnl PID d1002131	3.5
12	X76056	N. sylvestris DNA for spacer region between 25S and 18S ribosomal RNA genes	0.62	2661176	(U76671) putative cds	
3	X74501	B.taurus mRNA for ACTH receptor			[Rhodobacter sphaeroides] (AB001075) galectin-2 related	2.0
1	127 .501	AC 111 receptor	0.62	4249552	protein	2.0
		Rat FI-ATPase beta ubunit mRNA, 3'			transforming growth factor-beta type III receptor - chicken >gi 511843 (L01121)	
<u>. </u>	34	end.	0.62	2119692	transforming growth factor-beta type III receptor [Gallus gallus]	1.5

<u> </u>		est Neighbor (BlastN vs.	Genbank)	Nearest Nei	ghbor (BlastX vs. Non-Redundant)	Dage :
SEQ	2				Single Valuation value of the Control of the Contro	roteins)
ID	ACCESSI	ON DESCRIPTION	P VALUE	ACCESSION		P VAL
	 	 			ASPARTYL/ASPARAGINYL	
	1		1		BETA-HYDROXYLASE	
	1		Ĭ		(ASPARTATE BETA-	İ
	ł	1		1	HYDROXYLASE) (ASP BET	ما
	J		1		HYDROXYLASE) (PEPTIDE	. 1
	ŀ	Home and a	1	ł	ASPARTATE BETA-	ł
	ļ	Homo sapiens	1	i	DIOXYGENASE) beta-	
285	Y15724	SERCA3 gene, exons		i	dioxygenase (EC 1.14.11.16) -	j
	113/24	1-7 (and joined CDS) Plasmodium	0.62	2498164	bovine >gi 162694 taurus]	0.52
	l	falciparum DNA ***	1	1		V.J2
			İ	1	1	
		SEQUENCING IN	1	l ·		1
		PROGRESS ***	·	l	J	
286	AL010142	from contig 3-72,	1 . 1		HYPOTHETICAL PROTEIN	
	AL010142	complete sequence	0.62	3183206	KIAA0009 sapiens)	4e-07
		1			HYPOTHETICAL 63.5 KD	76-07
- 1		1	i		PROTEIN ZK353.1 IN	1
					CHROMOSOME III	
- 1			1		>gi 1078903 pir S44654]
		Mus musculus Stat3	ļ ļ		ZK353.1 protein -	
ł		gene, 5'-flanking			Caenorhabditis elegans	
287	4 B000160	region and exon 1	' I		>gi 289757 (L15313) putative	
·•′ 	AB008160	partial sequence	0.62	466097	[Caenorhabditis elegans]	le-35
ı		1	1		(Z48583) similar to ATPases	10-33
- 1			İ		associated with various cellular	
- 1			i		activities (AAA); cDNA EST	
ı			1		EMBL:Z14623 comes from this	
- 1			i i		gene; cDNA EST	
		Halaman	1	,	EMBL:D75090 comes from this	
- 1		Halomonas marina	1	•	gene; cDNA EST	
88	AB018795	gene for alginate			EMBL:D72255 comes from this	
~ -	VD019/A2	lyase, complete cds Human DNA	0.62	3877493	gene; cDNA EST yk200e4	3e-46
	•		. [.			JU-70
- 1		sequence from	1			
j		cosmid E141E2, on	1		1	
		chromosome 22,	- 1			
9	Z69906	complete sequence	ſ			
- -	203300	[Homo sapiens]	0.61	<none></none>	<none></none>	<none></none>
1	ĺ	Uman alama Oliva				
- 1		Human clone CIITA-	- 1		 	
ı		8 MHC class II	1			i
5		transactivator CIITA	ł		(X79983) viral proteinase	
+	U18259	mRNA, complete cds.	0.61	1483567	[Pseudorabies virus]	9.8
j		S.tuberosum mRNA	T			2.0
	1	for inorganic	1	l	i	1
		phosphate	٠- [le	(U08884) protein VIII precursor	
ш.	X98890	ransporter, StPT1	0.61	475724	[Bovine adenovirus type 3]	7.6

Nearest Neighbor (BlastN vs. Genbank) Nearest Neighbor (BlastX vs. Non-Redundant Property of the complete cds of the cds of the cds of the cds of	
Rattus norvegicus 5- oxo-L-prolinase mRNA. complete cds MRNA. complete cds MP 1 H49) DNA sequence 293 L81667 sequence AE000760 the complete genome Mus musculus Rho- associated, coiled- coil forming protein kinase p160 ROCK-1 MISS12 mRNA, complete cds Mus musculus Rho- associated coiled- coil forming protein kinase p160 ROCK-1 MISS12 mRNA, complete cds MU27459 complete cds Pisum sativum S- adenosylmethionine synthase mRNA, 3' end. AE000763 the complete of 109 of L36680 AE000760 AE000760 AE000760 AE000760 AE000760 AE000760 AE000760 AE000760 AE000760 AE000760 AE000760 AE000760 AE000760 AE000760 AE000760 AE000760 AE000760 AE000760 AE0	oteins)
292 U70825 mRNA. complete cds 0.61 733543 polyprotein (SP:POLG_BVDVN, P19711); alternative splicing to C04A2.7a Homo sapiens (subclone 2_a9 from P1 H49) DNA sequence 0.61 2565087 protein (2 0 open reading frame [Homo sapiens] HOMEOBOX PROTEIN HOX-A3 (HOX-1.5) homeobox-containing transcription factor [Mus musculus] musculus] Mus musculus Rhoassociated, coiled-coil forming protein kinase p160 ROCK-1 mRNA, complete cds 0.61 295671 protein 2 homolog hORC2L mRNA, complete cds 0.61 295671 protein 2 homolog hORC2L mRNA, complete cds 0.61 200285 protein 2 homolog hORC2L mRNA, complete cds 0.61 200285 protein 2 homolog horc2 massivum S-adenosylmethionine synthase mRNA, 3' end. 0.61 2285790 protein 2 homolog horc2 mr.A quifex aeolicus section 5 of 109 of the complex period of the complex protein 2 homolog horc2 mr.A quifex aeolicus section 5 of 109 of the complex period of the complex period of the complex protein 2 homolog horc2 mr.A quifex aeolicus section 5 of 109 of the complex period of 10	P VALUE
292 U70825 MRNA, complete cds MRNA, complete cds MRNA, complete cds MRNA, complete cds MRNA, complete cds MRNA, complete cds MRNA, complete cds MRNA, complete cds MRNA, complete cds MRNA, complete cds MRNA, complete cds MRNA, complete cds MRNA, complete genome MRNA, complete cds	1
(subclone 2_a9 from P1 H49) DNA sequence 293 L81667 Aquifex aeolicus section 92 of 109 of the complete genome 294 AE000760 Mus musculus Rhoassociated, coiled-coil forming protein kinase p160 ROCK-1 mRNA, complete cds protein 2 homolog hORC2L mRNA, complete cds protein 2 homolog hORC2L mRNA, complete cds 296 U27459 L36680 (Subclone 2_a9 from P1 H49) DNA sequence 0.61 2565087 BHOMEOBOX PROTEIN HOX-A3 (HOX-1.5) homeobox-containing transcription factor [Mus musculus] (L11275) selected as a weak suppressor of a mutant of the subunit AC40 of DNA dependant RNA polymerase I and III (M97900) putative open reading frame [Mus musculus] (M97900) putative open reading frame [Mus musculus] (AB002086) p47 [Rattus norvegicus] Aquifex aeolicus section 5 of 109 of the complete cds of 109 of 109 of 109 of 109 of 109 of 109 of 109 of 109 of 109 of 109 of 109 of 109 of 109 of 109 of 109 of 109 of 109 of 1	
Aquifex aeolicus section 92 of 109 of the complete genome 0.61 2811092 HOMEOBOX PROTEIN HOX. A3 (HOX-1.5) homeobox-containing transcription factor [Mus musculus] Mus musculus Rho-associated, coiled-coil forming protein kinase p160 ROCK-1 mRNA, complete cds 0.61 295671 Ecognition complex protein 2 protein 2 protein 2 homolog hORC2L mRNA, complete cds 0.61 200285 [M97900] putative open reading frame [Mus musculus] Pisum sativum S-adenosylmethionine synthase mRNA, 3' end. 0.61 2285790 [AB002086] p47 [Rattus norvegicus] Aquifex aeolicus section 5 of 109 of the complete case of 109 of	4.4
Mus musculus Rho- associated, coiled- coil forming protein kinase p160 ROCK-1 mRNA, complete cds 1 Human origin recognition complex protein 2 homolog hORC2L mRNA, complete cds 1 Pisum sativum S- adenosylmethionine synthase mRNA, 3' end. 298 AF000673 the complete case of the submit AC40 of DNA dependant RNA polymerase I and III (M97900) putative open reading frame [Mus musculus] (AB002086) p47 [Rattus norvegicus]	3.3
Mus musculus Rho- associated, coiled- coil forming protein kinase p160 ROCK-1 mRNA, complete cds protein 2 homolog hORC2L mRNA, complete cds protein 2 homolog hORC2L mRNA, complete cds protein 2 homolog hORC3L mRNA, complete cds protein 3 homolog hORC3L mRNA, complete cds protein 3 homolog hORC3L mRNA, complete cds protein 4 hom	2.6
Human origin recognition complex protein 2 homolog hORC2L mRNA, complete cds Pisum sativum S-adenosylmethionine synthase mRNA, 3' end. Aquifex aeolicus section 5 of 109 of 298 AE000673 the complete case of the case of th	2.0
recognition complex protein 2 homolog hORC2L mRNA. 296 U27459 complete cds 0.61 200285 frame [Mus musculus] Pisum sativum S-adenosylmethionine synthase mRNA, 3' end. 0.61 2285790 (AB002086) p47 [Rattus norvegicus] Aquifex aeolicus section 5 of 109 of section 5 of 109 of the complete content of the content of the complete content of the c	1.5
adenosylmethionine synthase mRNA, 3' end. 0.61 2285790 (AB002086) p47 [Rattus norvegicus] Aquifex aeolicus section 5 of 109 of 298 AE000673 the complete over the complete ov	0.66
section 5 of 109 of (AF058446) histone	4e-12
AE0006/3 the complete genome 0.61 3395782 macroH2A1.2 [Gallus gallus]	6e-27
Homo sapiens full (AL031603) conserved hypothetical protein.	
Agrotis ipsilon mRNA for 3-hydroxy- 3-methylglutaryl coenzyme A 300 A 1009675	8e-29
1176370 Land	2e-73
chromosome 19. cosmid F18382B. centromeric end. complete sequence	
Land Sapicipi (16)	ONE>

-	Near	est Neighbor (BlastN vs	. Genbank)	Nearest N	eighbor (BlastX vs. Non-Redundan	
SEQ	I	1		3.11	Vs. Non-Redundan	t Proteins)
ID	ACCESSI		P VALUI	ACCESSIO	DESCRIPTION	
		Candida albicans		7	DESCRIPTION	P VAL
1	j	topoisomerase type	I			
302	****	(CATOP1) gene,	1	I		1
302	U40454	complete cds	0.60	<none></none>	<none></none>	
	1	Emericella nidulans	1		- CNOINES	<noni< td=""></noni<>
		mtDNA between	j	1		
- 1	Ī	h2/h5 and bh2/b2	ı	1		1
		junctions, genes for	f	1	1	1
- 1		ATPase subunit 6,	1	1		i
I		cytochrome oxidase	1	j		
		subunit 3, seven.	i			1.
ł		unidentified proteins	.	Į.	1	
		twentyfour tRNA's	'	1	1	1
303	J01390	and L-rRNA.	0.60	NOVE	1	
		Plasmodium	0.00	<none></none>	<none></none>	<none:< td=""></none:<>
- 1		falciparum RNA				
		polymerase I gene,	j		1	
304	L11172	complete cds.	0.60	<none></none>	ALONE.	
- 1		Caenorhabditis		a.tortes	<none></none>	<none:< td=""></none:<>
1		elegans cosmid	l		1	1
ſ		F39H11, complete	1 1		1	1
- 1		sequence	i 1			1
305	Z81079	[Caenorhabditis	1		ł	í
-	2010/9	elegans]	0.60	<none></none>	<none></none>	<none></none>
- 1		S.cerevisiae			MAJOR DNA-BINDING	Tanoline S
- 1		chromosome X			PROTEIN herpesvirus 1 (strain	1
- 1		reading frame ORF	1		11) >gi 60327 (X64346) major	j
06	Z49627	УЛR127c	0.60	110251	ssDNA-binding protein]
		Rattus norvegicus H-	0.00	118751	[Saimiriine herpesvirus 2]	9.6
1		K-ATPase alpha 2	1			
ŀ		gene, alternatively	j			i
[spliced products and	J		(AF003086) PfSNF2L	
07	U94911	partial cds	0.60	2213862	[Plasmodium falciparum]	
		Methanococcus			[[* asmouldin falciparum]	7.4
		jannaschii section 18				
8	_	of 150 of the	J		(D89240) unnamed protein	
~		Complete genome	0.60	1749688	product	5.7
1		Methanococcus annaschii section 55	<u> </u>			J./
ſ		of 150 of the	1			
9 T		complete genome	0.60		(U97068) zonadhesin [Mus	I
—			0.60	3327421	musculus]	4.3
	ŀ	laemophilus ducreyi	·	_		
1		poprotein gene,	- 1		(AL034491) conserved	ľ
		omplete cds	0.60	4000577	hypothetical protein	
			<u> </u>	4008577	[Schizosaccharomyces pombe]	2.5

-	Near	est Neighbor (BlastN vs	. Genbank)	Nearest Nais	phos (Planty	
SEQ	Í			THE TEST IN ET	hbor (BlastX vs. Non-Redundant	Proteins)
ID	ACCESSI	ON DESCRIPTION	P VALUE		i	
			T P VALUE	ACCESSION	DESCRIPTION	P VAI
				+	probable protein-tyrosine kinas	6
311	X80700	H.sapiens G17 gene		1	(EC 2.7.1.112) RTK - Pacific	-
		Mus musculus (clon	0.60	422541	electric ray >gi 290858	1.5
		R24) rds gene, parti				
312	L42167	cds		i	(AF033823) moira [Drosophila	
			0.60	4220848	melanogaster)	0.51
- 1		Human hMSH6	J	i		0.51
313	U54777	mRNA, complete cd	0.00		(AF031087) mismatch repair	
		Human mRNA for	s 0.60	2665637	protein MSH6 [Mus musculus]	5e-07
ł		KIAA0232 gene,	1			1 200,
314	D86985	complete cds	0.60		(U97006) No definition line	
		Tompiete eds	0.60	1938462	found [Caenorhabditis elegans]	2e-07
- 1			1 .		(USS376) coded for by C.	
1			1		elegans cDNA cm21e6; coded	
1					for by C. elegans cDNA	i
- 1			i 1		cm01e2; similar to melibiose	İ
- 1		Rat liver mRNA for	1 1		carrier protein	
315	D43964	Kan-1, complete cds	0.60		(thiomethylgalactoside permease	
		Rattus norvegicus	0.00	1280135	II)	5e-15
- 1		CTD-binding SR-like	1 1			
- 1		protein rA4 mRNA.	1			
16	U49058	partial cds	0.60	21.1500.	(U37500) RNA polymerase II	
ſ		U.ruddi	0.00	2145091	largest subunit [Mus musculus]	le-19
[mitochondrial 12S	ľ			
17	X84388	ribosomal RNA	0.60	207.12.47	(Z70205) predicted using	
- 1		Caenorhabditis	0.00	3874247	Genefinder	2e-37
1		elegans cosmid	j			
18 /	AF125447	Y14H12B	0.59	<none></none>		
- 1		Hyoscyamus muticus		- GAOINES	<none></none>	<none></none>
- 1		clone cVS2	j	!	T	
1.		vetispiradiene	- 1	l	1	
ا ،		synthase mRNA,	1	į.	1	
9		partial cds.	0.59	<none></none>	J.	
J		Human gastric H,K-		4.01.12	<none></none>	NONE>
1		ATPase catalytic	1	1		
0 1		subunit gene,	J		1	•
- N	163962	complete cds.	0.59	<none></none>	ANONE:	
	1.				<none></none>	NONE>
1		lelicobacter pylori	1	[1	1
1		strain P1) comB and	I	j		- 1
	Į P	mi/algA (partial)	i		i	
AI		enes, and partial DRF1 and ORF2	· 1	İ	1	1

	Neare	st Neighbor (BlastN vs.	Genbank)	Nearest Neis	phbor (BlastX vs. Non-Redundant P	
SE					Non-Redundant P	roteins)
П	ACCESSIO		P VALUE	ACCESSION	DESCRIPTION	P VALUI
-		Mus musculus				1 174201
- 1		transcription factor				
J	ł	AP-2 (AP-2) gene,	1	1		ļ
- 1	ı	alternative exon 1a,	ļ			
32:	, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	and isoform 2, partia	.1	ł	(AC002332) hypothetical	I
32	2 U17289	cds. S.cerevisiae	0.59	2459419	protein [Arabidopsis thaliana]	9.4
1	1	12.02.00.00	1	i		
ı	[chromosome XIV			(Z67990) Similarity to Rat	ŀ
323	3 Z71466	reading frame ORF YNL190w	1	1	amiloride-sensitive sodium	İ
1	2/1400	TINLIYUW	0.59	3875542	channel beta-subunit	7.3
	1	Beet soil-borne virus		,		
1	· I	genes for 13K, 22K	1			
324	Z66493	and 48K proteins	0.59	2110067	cryV465 protein - Bacillus	
		Homo sapiens	0.59	2119867	thuringiensis thuringiensis]	7.2
		prostasin mRNA,			CRYSTALI DI IIG	
325	L41351	complete cds	0.59	729212	CRYSTALLIN JIC crystallin	
1		S.lincolnensis gene	7.27	727212	[Tripedalia cystophora]	4.2
1	1	for 16S ribosomal	j j		(AF056577) high mobility	
326	X79854	RNA	0.59	3702828	group protein 1.2	
1	1	Strongylocentrotus			HYPOTHETICAL PROTEIN	3.2
1 227		purpuratus mRNA for	1 1		KIAA0129 product is novel.	
327	AJ223356	SuDp98 protein	0.59	2495704	[Homo sapiens]	2.5
328	X86019	H.sapiens mRNA for			(Y10027) transcription factor	
328	7,00019	PRPL-2 protein	0.59	1743341	TEF-1 [Mus musculus]	2.5
i	ľ	Xiphias gladius				
ł	1	creatine kinase gene,			(U69477) envelope glycoprotein	ŀ
329	U75528	partial cds	0.59	1045005	[Human immunodeficiency virus	
		partial cus	0.39	1845995	type 1] DNA POLYMERASE	2.4
1 :			İ		EPSILON SUBUNIT B DNA.	
			1		directed DNA polymerase (EC	ļ
					2.7.7.7) II chain B - yeast.	ľ
			ł	•	(Saccharomyces cerevisiae)	1
	à				>gi 786319 (U25842) DNA	l
			f		Polymerase epsilon, subunit B	
		Homo sapiens	i	ĺ	(Swiss Prot. accession number	
,,,		chromosome 5, PAC	ĺ		P24482) [Saccharomyces	1
330		clone 202e13	0.59	2506366	cerevisiae	14
		Rat receptor-linked				1.4
331		protein tyrosine	ł	ĺ	(X96713) collagen [Globodera	
221	L19180	phosphatase	0.59		pallida]	1.1_
Į		Listeria	f			
ĺ		monocytogenes secA	İ			
332		gene, complete cds.	0.50		(AF016415) No definition line	- 1
		, complete eds.	0.59	2291129	found [Caenorhabditis elegans]	0.83

-	·· Neare	st Neighbor (BlastN vs.	Genbank)	Nearest Nei	ghbor (BlastX vs. Non-Redundant P	
SE	Q				Liter (Blascx Vs. 140n-Redundant P	roteins)
I	ACCESSIO		P VALUE	ACCESSION	DESCRIPTION	P VALUE
-		Xenopus laevis			(AL031124) hypothetical	†
33	3 U24433	syndecan-2 mRNA,	1		protein SCIC2.25c	
133	024433	complete cds.	0.59	3355692	[Streptomyces coelicolor]	0.64
33	4 M23412	Drosophila muscarinic acetylcholine recepto mRNA, complete cd		168237	(M76546) hydroxyproline-rich	0.00
		Synaphea media chloroplast atpB-rbcI intergenic spacer region, partial			protein [Helianthus annuus] HYPOTHETICAL 67.5 KD PROTEIN IN PRPS4-STE20 INTERGENIC REGION >gi 626567 pir S46825 hypothetical protein YHL010c - yeast (Saccharomyces cerevisiae) >gi 2289881 (U11582) No definition line found [Saccharomyces	0.22
335	AF060729	sequence	0.59	731596	cerevisiae]	0.16
336	AF029734	Xanthobacter autotrophicus transcriptional activator AldR (aldR) gene, partial cds; and NAD-dependent chloroacetaldehyde dehydrogenase (aldB) gene, complete cds	0.50		PERIAXIN >gi 2143901 pir I58157 periaxin - rat >gi 505297 (Z29649)	
			0.59	2498801	periaxin [Rattus norvegicus] HYPOTHETICAL 34.3 KD PROTEIN IN TAF145-YOR1 INTERGENIC REGION >gi 2131717 pir S64612 hypothetical protein YGR277c - yeast (Saccharomyces cerevisiae) >gi 1323505 gnl PID e243248	0.13
337	3/06000	C.reinhardtii LI818r-	0.59	İ	(Z73062) ORF YGR277c	ĺ
338] (Dictyostelium discoideum tRNA- Glu-GAA gene, clone (GluGAA8.	0.59		[Saccharomyces cerevisiae] HYPOTHETICAL 43.3 KD GTP-BINDING PROTEIN IN DACB-RPMA INTERGENIC REGION >gi 606121 coli]	1e-04 3e-06
339		łuman hMSH6 gene. xon 2	0.59		(AF031087) mismatch repair protein MSH6 [Mus musculus]	5e-07

\vdash	1	Vearest	Neighbor (BlastN vs.	Genbank)	Nearest Ne	ighbor (BlastX vs. Non-Redundant)	
	EQ					Volume VS. Non-Redundant	Proteins)
	D ACCE	10122	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	İ
			Escherichia coli	+	1	DESCRIPTION	P VALU
			genomic DNA. (25.3	2	 		
34	10 D90	0747	25.6 min)	0.59	134286	DOLIGHOU MINI ST	
	İ				134200	DOLICHOL KINASE major centromere protein.	6e-08
١.,			Human desmoplakin	1	j	CENP-B [human, Peptide, 594	i
34	J05	211	mRNA, 3' end.	0.59	246796	laa]	4 00
	ļ					KINESIN LIGHT CHAIN	4e-08
1			Loligo pealii kinesin	1	l	(KLC) sea urchin	1
34	2 L24	441	light chain mRNA,	1 .		(Strongylocentrotus purpuratus)	ł
J	- 1224	741	complete cds. Human cardiac alpha	0.59	547800	>gi 161530	5e-14
1		i	myosin heavy chain	7	1.		1
			(MYH6) gene, exons	1	i '		
34:	3 M25	140	2. 3 and 4.	0.58		1	1
			Homo sapiens	0.38	<none></none>	<none></none>	<none></none>
l	ļ		(subclone 9_h2 from	1			
ļ	<u> </u>		PI H21) DNA	l i		[
344	L819	[sequence	0.58	<none></none>	1	
	1		Homo sapiens full		CHOILES	<none></none>	<none></none>
	. [length insert cDNA	1		•	
345	AF087		clone YU51G04	0.58	<none></none>	<none></none>	210215
	1		H.sapiens flow-sorted			CHOILE	<none></none>
	1		chromosome 6 TaqI			1 .	
.346	Z785		fragment,	j			
.540	2/83		SC6pA10G11 Blattella germanica	0.58	<none></none>	<none></none>	<none></none>
			Ilatostatin				
	ł		europeptide	- 1		1	1
	l		recursor, gene,	ł		1	
347	AF0680		omplete cds	0.58	MONT		- 1
			Iomo sapiens Cdc7	0.58	<none></none>	<none></none>	<none></none>
			CDC7) mRNA,	1		1	
348	AF0155		omplete cds	0.58	<none></none>	21027	
					THOMES	<none></none>	<none></none>
			lethanosarcina	i		1	1
		ba	irkeri atp operon:	i		† i	1
			TP synthase beta	ł		1	}
			bunit (atpD), ATP	i		1	ľ
ľ		sy	nthase epsilon	j		ļ	i
l			bunit (atpC), ATP	j]	1
			nthuse gene 1	i			I
349	AF02800		pl). ATP synthase	0.50		(AC004136) putative DNA	
-1	02000	, J 14 S	ubunit subunit (0.58	3184291	polymerase III gamma subunit	9.4
- 1		M	is musculus gene	1			
			pancreatic trypsin,	j	ļ		1
50	AB01703		nplete cds	0.58		(AF056704) synapsin IIIa	1
				9.50	3170561	[Rattus norvegicus]	9.2

	Neares	Neighbor (BlastN vs.	Genbank)	Nearest Neig	ghbor (BlastX vs. Non-Redundant P	rotoi
SEC					Total VS. Non-Redundant P	roteins)
ID	ACCESSION		P VALUE	ACCESSION	DESCRIPTION	P VALU
-	-}	Dictyostelium discoideum				
1	J	developmental	1	i		
1		protein DG1110	1			
1	1	(DG1110) gene,	l			1
351	AF081585	partial cds	0.50		basic proline-rich peptide IB-8a	ł
	12 001303	partiar cus	0.58	105417	· human	9.2
1	i		1	1	hypothetical protein - African	
	1	,	Ī		swine fever virus (strain Malawi	ĺ
	i .			•	Lil-20/1) >gi 450758 (X71982)	ł
	I		ł	i	myeloid differentiation antigen	
1		Homo sapiens full	l	i	homologue [African swine fever	
l		length insert cDNA	j .	1	virus] >gi 903686 (M95672)	
352	AF086322	clone ZD53E01	0.58	93026	unknown protein	7.1
	1	Homo sapiens full			Giantie wa protein	/.1
		length insert cDNA			(U92805) thrombospondin-3	
353	AF088025	clone ZC19C04	0.58	2384644	[Xenopus laevis]	7.0
		Human mRNA for				
354	4 D000000	KIAA0341 gene,			M130 antigen (cytosolic variant	
334	AB002339	partial cds	0.58	2135587	2) - human	5.4
		Methanococcus jannaschii section 90		-		
		of 150 of the			1	
355	U67548	complete genome	0.58	2011001	(AL021957) hypothetical	
	00,0,0	complete genome	0.38	2911094	protein Rv2174 PYRUVATE	4.2
		i	ľ		DECARBOXYLASE (8-10 NM	
			i		CYTOPLASMIC FILAMENT-	
			1		ASSOCIATED PROTEIN)	!
	ľ		ſ		(P59NC) 4.1.1.1) - Neurospora	1
		Homo sapiens	- 1		crassa >gi 293948 (L09125)	
ľ	1	receptor tyrosine	Į.		pyruvate decarboxylase	i
		kinase (ERBB4)	I		[Neurospora crassa]	ł
356	L07868	gene, complete cds.	0.58.	461922	>gi 1655909.	4.2
- 1		Danillon or belle				
ľ		Bacillus subtilis	1			
· [sigma 43 operon with				
- 1		P23-dnaE-rpoD genes dnaE for DNA			(U55387) similar to C. elegans	ł
ĺ		primase, rpoD for	- 1		F38E1.9 gene product encoded	
357		RNA polymerase)	0.50	1202704	by GenBank Accession Number]
		stri potymerase)	0.58	1323704	U41996 [Cricetulus griseus]	4.1
- 1	lı.	Desulfovibrio	ł			
j		ulgaris rbo gene for	1			}
		esulfoferrodoxin and	i			
J		ub gene for	1	ļ		
	ļr:	bredoxin, complete			(AC004680) putative protein	
358		ds	0.58		kinase [Arabidopsis thaliana]	2.4

·	Neares	t Neighbor (BlastN vs.	Genbank)	Nearest Neis	hbor (BlastX vs. Non-Redundant F	
SEC			1	Troutest (ve)	Blasta vs. Non-Redundant F	roteins)
ID		N DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	
		Human DNA	+	i i i i i i i i i i i i i i i i i i i	DESCRIPTION	P VALU
		sequence from	 			
1]	cosmid B20F6 on		1		
1	1	chromosome 22,	1	}		
	1	complete sequence	1			1
359	Z82174	[Homo sapiens]	0.58	2145455	(Y07866) catalase-peroxidase	2.4
1	1	F.solani STI35			(= 0.000) catalase-peroxidase	2.4
		protein gene,		1	(AL021897) hypothetical	
360	M33642	complete cds.	0.58	2896706	protein Rv1069c	2.4
	ł	Mus musculus				
1	1	transforming growth	1	i	(Z81038) predicted using	1
		factor alpha (TGF	1	٠.	Genefinder; cDNA EST	ļ ·
361	1164072	alpha) gene, partial			yk488a2.5 comes from this gene	.}
301	U64873	cds Macrophthalmus	0.58	3874437	[Caenorhabditis elegans]	1.8
	1	banzai mitochondrial				
	f	DNA for 12S and	!	ĺ	ł	1
		16S rRNA, partial	! !		1	1
	Î	and complete	1		(4.700.4676)	
362	AB002132	sequence	0.58	2960022	(AJ224676) rho type GEF	_
		Caenorhabditis		2900022	[Drosophila melanogaster]	1.8
		elegans MutS			1	
		homolog (msh-5)			(U75869) Omp22 [Helicobacter	
363	AF070070	mRNA, partial cds	0.58	4098205	[pylori]	1.8
		Staphylococcus			P2	1.0
i		epidermidis plasmid	I			
ı		pIP1629 mobilization	j		1	
364	A E045240	protein (mobC1),	1		1	
304	AF045240	(orf69-1), (mobA1), H.sapiens Wilms	0.58	4218117	(AL035353) protein (fragment)	0.62
ļ		tumor gene 1, exons 8	1			
365		and 9	0.50	2221242	(U88211) unknown [Gallus	Į
-	.101057	and 9	0.58	2331059	gallus]	0.62
		•	J		l · · l	Į.
- 1	į.	Moraxella catarrhalis	ļ		1	
- 1	į.	strain 4223 transferrin	Į.		1	j
- 1		binding protein A	1		1	
_ [(tbpA) and transferrin	1		FIBER PROTEIN	- 1
`]		binding protein B			>gi 74229 pir ERADFM fiber	1
į		(tbpB) genes,	- 1	•	protein - mouse adenovirus 1	ŀ
,,,		complete cds; and	1		>gi 209758 (M30594) fiber	ļ
366		inknown gene	0.58	120155	protein [Mastadenovirus mus1]	0.27
	T I	luman mRNA for				
367		CIAA0273 gene,			(U94177) androgen receptor	
~~	D87463 c	complete cds	0.58	3861477	[Pan troglodytes]	0.12
	l,	lus musculus ninein	l	l		
68		nRNA. complete cds.	0.50	4115026	(AF118223) No definition line	
	3 70372 M	itti i A. Complete cus.	0.58	4115936	found [Arabidopsis thaliana]	0.004

2509

	Neares	t Neighbor (BlastN vs.	Genbank)	Nearest Neio	hbor (BlastX vs. Non-Redundant P	<u> </u>
SE			7	1	Total Vs. Non-Redundant P	roteins)
II	ACCESSIO	N DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALU
-		000				IF VALU
	1	CD68=110kda	1			+
1	1	transmembrane	1	1	1	
		glycoprotein [human		· ·		1
	į.	promonocyte cell lin U937, mRNA, 1722	e	1	1	
369	S57235	nt]	0.50		(U96113) WWP1 [Homo	
	937233		0.58	2072501	sapiens]	le-04
1	<u>I</u>	Mus musculus	ĺ		(D(2401) 771 - 172 - 172 - 172	
1	1	serotonin1A receptor	1	Ī	(D63481) The KIAA0147 gene	}
370	U39391	mRNA, complete cds		1469876	product is related to adenylyl	
			0.50	1403070	cyclase. [Homo sapiens]	le-07
1	1	Monkey B-	1]	İ]
ĺ	1	lymphotropic		i		
1	1	papovavirus genes for				
	1	VP-1, 2, 3 and large	Į	ľ		
ĺ		T antigen, complete	l i			
l	1	and partial cds, strain LPV-76 > ::	1			
ļ		gb M14494 PPMVP1				
İ	[M Monkey B-			}	
		lymphotropic			1	
	ſ	papovavirus mutant				
	! .	(LPV-76) PstI B			1	
	1 .	fragment encoding				
		VP1, VP2, VP3 and	j		(41001774)	
371	D00056	T-antigen.	0.58	2462069	(AJ001774) vanadium	
				2402009	chloroperoxidase HYPOTHETICAL 43.8 KD	1e-08
		Amsacta	į.		PROTEIN IN NCE3-HHT2	
		entomopoxvirus			INTERGENIC REGION	
		spheroidin gene,	I		>gi 2131871 pir S62957	
		complete cds, and	- 1		hypothetical protein YNL035c -	
		four vaccinia related	i	l	yeast (Saccharomyces	
- 1	1	orfs. > ::	ļ	` I	cerevisiae)	
- 1		gb 116670 116670	ſ		>gi 1301880 gn1 PID e239670	ļ
372		Sequence 1 from			(Z71311) ORF YNL035c	
 		gloo-S=growth-	0.58	1730722	[Saccharomyces cerevisiae]	8e-14
		ssociated protein	i	1		
373		GAP-43 homolog	0.58		(AF037168) DnaJ homologue	.]
		aoimione	0.38	2689720	Arabidopsis thaliana]	7e-14
1	rl	etraodon fluviatilis	1		HYPOTHETICAL 34.9 KD	1
		myloid precursor			PROTEIN C57A10.11C IN	
1		rotein mRNA.			CHROMOSOME I	ſ
374	AF018165 c	omplete cds	0.58		egi 2058378 gn1 PID e314002	
					onioej	5e-22

Ļ	. 1-1	Neares	t Neighbor (BlastN vs.	Genbank)	Nearest Neig	hhos (Plany)	
- 1	SEQ			1	THE TEST THEIR	thbor (BlastX vs. Non-Redundar	t Proteins)
ļ	ID	ACCESSIO	N DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
┝		-					IF VALUE
		į	Filobasidiella				
		Í	neoformans		Í	i	1
- [l	translation elongation	1	ľ		
		ļ	factor EF1-alpha	1	j ·	1	j l
- [375	U81803	(CnTEF1) mRNA,	ł			
⊢	3/3	081803	complete cds Candida albicans	0.57	<none></none>	<none></none>	<none></none>
- 1	- 1		ATCC 18804, CBS	1			- 3.0.0
- 1	I			1	i	İ	
			562 peptide				- [
-	376	U09781	transporter gene,			ĺ	1 1
尸		009781	complete cds. Homo sapiens	0.57	<none></none>	<none></none>	<none></none>
1.							
1	- 1		(subclone 4_b10 from BAC H102) DNA	i i			1 1
1 3	77	AC002143	1				1 1
F		11002143	sequence Tetrahymena	0.57	<none></none>	<none></none>	<none></none>
1	- 1		thermophila RR		'		
1			internal deletion	l .		i	1 1
3	78	U23442	sequence.	0.67			ŀ
			Mus musculus	0.57	<none></none>	<none></none>	<none></none>
	- 1		transcription factor	·			
1	- 1		AP-2 (AP-2) gene,	Ī			1 1
1	- 1		alternative exon 1a.	1			1 1
1			and isoform 2, partial	ı			
<u>_3</u> 7	79		cds.	0.57	NONE	1	1 1
Γ	T				<none></none>	<none></none>	<none></none>
ı		į:	Buzura suppressaria			i	
l			nuclear polyhedrosis				1 1
l	- 1		virus gene for	f			1 1
38	0		oolyhedrin protein	0.57	<none></none>	***O>#	1
l		T			CHOILE	<none></none>	<none></none>
	1	. 1	Homo sapiens 5T4	ı	ſ		
	1	İc	ncofetal trophoblast		j		1 .1
38	1 4	AJ012159 g	lycoprotein gene	0.57	<none></none>	<none></none>	1,70,75
	1		I.sapiens simple			CINOINES	<none></none>
5 .0.	.		NA sequence region	ĺ	l		
382		X76571 c	lone wg1a8.	0.57	<none></none>	<none></none>	<none></none>

<u> </u>	Near	est Neighbor (BlastN vs	Genbank)	Negrect M.	pighhar (DI, aV	
s	EQ			rearest M	eighbor (BlastX vs. Non-Redundant	Proteins)
	D ACCESSI	ON DESCRIPTION	P VALUE	ACCESSIO	N DESCRIPTION	P VALUE
\vdash	 	Vibrio cholerae				IF VALUE
		pathogenicity island				
- 1	ľ	putative transposase		f		
		aldehyde	·		1	ĺ
	1.	dehydrogenase	1		1	i i
1	i	(aldA), toxR-	ł	1	. [1
- 1	1	activated gene A		1		-{
1	1	protein (tagA),	İ		ł	1
-	į	putative inner	ł	I		1
		membrane protein.	ı	1 '		1
	1		ł	i		
1		and putative zinc	1	' '	!	1 .
	1	metalloprotease]		
38:	3 AF034434	genes, complete cds;		ł	1	1 1
1	12 034436	and Mus musculus gene	0.57	<none></none>	<none></none>	<none></none>
ļ	1	for TESP4, complete	1			1
384	AB017031	cds]]
	1 2 2 7 0 2 7	S.hispidus	0.57	<none></none>	<none></none>	<none></none>
1	1	mitochondrial DNA	1			
	1	for SSU ribosomal				1
385	X89788	RNA gene	0.57	*NONE		1 1
		Rat progesteron	0.57	<none></none>	<none></none>	<none></none>
İ]	receptor gene, 5'	1		(15001051)	
386	L16921	untranslated region.	0.57	3323116	(AE001251) femA protein.	1 1
1			9.57	3323110	putative [Treponema pallidum]	8.9
	İ	Homo sapiens	ı		(S48157) DNA polymerase- primase 180 kda subunit	1 1
	Í	interferon regulatory			Desception and subunit	i i
387	AF027292	factor 6	0.57	259790	[Drosophila melanogaster, Peptide, 1490 aa]	
	l	Cicer arietinum			hypothetical protein YDR446w -	6.7
200		mRNA for	[yeast CAI: 0.11 [Saccharomyces]	
388	AJ012581	cytochrome P450	0.57	2131498	cerevisiae]	
		11.				5.3
	l	Human transfer RNA-	- 1]	j
		Met (TRMEPI)	1			i
389	L15363	pseudogene, complete			(AF070935) GABA receptor	l
	213303	gene Helicobacter pylori	0.57	3228680	subunit [Musca domestica]	5.2
	1	26695 section 3 of	ł		(U97008) weak similarity to	
		134 of the complete	1		family 1 of G-protein coupled	1
390	AE000525	genome	0.57	1020	receptors [Caenorhabditis	i
		23	0.57	1938478	elegans]	4.0
I	ļ	Amblyomma	1			
1		americanum	1		1	ļ
ĺ]	ecdysteroid receptor	1	٠	·	j
	,	(AamEcR) mRNA,	I		(1104975) - 10 (D	1
391		3'UTR, region 1	0.57	2072224	(U94875) p40 (Borna disease	
					virus)	4.0

<u> </u>	Near	rest Neighbor (BlastN vs	. Genbank)	Nearest N	eighbor (Planty	
SEQ	2	-			eighbor (BlastX vs. Non-Redundant I	Proteins)
ID	ACCESS	ION DESCRIPTION	P VALU	į –		
	1	Human UbA52 gen	1 4 4 7 7 1 1 1	E ACCESSIO	N DESCRIPTION	P VAL
		coding for ubiquitin				1
	Ī	52 amino acid fusio		I		 -
392	X56997	protein	1		(AL022121) hypothetical	1
		- Protein	0.57	2960113	protein Rv3689	4.0
	1	Plasmodium		1	CYTOCHROME P450 2C14	7.0
	1	falciparum DNA ***	•	1	(CYPIIC14) phenobarbital-	1
	ĺ	SEQUENCING IN	1	1	inducible, hepatic - rabbit P-450	1
		PROGRESS ***	1	ı	[Oryctolagus cuniculus]	ł
		from contig 4-81,	1	i	>gi 358265 prf 1306317A	1
393	AL01026	complete sequence	0.57		cytochrome P450 [Oryctolagus	ł
		- suprete sequence	0.57	117233	[cuniculus]	3.9
ł		Xenopus laevis	1	† ''	GASTRULA ZINC FINGER	- 3.7
- 1		gamma-crystallin	·.	ľ	PROTEIN XLCGF44.2	
ĺ		(gcry3) gene.	1	1	>gi 85736 pir S06571 finger	·
394	M99581	complete cds.	0.57	1	protein (clone XlcGF44-2) -	
T		Drosophila	0.57	141647	African clawed frog (fragment)	3.0
- 1		melanogaster seven in	j	i i	<u> </u>	J.U
- 1		absentia mRNA,	1	f	1	
395	M38384	complete cds.	1 000		(U80454) T16A1.1	
T		Tompiete eds.	0.57	1707127	[Caenorhabditis elegans]	3.0
ľ		Haemophilus				3.0
Ī		influenzae Rd section			IRON(III)-TRANSPORT	
- 1		110 of 163 of the			SYSTEM PERMEASE	
96	U32795	complete genome	0.57		PROTEIN SFUB >gi 152861	
$\neg \Gamma$		Klebsiella	0.57	1173433	(M33815) protein (sufB)	2.3
-		pneumoniae nifX,	1			
- 1		nifU, nifS, nifV and	1		1	;
97	X12600	nifW genes	0.57		(AL021925) hypothetical	
			0.37	2909562	protein Rv2256c	1.4
		Homo sapiens mRNA	J		insect-stage-specific protein -	
1		for KIAA0626	ł		Trypanosoma cruzi >gi 162099	
28 A	AB014526	protein, complete cds	0.57		(M65021) insect stage-specific	
T		Rhodococcus fascians	. 0.37	482390	antigen	0.61
-	İ	strain NRRL-B-	1			
- 1		15096 hypothetical	1		1	ı
1	ł	protein gene,	ł		1	ľ
9 A	F063587	complete cds	0.57	448.5-	(AF034582) vesicle associated	ı
			0.37	4104321	protein [Rattus norvegicus]	0.46
1	le	Guinea pig estrone	ł			
	L11117 s	sulfotransferase gene.	0.57	22.5	alpha/beta-gliadin precursor	
		and to ase gene.	0.37	82584	(alama 4010)	0.35

25	Near	est Neighbor (BlastN vs.	Genbank)	Nearest Nei	ghbor (BlastX vs. Non-Redundant	
SEQ					Endo (Blastx Vs. 14011-Redundant	Proteins)
ID	ACCESSI	ON DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	
			7		DESCRIPTION	P VAL
	į	Mouse complete gene		1		
		for a mouse kallikreir		Ì		1
		gene. Genes are mGK	9	ĺ	·	İ
v		1 (complete gene) and mGK-2 of		i		ı
		hormones, e.g.,	1	l	.1	1
ł		grow > ::	I	i	1	
1		gb J00390 MUSKAL	l		NUCLEAR HORMONE	1
1		07 Mouse pseudo-	l	ł	RECEPTOR NOR-2 receptor	1
- 1		kallikrein 2, exons 4	ľ		[Rattus norvegicus]	1
- [and 5, and kallikrein			>gi 1583604 prf 2121281A	
401	V00829	1 gene, complete cds.	0.57	2500016	NOR-2 protein [Rattus	1
1			0.27	2500916	norvegicus]	0.20
1		Chicken mRNA for	J		(1140053) similar as a similar	
		beta-2 subunit of			(U40953) similar to matrin F/G (SP:Q00910) containing C4-	İ
102	Venne	neuronal nicotinic	· · · · · · · · · · · · · · · · · · ·		type zinc-fingers	
102	X53092	acetylcholine receptor	0.57	1072256	[Caenorhabditis elegans]	0.00.
		[(281035) predicted using	0.031
					Genefinder; Similarity to	l
					dehydrogenases; cDNA EST	
			1		EMBL:D65800 comes from this	
- 1		1	1		gene; cDNA EST	
- 1		1	ł		EMBL:D76184 comes from this	
- 1		Ovis ovis granulocyte			gene; cDNA EST	
,,		colony stimulating	ŀ		EMBL:D69322 comes from this gene; cDNA EST	
03	L07939	factor	0.57	3874345	EMBL:C08158 comes f	
J		Colletotrichum	1		EMBE. CO8138 comes 1	3e-07
- .		gloeosporioides	I		l	
14	U18061	CAP20 (cap20) gene,			(AC003974) putative ubiquitin	
\top	010001	complete cds.	0.57	2914695	specific protense	9e-08
-			· 1		TUMOR NECROSIS FACTOR,	
-	l		- 1	• •	ALPHA-INDUCED PROTEIN	•
1	1	1	<u> </u>	ĺ.	3 (PUTATIVE DNA BINDING	- 1
-			1	[;	PROTEIN A20) (ZINC	
1	j:	L.japonicus mRNA	1	,	FINGER PROTEIN A20)	
		for small GTP-		<u>[</u>	>gi 107549 pir A35797	1
1	ļį.	binding protein,	j	.	probable DNA-binding protein A20 - human >gi 177866	- 1
5 2	Z73955 II					

		st Neighbor (BlastN vs.	Genbank)	Nearest Neigh	bor (BlastX vs. Non-Redundant F)
SEC					Ton-Redundant F	roteins)
ID	ACCESSIO	ON DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
<u> </u>	 			 		T
	j		1		(277660) Similarity to Human	
	1		ļ	i	enoyl-CoA hydratase	
	1				(SW:ECHM_HUMAN); cDNA EST EMBL:T00611 comes	· }
	I		j ,	i	from this gene; cDNA EST	Í
	•				yk203d10.3 comes from this	1
		Petunia grp-1 gene	1		gene; cDNA EST yk203d10.5	1 1
	İ	for glycine-rich	Į i		comes from this gene; cDNA	1 1
406	X04335	protein	0.57	3876901	EST yk457h5.3 comes from t	
	1	Rattus norvegicus S-			231 yk437113.3 comes from t	le-27
	l	adenosylmethionine		٠,		. · [
	ľ	decarboxylase	1 1			1 1
407		(AMDP2)	1 . 1		1	
407	U40718	pseudogene S.cerevisiae SSD1	0.56	<none></none>	<none></none>	<none></none>
	ł	protein gene,	1 1			
		complete cds. > ::	1 1			1
		gb AR013983 AR013				i j
		983 Sequence 8 from	1			
408	M60318	patent US 5773245	0.56	2/01/2		
		Nicotiana tabacum	0.30	<none></none>	<none></none>	<none></none>
		blp4 mRNA for		j	j	
		luminal binding	ŀ			į.
409	X60057	protein (BiP)	0.56	<none></none>	<none></none>	
		Homo sapiens full			NONES	<none></none>
		length insert cDNA	i	I		Ì
410	AF085930	clone YR55A09	0.56	<none></none>	<none></none>	<none></none>
- 1		Plasmodium				STOTIL
- 1		falciparum DNA ***				1
ı	•	SEQUENCING IN	1		1	I
		PROGRESS ***	1	1	. 1	5
111	AL010189	from contig 3-102, complete sequence	255			- 1
-	AE010169	Murine G-CSF gene	0.56	<none></none>	<none></none>	<none></none>
ł		for granulocyte		j		
j		colony stimulating		ł		1
12	X05402	factor precursor	0.56	NONE-	1	
T		Rattus norvegicus		<none></none>	<none></none>	<none></none>
ĺ		regulator of G-protein	1			
	ſ	signalling 12	j	1	1	ł
. 1		(RGS12) mRNA,	į		i i	ł
13		complete cds	0.56	<none></none>	<none></none>	NONE>
		Human				1101127
- 1		papillomavirus strain	i l	[ŀ	ł
4		RTRX7 complete	1	}	į	İ
	093000	genome	0.56	<none></none>	<none> <</none>	NONE>

-		st Neighbor (BlastN vs.	Genbank)	Nearest Ne	ighbor (BlastX vs. Non-Redundant F	
SE	`				-sinos (Diasez Vs. 140n-Redundant I	roteins)
ID	ACCESSIO	N DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	
<u></u>			1	T HEELEGICIN	DESCRIPTION	P VALUE
	1	M. javanica	T			
	1	mitochondrion	1	ł	* •	1
		ATPase 6, and	1	1		1
415	V67606	putative tRNA-f-Met	1	I	1	j
1	X57626	and tRNA-His genes	0.56	<none></none>	<none></none>	<none></none>
416	AB003363	Sus scrofa \$100C	1			CHOINES
	/ AB003303	gene, complete cds	0.56	<none></none>	<none></none>	<none></none>
j		Danio rerio DANA	1	1	(AE001062) conserved	
417	L42291	element, intron 4.	0.56	2650000	hypothetical protein	1 1
		The state of the s	0.36	2650002	[Archaeoglobus fulgidus] L-LACTATE	8.7
1	I	1.		İ	DEHYDROGENASE	
	ı	1	· ·		(IMMUNOGENIC PROTEIN] <u> </u>
	1				P36) >gi 479296 pir S33362 L-	i I
	l	Mus musculus			lactate dehydrogenase (EC	1 1
410		leukocystatin gene,			1.1.1.27) - Mycoplasma	
418	AF031826	complete cds	0.56	462493	hyopneumoniae	6.7
i ,		Pennisetum glaucum				0.7
419	U17068	Ac-like element, AcL2.		ı	ESCARGOT/SNAIL PROTEIN	
· • • •	017008	H.sapiens mRNA	0.56	399449	HOMOLOG	6.7
İ		encoding GPI-			HYPOTHETICAL 8.7 KD	
		anchored protein	I		PROTEIN (READING FRAME	
420	Z48042	p137	0.56	141232	D) >gi 76316 pir QQSA7C	ŀ
		Choristoneura	0.50	141232	hypothetical protein E-74	6.7
		fumiferana	J		ACETYLCHOLINE	
I		entomopoxvirus	1		REGULATOR UNC-18	1
1	ľ	nucleotide			>gi 480359 pir S36747	1
j		triphosphate	1		acetylcholine regulator unc-18 -	ĺ
		phosphohydrolase I	1		Caenorhabditis elegans	J
421	4 220	(NPHI) gene,			>gi 247392 bbs 100294 putative	
	12 027037	complete cds	0.56	464999	acetylcholine regulator unc-18	5.1
- 1			i		URACIL-DNA	
1	/3	Homo sapiens mRNA	i		GLYCOSYLASE (UDG)	ľ
1		or MEGF7, partial	[herpesvirus 2 >gi 695219	j
122		ds	0.56	1718033	(U20824) uracil DNA	
	T			1710033	glycosylase COMMON PLANT	5.1
	j		ſ		REGULATORY FACTOR	1
					CPRF-1 >gi 515621 (X58575)	J
		Cmaculatus NGF	-		light-inducible protein CPRF-1	- 1
23		ene for nerve growth		į	[Petroselinum crispum]	
<u></u> _L	V725541 K	ictor	0.56	1169081	>gi 1498301 (U46217) CPRF1	3.8

<u> </u>		Neare	st Neighbor (BlastN	vs. G	enbank)		Neares	N-:-	hh- (Di		
	EQ		}				11021031	14618	hbor (BlastX vs. Non-Redunda	nt Proteins	s)
<u> </u>	ID ACC	<u>ESSIO</u>	N DESCRIPTIO	N	P VAL	I DE	1		1		
-				+			ACCESS	ION	DESCRIPTION	P V	AT
- 1	ĺ		Rat transcriptiona								=
1	- 1		repressor of myeli	n-							
10	24 M7		specific genes (SC	IP)					1440.000	- 1	
1-	M	2711	mRNA, complete	cds.	0.56		501027	7	(U01849) ORF2 [Trypanoso	ma	
1	- 1			T		\neg	301021		brucei] CHURISMATE MUTASE	2.	.3
1			1			- 1			(CM) / PREPHENATE		
1	ı		Caenorhabditis	- 1		- 1			DEHYDRATASE (PDT) (P-		
1	ı		elegans cosmid	- 1		- 1			PROTEIN)	1	
1	1		Y67D11A, comple	.					>gi 281791 pir S26053	- 1	
1			sequence	te		- 1			chorismate mutase (EC 5.4.99	. 5	
l	1		[Caenorhabditis	j		- 1			P / prephenate dehydratase (E	()	
425	AL02	3850	[elegans]	- 1	0.55				4.2.1.51) - Erwinia herbicola		
			J. Ogunsj		0.56		266771		>gi 43344	1	
	1			-		1				2.3	<u>_</u>
l	1		Schistosoma mansor	ni l		-			ATP synthase chain 6 -	1	
	1	l	gynecophoral canal	"		1			Platymonas subcordiformis	1	
	j	- 1	protein mRNA.	1				- 1	mitochondrion >gil633582	1	
426	U478	62	complete cds		0.56		2142122	- 1	(Z47797) ATP synthase subuni	:	
	1			+	0.50	+-	2147138		6 [Platymonas subcordiformis]	2.3	
	ł		luman germ line	1		1		- 1		1	_
	l	٤	tene homologous to			1		- 1		1	
	ł	Jb	ladder carcinoma	1		1		- 1	•	1	
	ĺ	lo	ncogene T24 (Gene			1	•	1	1160380)	1	
427	V0057	م اد	ode c-Ha-ras-1) with	1		1			U60289) receptor protein	1	
	, 003/		our exons.		0.56		1518672	1,7	yrosine phosphatase psi [Homo		į
128	Z7150	- '	laevis H1(0)-1	1				$-\frac{3}{0}$	D90899) ferrichrome-iron	1.7	
\neg		- 186	ile	 9	0.56	↓_	1651674	re	ceptor	١	
- 1		R	norvegicus renin			1		(4	AF045141) putative serine	1.3	4
29	M3727	3 ge	ne, exons 1-9.	_	1 5 6	l		pr	oteinase [Scirpophaga		ı
П		16.	.,).56	├	2853019	line	certulas]	1.0	-
- 1		Th	ermus		į			Γ		1.0	\dashv
		the	rmophilus polA		j	l		- [·		1
- 1		ger	ne for thermostable	•	ı	1		-		•	
30	Dan==	DN	A polymerase I,		l			1			1
"	D28878	con	nplete cds	0.	56		3659692	(Al	F068748) sphingosine kinase		ı
\mathbf{I}	715027	H.s	apiens HLA class				- 337072	_ II w	us musculus)	0.77	1
+	Z15027	1011	DNA	0.:	56		1304141	cha	13758) fibrinogen A-alpha-		1
-		11	T "					Tena	1(1	0.76	
- [Linu	nan T-cell surface		- 1			1	•		
2	M14362	mp	gen CD2 (T11)		- 1			CYL	1915) Tenascin-X [Bos		
\top		Time	NA, complete cds.	0.5	6	3	2462979	taur	us]		1
		Z.m:	ys mRNA for					1	1	0.59	
1			rophyll a/b-		- 1			1	1	1	
1_	Z50801	bindi	ng protein CP29	0.5	.			colla	igen alpha 1(I) chain -	1	
			F. 010111 C1 29	0.5	0	j	109677	l	se >gi 50487	ſ	

l	-	N	earest	Neighbor (BlastN	vs. Gen	bank)	Neares	Nai-	hhar (D)	
	SEQ ID	ACCES		į.	[1	LICIE	hbor (BlastX vs. Non-Redunda	nt Proteins)
		Ι		T DESCRIPTION	<u> </u>	VALU	E ACCESS	ION	DESCRIPTION	J.,,,
				 					HYPOTHETICAL 86.0 KD	PVAL
- 1		1					1		PROTEIN IN GLK1-SRO9	 -
- 1		ľ			- 1		ł		INTERGENIC REGION	- 1
- 1				S.cerevisiae	- 1		1		>gi 83159 pir \$19367	1
- 1			1	chromosome XIII	- 1		1		hypothetical protein YCL030	ow -!
 -	434	Z381	14	cosmid 9745	- 1	0.56			yeast (Saccharomyces	
ı			- 1			0.50	140372	<u> </u>	cerevisiae)	0.35
- [- 1	Escherichia coli D	NA		i			0.55
1,	135	4 F0 ===	8	gyrase A (gyrA) ge	ne.		1			- 1
F	+33	AF0522	254	partial cds	- 1	0.56	2724126		(AF038535) synaptotagmin V	'II
-	- 1		- 1	egula pulligo 12S			2/24120		[Homo sapiens]	0.12
1	- 1			mall subunit	- 1		ĺ			
	- 1			bosomal RNA ger	ne,	٠.	l		1	
			In	nitochondrial gene	- 1		ľ			1
			In D	or mitochondrial NA, partial	- 1	i		l	CYCLIN-DEPENDENT	
43	36	AF08064		quence	- 1			- 1	KINASE INHIBITOR I	- 1
				anio rerio mRNA		.56	3913223	ı	p21/WAF1 [Felis catus]	1 _
	- [fo	r protein tyrosine	1				- a r (r ens catus)	0.11
43	37	AJ00569	0 ki	nase	1 .	. 1		- I	(AF030962) unknown	1
1			H	man noggin	1-0	.56	2623830	[Schistosoma mansoni]	7e-06
1	٠		(N	OGGIN) gene,	1	- 1		1		76-06
43	<u>* -</u>	U31202	COI	nplete cds.	Ó.	56	3875475	[0	Z78411) F02D8.3	
1	- 1		1.			-	36/34/3		Caenorhabditis elegans]	le-06
439	.	X51695	JO _v	is sp. trichohyalin	1	- 1			A COO 4 6 6 5	
	+-	V31093	- mR	NA, partial	0.5	56	3386622		AC004665) unknown protein	1 :
			Par						Arabidopsis thaliana]	le-10
	1		Droi	tus norvegicus ein tyrosine	1	- 1				
	1		pho	sphatase D30	1	- 1		(A	F072709) putative	1 1
440	t	J28938		VA. complete cds				ОX	idoreductase [Streptomyces	
			 	Complete cds	0.5	<u> </u>	3293547	liv	idans]	, <u>,</u> ,
	1	٠.	Воп	elia burgdorferi		ı		T		le-1↓
4	1		(sect	ion 57 of 70) of	•	ı		- 1		
441	AE	001171	the c	omplete genome	0.56	. 1	221650	(Al	F016452) similar to the beta	1
					0.50	-	2315521	trar	isducin family	4e-16
	1			orhabditis		- 1		100	67951) contains similarity to	
142	ΔE	036685		ns cosmid		- 1		AT	P/GTP-binding site motif	1
. 72	AF	030082	C05B	10	0.56	_	1519671	(PS	:PS00017) [Caenorhabditis	1
- 1		İ	Yann	T		1	22.7071	leieğ	ans)	6e-20
- 1		j	vitella	ous laevis genin gene A1		- 1		(U4	1558) K02B2.3 gene	7
43	XO	1173	S' flan	king region	_	1		prod	luct [Caenorhabditis	1
\neg		-=:-	o man	ving region	0.56		1118102	elega	ans	
		l:	Mus m	usculus DNA		1		1		2e-31
- 1		- li	for MS	2 protein.		- 1		1	j	1
14	D10	0911	omple	te cds	055	- 1		1	·.	- 1
					0.55	1	<none></none>	í	<none></none>	NONE>

Ę	···	Near	est Neighbor (BlastN v	/s. Genbank)	Negreet Na	aichte (D)	
J :	SEQ]		1	1400003(146	eighbor (BlastX vs. Non-Redundan	t Proteins)
L	ID	ACCESSI			E ACCESSION	N DESCRIPTION	DVALLE
⊢	115		Rice mRNA ENI	17,			PVALUE
<u> </u>	445	D30010		0.55	<none></none>	<none></none>	
- 1			Escherichia coli			CHOINES	<none></none>
	146	775.00.	phosphoprotein	1			- 1
<u> </u>	***0	U51991	phosphatase	0.55	<none></none>	<none></none>	
ı	ł		Mouse T cell recep			CNOINES	<none></none>
- 1.	47	1410050	C-gamma-7.1 mRN	VA,	j	•	}
<u> </u>	"/	M18858	3' end.	0.55	<none></none>	<none></none>	
i	- 1		Homo sapiens T ce	:11-		THORES	<none></none>
- 1			death associated	i	İ	1	
1.	48	Mosara	protein gene.		1	1	1 1
<u> </u>	* *	U95218	complete cds	0.55	· <none></none>	<none></none>	
1	49	1414040	Human R-ras gene,			SHORES	<none></none>
1-4	***	M14948	exon 1.	0.55	<none></none>	<none></none>	1 1
ı	1		Human mRNA for			THORES	<none></none>
45	50	4 D0000	KIAA0355 gene,		1	- 1	1 1
\ 	"	AB002353	Taginbiete eda	0.55	<none></none>	<none></none>	- NOVE
J	- 1		Homo sapiens			SNONE	<none></none>
- 1	- [(subclone 1_d6 from	n	1	}	1 1
45	.	T 01 600	PI H54) DNA		1	1	1 1
1-3	` +	L81689	sequence	0.55	<none></none>	<none></none>	NOVE
1	- 1		1			T. C. C. C. C. C. C. C. C. C. C. C. C. C.	<none></none>
- 1			77	.		1	1 1
1	- 1		Human myristoylated	d			1 1
Í	ı		alanine-rich C-kinase	? [i	(AE001220) V-type ATPase,	1 1
45:	,	M68955	substrate (MACS)	1	Ī	subunit B (atpB-1) [Treponema	
13.	+	14108933	gene, 5' end.	0.55	3322710	pallidum	5.0
1	-		P momunations and a	ł			
1	1		R.norvegicus mRNA (pJG116) with				1 1
453		X62953		1	•	extensin-like protein - maize	1
	1	2102933	repetitive elements Synechocystis sp.	0.55	1076802	>gi 600118 mays]	5.0
1	1		mntABC transporter	1			5.0
1	ł		system: periplasmic-	1			1 1
1	1		binding protein	1 1	•		l · 1
1			(mntC), complete cds;	1			l l ·
1	1	j	(mntA) gene,	i 1		1	l [
	1		complete cds;	1		hydrogen dehydrogenase (EC	İ
1	l		membrane protein	1		1.12.1.2) - Clostridium	1
	l	J.	(mntB) gene,	ŀ		acetobutylicum >gi 557064	1
454	l I		complete cds.	0.55		(U15277) hydrogenase I	1
	<u> </u>		Plasmodium berghei	0.55	2117632	[Clostridium acetobutylicum]	5.0
	l		nerozoite surface	{			
	ł		rotein-1 gene.				ı
455	ι		omplete cds	0.55	10745		i
			1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	0.55	127654	MYOGLOBIN	4.9

V

	Nearest	Neighbor (BlastN vs. G	enbank)	Nearest Neigh	hhor (BlassY us No- D-t. I	
SEC		T SHOOT (SHOOT)	T T	ricarest Neigh	hbor (BlastX vs. Non-Redundant P	roteins)
Ð	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
<u> </u>						1
456	Z64937	H.sapiens CpG DNA, clone 17g7, reverse read cpg17g7.rt1a.	0.55	417298	MFS18 PROTEIN PRECURSOR	3.8
457	1110014	Macaca mulatta clone irh83 T-cell receptor alpha chain mRNA,			(L09212) tat protein [Simian	3.6
437	U10914	partial cds. Homo sapiens	0.55	310406	immunodeficiency virus] virus]	3.8
458	AF022838	multidrug resistance protein	0.55	1585251	traB gene [Amycolatopsis methanolica]	2.8
459	M35603	Mouse Hox-3.1 gene and Hox-3.2-Hox-3.1 intergenic region.	 0.55	 818849	(U25430) nucleotide pyrophosphatase precursor [Oryza sativa]	2.0
460		Plasmodium falciparum chromosome 2. section 32 of 73 of the complete sequence Plasmodium	0.55	137532	PROTEIN C2 >gi 74386 pir WZVZB6 59K HindIII-C protein - vaccinia virus (strain WR)	1.7
461		falciparum chromosome 2, section 32 of 73 of the complete sequence	0.55	137532	PROTEIN C2 >gi 74386 pir WZVZB6 59K HindIII-C protein - vaccinia virus (strain WR)	1.7
462		Human transcription factor (NFATc.b) mRNA, complete cds	0.55	3327144	(AB014565) KIAA0665 protein [Homo sapiens]	0.096
	; ;	Saccharomyces cerevisiae origin ecognition complex arge subunit (ORC1)			HYPOTHETICAL 86.0 KD PROTEIN IN GLK1-SRO9 INTERGENIC REGION >gi 83159 pir S19367 hypothetical protein YCL039w - yeast (Saccharomyces	
463	U34860 g	tene, complete cds	0.55	140372	cerevisiae) (U46674) coded for by C.	0.017
16:	<u> </u>	Homo sapiens clutaryl-CoA lehydrogenase GCDH) gene, exons			elegans cDNA yk27d9.5; coded for by C. elegans cDNA yk27d9.3; short region of weak homology to drosophilia	
464	AF012341 6	. 7. 8, 9, and 10	0.55	1166611	suppressor of sable protein	0.008

	Neares	Neighbor (BlastN vs. C	Genbank)	Nearest Nei	ghbor (BlastX vs. Non-Redundant	Description
SEQ			T		LION (Diasex Vs. Non-Redundant	Proteins)
ID	ACCESSIO	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	D
		HIV-1 isolate Q98-	1	1	DESCRIPTION	P VALU
		CxA from Kenya,		 		_}
1		envelope		ł	1	
1	ł	glycoprotein C2V3		ł		1
1		region (env) gene,		ł	1	1
465	AF004891	partial cds	0.54	<none></none>	<none></none>	2:02
j	ł	D.discoideum			CNONES	<none></none>
466	Y 10159	racGAP gene	0.54	<none></none>	<none></none>	ANONIE
ł		Homo sapiens mRNA			CHOINES	<none></none>
1	ł	for B120, complete		[I
467	AB001895	cds	0.54	<none></none>	<none></none>	<none></none>
		Bovine gene for			3.0.0.2	TONOINES
i i		aspartyl protease				1
ŀ		NM1 exons 3 and 4 >	٠.		1	j
		:: Icl X12357 Bovine			1	1
		aspartyl protease				
460	••••	NM1 gene, exons 3			1	ľ
468	X12357	and 4.	0.54	<none></none>	<none></none>	<none></none>
ſ			í			
ľ		Borrelia burgdorferi			ļ	1
469	AE001151	(section 37 of 70) of				f .
409	AE001131	the complete genome H.sapiens mRNA for	0.54	<none></none>	<none></none>	<none></none>
f		T cell receptor alpha	1	•	·	
470	X92052	chain	254	2702		1 1
	7132032	Mus musculus ileal	0.54	<none></none>	<none></none>	<none></none>
		lipid-binding protein	ŀ			
471	U00938	gene. complete cds	0.54	1000710	(U27698) calreticulin	1 1
		gener complete cus	0.54	1009712	[Arabidopsis thaliana] CASEIN KINASE II, ALPHA	4.9
1			ł		CHAIN (CK II)	1
	}	•	ľ		>gi 419938 pir A43297 casein	1
- 1			Ì		kinase II (EC 2.7.1) alpha	1 1
ı	į		1		chain - Theileria parva	1 1
	[1	M.thermoformicicum	· . *		>gi 161871 (M92084) casein	j . I
	ļ.	complete plasmid	. [kinase II alpha subunit]
472	X68367	FZI DNA	0.54	125272	[Theileria parva]	4.7
					(purtu)	7./
- 1		H.sapiens CpG DNA.	Į.			
472		lone 44c4, reverse	j		(AJ131094) Xvent-1B protein	
473		ead cpg44c4.rtla.	0.54	4191274	[Xenopus lacvis]	3.7
		luman gastric H.K-	. T			
		ATPase catalytic	1	•	(Z70757) similar to serine	ŀ
174		ubunit gene,	- 1		protease inhibitor	ŀ
174		omplete cds.	0.54	3881648	[Caenorhabditis elegans]	3.7
175		I.sapiens mRNA for			(D87963) ETF-related factor-1	
	700013 P	RPL-2 protein	0.54	1648828	(ETFR-I)	2.1

		Neares	t Neighbor (BlastN vs.)	Genhank)	Negrest Naid	hhor/Disay. N. D.	
	SEQ			T T	rearest reig	hbor (BlastX vs. Non-Redundant)	Proteins)
	ID	ACCESSIO	N DESCRIPTION	D.V.4.1.III	4.66770000		ŀ
		1.10023310	S.glaucescens genes	P VALUE	ACCESSION	DESCRIPTION	P VALUE
			strU, strX, strV and	 	<u> </u>		T
		l	strW for 5'-	ļ			
ı		i	hydroxystreptomycin	1	İ		I
			pruduction and				Ì
- 1			transport	1	ľ	(AF084524) cellular repressor	1
ı	476	X89010	polypeptides	0.54	25502.46	of E1A-stimulated genes CREC	}
Ì		1105010	porypeptides	0.54	3550345	[Mus musculus]	0.25
			Homo sapiens mRNA	•		CDE LEG	
۱.	477	AB007836	for Hic-5, partial cds	0.54	1097213	ORF 1 [Streptomyces	
ſ			The or partial cas	0.54	1097213	lavendulae]	0.15
1	ı				1		1 .1
ı			Comamonas		!		
-	•		testosteroni TsaR	· · ·	Ì		
-			(tsaR),	ĺ		į	1
1			toluenesulfonate	ł			
ı	ı		methyl-			İ	1 1
1			топоохуделаѕе			1	1 1
1			oxygenase component] [
	- 1		component (tsaB),				1
	ı		toluenesulfonate zinc-				1 1
1	478	1122622	indepedent alcohol			(Z96047) DY3.6	1
H	~ /°	U32622	dehydrogenase	0.54	3875351	[Caenorhabditis elegans]	0.006
1	ł		Arabidopsis thaliana				
	j		gene for beta-VPE,				1
1.	479	D61394	complete cds	0.53	NONE	,	1 1
Γ			complete eus	0.55	<none></none>	<none></none>	<none></none>
	- 1		Arabidopsis thaliana	Į.			1 1
	ł		gene for beta-VPE,			1	
Ŀ	180		complete cds	0.53	<none></none>	NONE	
ĺ			M.capricolum DNA	- 3,55	C. TOTTLES	<none></none>	<none></none>
Ľ	181	Z33072	for CONTIG MC097	0.53	<none></none>	<none></none>	<none></none>
						4,0,45	KNONES
l	1		Human	•			
1	- 1		phosphatidylinositol	i		į į	ľ
			(4,5)bisphosphate 5-	j			I
؍ ا	82		phosphatase homolog	1	i		Ī
4	82		nRNA, partial cds.	0.53	<none></none>	<none></none>	<none></none>
			S.cerevisiae	i			
	ı		chromosome XIV eading frame ORF	I			}
4	83					M130 antigen (cytosolic variant	1
		2/13/4	YNL048w	0.53	2135586	1) - human	2.1
	1	,	Listeria	1			
		4	nonocytogenes secA	j			1
48	34		ene, complete cds.	0.53		(AF016415) No definition line	<u> </u>
_			The complete cus.	0.55	2291129	found [Caenorhabditis elegans]	0.70

\vdash		Nearest Neighbor (BlastN vs. Genbank)					Nearest Na	ei o h l	or (Plany :	
SI	EQ					\dashv	r-curest 140	C1811(oor (BlastX vs. Non-Redundan	Proteins)
	D /	ACCESSI		DESCRIPTION		UE	ACCESSIO	N	DESCRIPTION	P VAL
\vdash				lus musculus mRi	NA					IF VAL
48	25	D06400		or HGT keratin.					(X96713) collagen [Globoder	_
1	"	D86423		artial eds	0.53		1235974		[pallida]	1
1	i			lus musculus V	i					0.41
48	,_	3/15040		ippa 21-6 gene,	1					ſ
1	"	Y15969	pa	rtial	0.52		<none></none>		<none></none>	ANONT
ĺ	1		M	110 - 110 -111 (-1-						<none< td=""></none<>
ĺ	ł			us musculus (clori	ie j	- [1
l	1			9) transcribed rmline T cell	ļ	- 1		- 1		1
ı	- 1				.	1		ı		ĺ
	1			ceptor gamma cha				- 1	(Z67990) Similarity to Rat	1
487	, I	M27480		er-g) mRNA, VJ4 region.	1	- 1	•	- [:	amiloride-sensitive sodium	1 .
	1	1/12/400		man (lambda)	0.52		3875542		channel beta-subunit	4.6
Ī	1			IA for	1	1		T		 •••
	1			nunogloblin light	1			- 1		
488	3	D87004	cha			- 1		- 10	U37272) winged helix protein	1
	1			man DNA	0.52		1766073		CWH-1 [Gallus gallus]	3.5
	1			uence from	1			- 1		
	1			mid E75B8 on	1	- 1		- 1		1
	1			omosome 22,	1				•	1
				plete sequence	1	1	•			1
489		Z99704		mo sapiens]	0.51	1	-MONTE	- 1		1
			T		1 0.51	+-	<none></none>	- -	<none></none>	<none></none>
	1		Sam	bucus nigra lectin	.	1				1
	1		prec	ursor mRNA,	}				*	i
490		J76523	com	plete cds	0.51	1	<none></none>	- [NONE	1
	l		1			1		┰	<none></none>	<none></none>
			Haer	nophilus	1	1		1		
	•		influ	enzae Rd section	İ	1		1		f I
491	١,,	120707	1	of 163 of the		1				
771	├ ──	32795	comp	olete genome	0.50	1_	<none></none>	1	<none></none>	<none></none>
			1	· , · · · · · · · · · · · · · · · · · ·				he	licase homolog g10L protein -	CINCINES
			LT				•	Af	rican swine fever virus	
192	м	14602		n myoglobin	_			>gi	414091 (X72951) G10L 125	
	171	17002	gene,	exon 2.	0.49	 	478384	KE	Da protein	7.0
Į		- 1		İ		1		(US	97002) similar to	
J		l		i		1		Sch	iizosaccharomyces pombe 4-	ļ
[Huma	n mRNA for		ı		nitr	ophenylphosphatase . [ļ
- 1				.0238 gene,		1		(PN	PPASE) (SP:Q00472,	1
93	D8		partial		0.24	l	1000		D:g5004) [Caenorhabditis	·
\neg					0.24	<u> </u>	1938429	eleg	ans]	2.5
		:	Xenop	us laevis		l				
- 1			nitotic		i		i			
[oprotein 90				1	}	1
)4	U9			. complete cds	0.23	١ .	NONE-			1
-				complete eus	0.23		<none></none>		<none></none>	<none></none>

	Neare	st Neighbor (BlastN vs.	Genbank)	Nearest Nei	ghbor (BlastX vs. Non-Redundant	Description
SE	Q				siles (Slastic Vs. Non-Redundant	Proteins)
	ACCESSIO		P VALUE	ACCESSION	DESCRIPTION	P VALU
<u> </u>	- 	N.crassa				T VALU
1		mitochondrial small				
495		(198) rRNA and Cys-		l	(L05670) clustrin [Mus	J
49.	J05254	tRNA.	0.23	192150	musculus]	5.1
l	l l	Gene for glutamate	1		/	
	İ	dehydrogenase (EC	.l	1	(L07867) invariant surface	İ
496	X16399	1.4.1.4), put. bacteria			glycoprotein [Trypanosoma	ı
1770	X10399	<u>Origin</u>	0.23	790933	brucei]	0.030
		Treponema pallidum	i	ĺ		
ľ	ł	section 67 of 87 of	i	i		1
497	AE001251		0.00		1	1
	1	the complete genome	0.22	<none></none>	<none></none>	<none></none>
	1	Homo sapiens	;	1		
	ł	amyloid lambda light				
	į.	chain variable region				1
498	AF026919		0.21	<none></none>	21025	1
		D.melanogaster	0.21	CHOINES	<none></none>	<none></none>
499	Z27247	mRNA for defensin	0.21	<none></none>	<none></none>	1
		Candida albicans			KNONES	<none></none>
500	Y15608	UBI3 gene	0.21	<none></none>	<none></none>	<none></none>
501	1,,,,,,,,	Human beta-tubulin			41.01.122	CNOINES
501	V00598	pseudogene.	0.21	<none></none>	<none></none>	<none></none>
		A.thaliana	1			
		microsatellite			1	
502	X79426	[repeated motif			1	}
-	1177420	A.caerulescens	0.21	<none></none>	<none></none>	<none></none>
		mitochondrial genes	1		1	
		for cytochrome b and				1
ı		NADH	- 1			
503	X75772	dehydrogenase 5	0.21	139626	DD OTEN TI DD TO TO	i i
				137020	PROTEIN T1 PRECURSOR	7.8
ł		j	· [*		(AL031583) 1-	Į Į
ł		•	1		evidence=predicted by content;	
i			i		1-method=genefinder;084; 1-	
- 1			1		method_score=47.46; I-	· ·
I	ļ		- 1		evidence_end; 2-	1
	- 1	[J		evidence=predicted by match; 2-	٠ .
- 1	1	S	į		match_accession=SWISS-	i
		Serratia marcescens	. 1		PROT:P23792; 2-	i
04		site specific		ļ	match_description=DISCONNE	i
 	11 020/30	recombinase	0.21	3645960	CTED PROTEIN.; 2-matc	4.6
1],	S.cerevisiae OST5	1			
05	3/07-15	zene	0.21	2275621	(AF014940) No definition line	
			<u> </u>	2275631	found [Caenorhabditis elegans]	2.7

ſ		Nearest	Neighbor (BlastN vs. C	ienhank)	Nearest Naio	phos (DL V N D L	
ı	SEQ		Tronginoor (Brasar vs. C	T T	realest reigi	hbor (BlastX vs. Non-Redundant F	roteins)
	ID	ACCESSIO	DESCRIPTION	D.V.A.L.I.E.	A COECCIO		
F		TreeL33IO	DESCRIPTION	PVALUE	ACCESSION	DESCRIPTION	P VALUE
H		 	Human prostate-	 	<u> </u>	(1107010)	
- 1		1	specific antigen (PA)			(U97012) C04E6.2 gene	
- [506	M24543	gene, complete cds.	0.21	1938527	product [Caenorhabditis	1
r		1	gene, complete cus.	0.21	1938321	elegans] RNA REPLICASE	2.7
ı				ļ		POLYPROTEIN 2.7.7.48) -	
- 1		•	Mouse			Erysimum latent virus	1
			thrombospondin			>gi 3892232 (AF098523)	I
- 1			(THBS1) gene,			replicase protein [Erysimum	J
L	507	M62470	complete cds.	0.21	548563	(latent virus)	2.1
1						(L40584) polyprotein	2.1
ı	[Homo sapiens cosmid			[Infectious pancreatic necrosis	
L	508	Y13544	Cl	0.21	1235710	virus]	2.0
1	i		Chicken MHC B	• •			1 - 2:0
1			complex protein (C12			1	1
Т			3) mRNA, complete			(AF090441) extracellular reelin	
\vdash	509	M24193	cds.	0.21	3600102	[Gallus gallus]	0.52
1	ا		H.sapiens TFE3 gene,			(X83413) U88 [Human	
F	510	X97161	exon 4,5 & 6	0.21	854065	herpesvirus 6]	0.30
	Ī		D DNA	· ·		TRANSCRIPTION FACTOR	
1	ı		R.norvegicus DNA	1		COUP 2 COUP-TFII - chicken]
	- 1		sequence for LFB1/HNF1	1		>gi 392817 (U00697) orphan	1
1.	511	X67649	promoter	0.21	2010111	receptor COUP-TFII [Gallus	1
F		207049	promoter	0.21	3913114	gallus]	0.004
			Fugu rubripes growth	ı		1	i i
ı			hormone (GH) gene,	I		(AE020881) 1 1 · ·	
1 5	512	U63807	complete cds	0.21	3510505	(AF030881) pol polyprotein	
Г			ompiete eas	- U.21	3310303	NAM7 PROTEIN (NONSENSE	3e-04
			,	ı		MEDIATED MRNA DECAY	
	ľ			Ī		PROTEIN I) (UP-	
ĺ	ł					FRAMESHIFT SUPPRESSOR	
l						1) factor NAM7 - yeast	. 1
	ı	•	H.sapiens mRNA for	Į.		(Saccharomyces cerevisiae)	
_5	13		laminin alpha 5 chain	0.21	400350	>gi 4023	le-07
	- 1		Mirounga leonina				
	- 1		major	Ī			j.
ı			histocompatibility				ł
l			complex class II		i		
_	, 1		(DQA) gene, partial		ļ	ļ	- 1
ᆣ	14		eds	0.20	<none></none>	<none></none>	<none></none>
			Fransmissible	· 1			
			gastroenteritis virus	1		•	
5	,	~~~~ l	TFI virion protein	0.00			ļ
ا و	-		zenes Drosophila virilis	0.20	<none></none>	<none></none>	<none></none>
			simple DNA	1	1	İ	1
51	16		equence (pDv-19)	0.20	NONTE		
-			edactice (DDA-13)	0.20	<none></none>	<none></none>	<none></none>

	Near	est Neighbor (BlastN vs.	Genbank)	None N		
S	EQ	3.00. (2.00 73.	Genbank)	Nearest Nei	ghbor (BlastX vs. Non-Redundan	t Proteins)
	D ACCESSI	ON DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
-						IF VALUE
		Homo sapiens biliar	У			-
5	17 M76741	glycoprotein (BGP)	1	1	1	
	17 M76741	gene, partial cds.	0.20	<none></none>	<none></none>	<none></none>
- 1	- 1	Mus musculus rae28	1			- CINONES
- 1	j	gene, exon 1 and	1	i	.1.	1
51	8 D78515	5'flanking region	0.20		1	1
		o tidikilig region	0.20	<none></none>	<none></none>	<none></none>
- 1	j	Drosophila	1			
	1	melanogaster RNA	1 1			- 1
-	j	polymerase II second	1 1		1	- 1 :
1	1	largest subunit	1 1		1	_ [·
	1	upstream (DmRP		·	j	. [
519	9 M62975	140) gene, exons 1-4.	0.20	<none></none>	<none></none>	
	ſ				CHONES	<none></none>
1	1	Chicken 78-kD	1 [
520	1427260	glucose-regulated	1 1			
1 320	M27260	protein, complete cds.	0.20	<none></none>	<none></none>	<none></none>
ĺ	1	Rice tungro		·		110112
1	l .	bacilliform virus				1 1
521	AF076470	Serdang strain, complete genome	0.00			1
-	12070470	Rice tungro	0.20	<none></none>	<none></none>	<none></none>
i	ł	bacilliform virus				
1	J	Serdang strain,	ſ	•	1	1 1
522	AF076470	complete genome	0.20	-MONTE:	1	1 1
		Human	- 0.20	<none></none>	<none></none>	<none></none>
	1	cyclooxygenase-2	I		1	1. 1
		(hCox-2) gene,	ı			
523	U04636	complete cds.	0.20	<none></none>	<none></none>	1 2/02/75
1		Plasmodium			CHOINES	<none></none>
		falciparum	[1 1
		chromosome 2,	j	•	,	1 1
		section 67 of 73 of	i		i	1
524	AE001430	the complete	I			
324	AE001430	sequence	0.20	<none></none>	<none></none>	<none></none>
			i	·	HYPOTHETICAL 15.5 KD	
		Mus musculus	ı		PROTEIN IN MOAE-RHLE] [
		phosphomannomutase	I		INTERGENIC REGION	1 1
		(Pmm2) mRNA,	ĺ		>gi 1787009 (AE000181) orf,	
525	AF043514	complete cds	0.20	3025004	hypothetical protein	
			0.20	3025006	[Escherichia coli]	9.8

	Neares	t Neighbor (BlastN vs.	Genbank)	Nearest Nei	ghbor (BlastX vs. Non-Redundant P	
SE	-				ghoof (Diaster vs. Ivon-Redundant P	roteins)
ID	ACCESSIO	N DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	BVALLE
├-	+					P VALU
	j	Xenopus laevis FTZ				
	j	F1-related nuclear	-	1	1	1
	1	orphan receptor			}	1
İ	j	variant (xFF1rAshor	D		(AB014477)	
526	U23144	mRNA, complete cd		3184402	(AB014477) period protein	
				3104402	[Chymomyza costata] PROBABLE MICKOSOMAL	9.6
1	1	1	1	į	SIGNAL PEPTIDASE 23 KD	ſ
	1	1	J	}	SUBUNIT (SPC22/23)	
l	ł	· ·	l		>gi 630688 pir S44854	1
1		1		· ,	K12H4.4 protein -	· ·
l	1			1	Caenorhabditis elegans	
l			[>gi 289708 (L14331) homology	
	l	D	[·	with signal peptidase; coded for	
	i	Paracentrotus lividus	f		by C. elegans cDNAs GenBank:	
527	U14621	Pax-6 (suPax-6)			M79661, M79662 and M79663;	
327	014021	mRNA, complete cds.	0.20	465894	putative	7.7
		Actinobacillus	1 1			
		pleuropneumoniae	1		j	
		MRP ATPase	}			
		homolog (mrp) gene.	1			
		partial cds; ApxIVA			HYPOTHETICAL 45.3 KD	
		var3 (apxIVA) gene,			PROTEIN IN THIS 5'REGION	
		complete cds; and			>gi 1084720 pir S56193	İ
		beta-galactosidase	1		probable membrane protein	1
		(lacZ) gene, partial			YFL062w - yeast	1
528	AF030511	cds	0.20	1175966	(Saccharomyces cerevisiae)	7.2
	l.				glyoxal oxidase (EC 1.2.3)	
		Homo sapiens clone	i		precursor - basidiomycete	
529	A F05050	24540 mRNA	1		(Phanerochaete chrysosporium)	. [
J27		Sequence	0.20	542394	>gi 1050302	5.8
[T.maritima pgK gene for 3-	ł			
- 1		hosphoglycerate	l l		1	1
530	3/	tinase	0.00	205540	(Z34531) coproporphyrinogen	
		imase	0.20	825648	oxidase [Homo sapiens]	5.8
- 1	1	łaemophilus				1
ł		nfluenzae Rd section	j	j	1	1
- 1		of 163 of the	1		(AE072979) ailia	Į.
531	U32686 c	omplete genome	0.20		(AF072878) ciliary outer arm	
					dynein beta heavy chain CARBON CATABOLITE	5.6
	i i	.cerevisiae	1		DEREPRESSING PROTEIN	- 1
		hromosome XI	•		KINASE >gi 1469803 (L78129)	
	Z28081 Y	ading frame ORF	i		serine/threonine kinase [Candida]	ſ
32		KL081w				

	· ;	Near	est Neighbor (BlastN v	(s. Genbank)	Nannas N		
s	EQ				inearest N	eighbor (BlastX vs. Non-Redundant	Proteins)
		CCESSI		V P VALI	i	i	
\vdash			Hordeum vulgare				P VALUE
ł	- 1		limit dextrinase				
5	,,	4 F000==	(HvLD99) gene,	1	1	(AF064077) adrenocorticotrop]
12	23	AF02272		0.20	3139154	hormone receptor (Sus scrofa)	
- 1	- 1		Drosophila			mormone receptor (Sus scrota)	4.3
53		1.00170	melanogaster cosm	nid	ł	(AC005623) putative argonaut	
133		AL021720		0.20	3885334	protein [Arabidopsis thaliana]	
j	İ		Brassica rapa mRN			(Duoidopsis manana)	2.6
53	5 / 4	B012106	for SRK45, comple	1	1	(Z92824) B0413.4	1 1
133	- -	IBU12106	cds	0.20	4008334	[Caenorhabdiris elevans]	1.5
- 1	ı			1		60S KIBOSOMAL PROTEIN	1.3
- 1					1 "	L30B (RP29) cytosolic - yeast	1 . 1
1	1				į.	(Saccharomyces cerevisiae)	1 1
ſ	1				1	>gi 171821 not determined)	1 1
- [1			i	1	[Saccharomyces cerevisiae]	ļ i
- 1	1				Ĭ	>gi 1045254 cerevisiae]	J - J
1	1		H.sapiens HLTF ger	ne		>gi 1323250 gnl PID e243708	1
536		Z46606	for helicase-like	1		(Z72933) ORF YGR148c	1 1
1-350	4-4	240006	transcription factor	0.20	132946	[Saccharomyces cerevisiae]	1.5
537	Ι,	797102	H.sapiens mRNA fo			DNA-REPAIR PROTEIN	 '
1-337	╂╾	(87193	2.19 gene	0.20	139820	XRCC1	1.5
-	1		1			HYPOTHETICAL 33.5 KD	1.5
	1			1	1	PROTEIN IN SEC53-ACT1	1 1
1	1				· ·	INTERGENIC REGION	1 1
İ	1		Į	1		>gi 1084703 pir S56211	1 1
1.	İ		Clostridium	1		probable membrane protein	
1	1		perfringens C beta 2	i	1	YFL044c - yeast	
1	l		toxin gene, complete	1	1	(Saccharomyces cerevisiae)	-
538	1.	77965	cds	1		>gi 836711 gnl PID d1009835	1
	<u> </u>	77703	cus	0.20	1175950	(D50617) YFL044C	1.4
1	1		Chicken neural cell-	ł			
1			adhesion molecule (N	1.	1	1	i
539	М	15938	CAM) gene, exon 18.	1			
			C. Livi) gene, exun 18.	0.20	2133082	regulatory protein MSR1 - yeast HYPOTHETICAL 55.9 KD	1.1
1 1				į i	I	HYPOTHETICAL 55.9 KD	
		- 1				PROTEIN C56G2.1 IN	Į
		į.	Solanum tuberosum		F	CHROMOSOME III	1
			mRNA for extensin-		•	>gi 726413 (U23177) C56G2.1	1
540	AJ0	03220	like protein, partial	0.20	2406020	gene product [Caenorhabditis	
			p. s.c, partial	0.20	2496932	elegans]	1.1
						EPIDERMAL GROWTH	
1		ŀ		Į.		FACTOR PRECURSOR	ļ
- 1		1	1	i		precursor - mouse >gi 309210	
541	_X9	8108	A.thaliana psbP gene	0.20	110007	(J00380) prepro-egf [Mus	l l
			7237 2010	<u> </u>	119227	musculus]	0.49

<u> </u>	Near	est Neighbor (BlastN v	s. Genbank)	Nearest Nai	ghbor (PlaneV	
SEQ	1			Treatest Ivel	ghbor (BlastX vs. Non-Redundant F	roteins)
ID.	ACCESSI	ON DESCRIPTION	PVALUE	1		P VAL
				 		1
	l		1	1	gene VGF protein - rat	
	1				>gi 205690 (M60525) nerve	1
	}		ı	1	growth factor inducible protein	1
	Ī	Homo sapiens mRI	NA	Í	[Rattus norvegicus] >gi 205701	ľ
		for KIAA0607	1	1	(M60522) nerve growth factor-	ĺ
542	AB01117	9 protein, partial cds	0.20	2143753	inducible protein (Rattus	l
í				2143/33	norvegicus] >gi 207651	0.39
j			1	1	RNA-binding protein mpD -	
		H.sapiens ITIH1 ge	ne	1	Arabidopsis thaliana (fragment)	
543	V755	(exon 22) and ITIH	3	· ·	>gi 510240 (X61108) RNA	
J43	X75318	gene	0.20	629557	binding protein [Arabidopsis thaliana]	_
- 1		Oncorhynchus myki	ss		(Harrana)	0.38
		mRNA for alpha 3		•	muf1 protein - human	
544	AB008374	type I collagen,	ļ ı		>gi 762953 (X86018) muf1	
-+	1100003/4	partial cds	0.20	1082610	[Homo sapiens]	0.37
ı		j	1 1			0.37
- 1		Limulus polyphemus	1 1		1	
		arginine kinase	1 1		1	
45	U09809	mRNA, complete cds	0.00		(AJ012650) CP [Papaya	
			0.20	3882016	ringspot virus]	0.37
		Homo sapiens mRNA] [
		for KIAA0864	1 1		(U93121) M-phase	
46	AB020671	protein, partial cds	0.20	2674350	phosphoprotein-1 [Homo	
- 1		Phytophthora	 	2074330	sapiens]	0.18
ł		megasperma	1			
		mitochondrial	j 1		1	
- 1		ORF152, complete	ļ į	ł		
- 1		cds, cytochrome c	ľ			
.		oxidase subunit I	1			
ľ		(cox1) gene,	1.			į
		complete cds,	1	- · · · · · · · · · · · · · · · · · · ·	(U23517) D1022.7	
7		cytochrome c oxidase subunit II	1	li	[Caenorhabditis elegans]	
\top		Phytophthora	0.20	746516	-: 12050651 1	0.043
		megasperma	1		5-1.10)	0.042
		mitochondrial	f	Ì		
1		ORF152, complete	ł			- 1
1	la	ds, cytochrome c	1	ļ	ŀ	ł
1		xidase subunit I	İ			i
1		cox1) gene,	i			ł
ı		omplete cds.	İ	ĺ		1
	lc.	ytochrome c oxidase	1		J23517) D1022.7	ı
L.	.04457 sı	ubunit II	0.20	7.165.16	Caenorhabditis elegans]	- 1
			0.20	746516 >9	gi[3258651 elegans]	.042

	- Nea	rest Neighbor (Blas	tN vs. Gen	ibank)	Nearest Nai	phor (BlockY V	
s	EQ			i	1.021031 1461	ghbor (BlastX vs. Non-Redundant F	roteins)
L	D ACCESS			P VALUE	ACCESSION	DESCRIPTION	
<u> </u>		Cdk3r=cyclin-				DESCRIPTION	P VALUE
- [ł	dependent kin	ase 5		 		-
	1	regulatory sub			Ī	<i>}</i>	1
	1	p35 [mice, bra	in,				1
- 1	1	129/SvJ, C57E				ļ	1
ر ۽ ا		Genomic/mRN	IA,			(AB007923) KIAA0454 protein	İ
54	9 S8281			0.20	3413870	[Homo sapiens]	
	ı	Streptomyces	riseus			(Azomo suprens)	0.020
- 1	1	DNA for	İ			ł	1
i	1 .	serine/threonin				(U29154) T07F12.2 gene	l i
55	D31792	protein kinases	.		•	product [Caenorhabditis	
1-55	D31792	Complete cds Homo sapiens		0.20	861405	elegans]	0.019
1	1	butyrophilin (B	T2 2				0.019
	1	gene, exons 5-1		- 1		(AF040954) putative protein	! !
55	U97499	complete cds	o, and		5 .	phosphatase 1 nuclear targeting	
	377433	Complete cas		0.20	2773341	subunit [Rattus norvegicus]	0.008
	1	Rattus norvegic	is .	j			
1	Ĭ	nonmuscle myo		1	•	,	1
1		heavy chain-A		i			1
552	U31463	mRNA. complet	e cds	0.20	2000111	(Z81130) predicted using	i
				0.20	3880111	Genefinder	0.002
1	1	Bacteriophage P			*	1	
1	1	right operon, orf	48,	1		1	1
1	Į.	replication genes	18			1	1
1	i	and 12, nin regio	n	1		i i	1
[I	genes, ninG	ı	1			- 1
l	ł	phosphatase, late					1
1		control gene 23,		i			I
i	1	60, complete cds,	late			(U42436) C49H3.3 gene	- 1
553	V70401	control region, sta	irt	1		product [Caenorhabditis	
333	X78401	of lysis gene 13	0	.20	1123087	elegans]	4e-04
	·	Nocardia	- 1				46-04
		lactamdurans peb	A D	ł		•]	1
		and pcbC genes for		1		1	
,		alpha-aminoadipy		[j		İ
		cysteinyl-D-valine		l	į i	PUTATIVE ENDONUCLEASE	1
ŀ		synthetase and	1			C1F12.06C yeast].
1		isopenicillin N		1.	Į(Schizosaccharomyces pombe)	
554	X57310	synthase	0.:	20		gi 1217980 (Z69944) unknown	
		S.epidermidis gene	s 0	-	1723511	Schizosaccharomyces pombe]	4e-09
- [epiY', epiY, epiA,			1		
- 1		epiB. epiC. epiD,		1		773 10 1) 0 1 100 1	ł
555	X62386	epiQ. epiP	0.2	20		Z73424) C44B9.1	
					3077727	Caenorhabditis elegans]	3e-10

-	Ne	arest N	leighbor (BlastN	vs. Ger	nbank)	Nearget Mai	abbas (DL 14	
SE	Q					Meglest [46]	ghbor (BlastX vs. Non-Redundant	Proteins)
ID.	ACCES	SION	DESCRIPTIO	N	P VALUE	i	· ·	
<u> </u>	 						(Z80220) similar to nucleotide	PVAL
1	1	- 1					binding protein; cDNA EST	
l	1	- 1		- 1		}	EMBL:M75897 comes from th	ie l
l	1					1	gene; cDNA EST	113
l	1			- 1		ł	EMBL:M89054 comes from th	is
ĺ	1	E	pizootic	- 1		1	gene; cDNA EST	1
	1		aemorrhagic dise			l	EMBL:D26713 comes from thi	s
	l	V	irus gene segmeni	6		İ	gene; cDNA EST	1
556	X5900	0 fo	or NS1	. "	0.20	2070-0-	EMBL:D26718 comes from this	s
_		Н	uman keratin I		0.20	3879755	gene; cDNA	80.16
557	M9877		ene, complete cds		0.20	1096000	(U41278) contains similarity to	
	· ·	M	us musculus	\neg		1086900	G beta repeats	2e-30
560		gr	anzyme K gene,				1	
558	AF01144	6 co	mplete cds	_	0.19	<none></none>	1	1
		١.,		T		2.01122	<none></none>	<none< td=""></none<>
		M	acaca mulatta clor	1e	- 1			
		IVI	MU1.5 FRG1-like		ı			
- [pse	eudogene, exons 7	'	1			ĺ
559	AF07470		1 8. partial Juence	1			1	
			dicago sativa		0.19	<none></none>	<none></none>	<none></none>
560	X13287	пос	lulin-25 gene	Ι,				CIVOIVE
			erevisiae	+-	0.19	<none></none>	<none></none>	<none></none>
- 1		chr	omosome X	1	i			
		reac	ling frame ORF	1				
61	Z49509	_ YJF	1009c	0).19	<none></none>		
			ine DNA for			VIVOINES	<none></none>	<none></none>
- 1		pros	taglandin	l .	ł		į.	
62	D89041	F2al	pha receptor,	l				
	D09041		al cds	0.	.19	<none></none>	<none></none>	
- 1			arius DNA for		1		Z1014E>	<none></none>
53	D29644	devi	anus DNA for anase					
丁		Helic	cobacter pylori,	0.	19	<none></none>	<none></none>	NONE>
-		strair	J99 section 22		ı			T-10(4E>
- 1		of 13	2 of the		- 1			ł
4 4	E001461		lete genome	0.1				j
		Homo	sapiens	U. I	-	<none></none>	<none></none>	NONE>
-		galaci	ocerebrosidase		1			
.		(GAL	C) gene, exon		1	1		- 1
5	L38559	17.	1	0.1	9	<none></none>		l
I			wazekii				<none> <:</none>	NONE>
			nic DNA		- 1			
. [fragme A405F	ent (clone		j	i	1	- 1
1 2				0.19				

<u></u>	Near	est Neighbor (BlastN vs.	Genbank)	Nearest Neig	phoor (BlastX vs. Non-Redundan	
S	EQ				Month (Blasta Vs. Non-Redundan	t Proteins)
	D ACCESSI	ON DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALU
-		T . (1. 47.0
1	ļ	Tetrahymena	ſ			
- [İ	thermophila		1		
- 1]	telomerase	İ	ł	i	j
15/	67 U25641	component p80	1	l	ł	Í
1-	67 U25641	mRNA, complete cds	0.19	<none></none>	<none></none>	<none></none>
		Human mRNA for	j			
56	8 AB00234	KIAA0345 gene,				ł
<u> </u>	AB00234	3 complete cds	0.19	<none></none>	<none></none>	<none></none>
Ţ	- I	E-winia	l			11011
		Erwinia carotovora	ł	l		1.
56	9 D10064	gene for pectate lyase		·	1	
1	D10004	III, complete cds Homo sapiens clone	0.19	<none></none>	<none></none>	<none></none>
1	ı	MF118 A4A10	, i			1.01.2
1		hypoxanthine			ļ	J
1	1	phosphoribosyltransfe			j	Í
		rase (hprt) 130 kb			1	1
		deletion mutant	1		1	
ŀ		mRNA, partial cds,	i		1	i
1	1	contains human Alu	1		1	. [
570	U31734	element	0.10			1
	1	Plasmodium	0.19	<none></none>	<none></none>	<none></none>
		falciparum	1			
ĺ	•	chromosome 2,	Ī		1	l i
l	i	section 23 of 73 of	Ì		1	1 1
l	ł	the complete	ı		1	1 1
571	AE001386	sequence	0.19	NONE		1
		Homo sapiens	0.19	<none></none>	<none></none>	<none></none>
i		hydroxymethylbilane	1			
İ	ľ	synthase gene,	j			}
572	M95623	complete cds.	0.19	<none></none>		
				CHONES	<none></none>	<none></none>
	ľ	(GC*IS)=vitamin D-	1			1. 1
	1	binding protein/group	I	j		1 1
		specific component	j			1 1
	İ	[human, peripheral	f			1 1
	i i	blood leukocytes,	1	ĺ		
		Genomic, 794 nt,	1	· [} I
573		segment 4 of 9]	0.19	<none></none>	<none></none>	LAYONTE L
ا		H.sapiens NRGN			THOMES	<none></none>
574		gene, exon 1	0.19	<none></none>	<none></none>	NONE
1		Homo sapiens			THORES	<none></none>
ł		breakpoint cluster	ł			[]
575		region BCRder14	1	1		
575	AF044775	sequence	0.19	<none></none>	<none></none>	<none></none>
					- SHONES	<none></none>

WO 01/02568

	Neares	Neighbor (BlastN vs. C	renhank)	Nearest Main	bbee (DI V)	
SEC			T T	14cmest (4618	hbor (BlastX vs. Non-Redundant P	roteins)
ID	ACCESSIO		P VALUE	ACCESSION	DESCRIPTION	P VALUE
L		Human mRNA for				I TALUE
1	1	KIAA0335 gene,				
576	AB002333	complete cds	0.19	<none></none>	<none></none>	<none></none>
		Macaca mulatta pit- 1/GHF-1				
577	U53566	transcription factor		ļ	probable membrane protein	İ
 3//	033300	mRNA, complete cds	0.19	1078068	YLR311c - yeast	9.2
		t(11;14)(q13;q32) breakpoint junction			COAT PROTEIN (CAPSID PROTEIN) virus >gi 58901	
578	U73664	sequence	0.19	116734	(X62133) CyMV coat protein	· ;
		Heterophyllaea		110/34	gene product	8.8
		pustulata rps 16 gene, chloroplast gene, partial intron	· .		(100015) 1	
579	AF004054	sequence	0.19	1928991	(U92815) heat shock protein 70 precursor [Citrullus lanatus]	
580	Z 27081	Caenorhabditis elegans cosmid M01A8. complete sequence [Caenorhabditis elegans]	0.19	2496247	HYPOTHETICAL ATP-BINDING PROTEIN MJ0625 >gi 2128413 pir A64378 hypothetical protein MJ0625 - Methanococcus jannaschii >gi 1591336 (U67510) M. jannaschii predicted coding	8.7
		S.cerevisiae	0.19	2496247	region MJ0625	8.6
581		chromosome IV reading frame ORF			TYROSINE-PROTEIN	
701		YDL097c Small round	0.19	1174425	KINASE SPK-1	6.7
		small round structured virus genomic RNA, 3'terminal sequence containing ORF2 and				
582		ORF3	0.19	071210	(Z48053) putative protein	
			0.17	971318	[Bovine herpesvirus 1]	5. l

	-25 L	Neare	st Neighbor (BlastN vs.	Genbank)	Nearest Neig	phos (Plant V No. 1)	
	SEQ				curest iven	phbor (BlastX vs. Non-Redundant I	roteins)
	ID	ACCESSIO		P VALUE	ACCESSION	DESCRIPTION	
			канзтопна епторна		T	DESCRIPTION	P VALUE
			DNA 16S ribosoma	- 	 		
			RNA > ::			1	1
- 1			dbj D88002 D88002	: 1	ł .	1	1
			Ralstonia eutropha	1	ĺ		1
- [•		DNA for 16S	1	I	.}	J
- 1	- I		ribosomal RNA > ::	ł			1
ļ	ŀ		dbj D88003 D88003	1			1
-	- 1		Ralstonia eutropha	-			1 1
			DNA for 16S			İ]
- 1	J		ribosomal RNA > ::	1		ł.	1 1
- [- 1		dbj D88004 D88004	1	'·		i i
-1	- 1		Ralstonia eutropha	1 . 1		1	İ
-	- 1		DNA for 16S			(AF100657) No definition line]
L	583	D88000	ribosomal RNA	0.19	3800952	found [Caenorhabditis elegans]	i I
1	- 1		Methanococcus		3000335	Tound [Caenornabditis elegans]	5.1
1	- 1		jannaschii section 4	1.		(AJ005586) MYB-related	i 1
			of 150 of the	1 1		transcription factor	i i
L	584	U67462	complete genome	0.19	3183617	[Antirrhinum majus]	
1			Gallus domesticus			(: diaminant majus)	4.0
1.			microsatellite DNA	1		(U93074) voltage-gated sodium	
H	585	L23906	marker.	0.19	1947094	channel homolog BdNa1	3.9
ı	ı		İ				3.5
	1		ľ			GLUCOSE-6-PHOSPHATE	
1			Haliaghana			ISOMERASE (GPI)	ľ
ı			Helicobacter pylori,	í <u>l</u>		ISOMERASE) (PHI)	i
	- 1		strain J99 section 23			>gi 2118333 pir I48073 glucose	1
١,	86	AE001462	of 132 of the			phosphate isomerase - Chinese	- 1
۲	-	AE001402	complete genome	0.19	1730177	hamster >gi 987046 griseus]	3.9
	- 1					(Z8ZZ56) CDNA EST	
]	- 1		j			yk251g7.3 comes from this	1
ĺ	- [P.putida catBC			gene; cDNA EST yk251g7.5	
1	- 1		operon encoding	. 1		comes from this gene; cDNA	
l	- 1		cis.cis-muconate			EST EMBL:D68223 comes	į.
ſ	ı		lactonizing enzyme I	·]		from this gene; cDNA EST	1
			and muconolactone	1		EMBL:C12737 comes from this.	
	1		isomerase genes,	I		gene; cDNA EST yk389c8.5	1
58	37		complete cds.	0.19	2072047	comes from this gene; cDNA	i
	T		Tetrahymena australis	0.19	3873843	E	3.9
			telomerase RNA	1	İ		1
		Į,	gene, complete	i	Í	(AE040033) PCP143-13	İ
58	8	• • • • · · · · · · · · · · · · · · · ·	sequence	0.19		(AF049922) PGP169-12	
					7103702	[Petunia x hybrida]	3.2

	. Nea	rest Nei	ghbor (BlastN vs. C	Genbank)	Nanson N		_
SE	EQ			1	Nearest N	eighbor (BlastX vs. Non-Redundant	Proteins)
	D ACCESS	ION	DESCRIPTION	P VALUE	ACCESSIO	N DESCRIPTION	P VALI
 		- 1	omo sapiens voltage				I VAL
1	ı	000	erated calcium				
	1	Chi	annel, alpha-1		1	1 '	
	j		ounit mRNA,		1	ł	1
_58	9 L27745		nplete cds.	0.10	l	(AC004450) unknown protein	1
			nis familiaris	0.19	3763926	[Arabidopsis thaliana]	3.0
1			apsin I gene,				
590	O AF04958	8 раг	tial cds	0.19	410400	(AF042196) auxin response	1
				0.19	4104931	factor 8 [Arabidopsis thaliana] PRE-NECK APPENDAGE	3.0
1	1	1.			ł	PROTEIN (LATE DE COMP	
	i	1			· ·	PROTEIN (LATE PROTEIN	
i	ł	- 1	į.			GP12) >gi 75856 pir WMBP22	1
1	1		1			gene 12 protein - phage phi-29	1
i	1	- 1	ł			>gi 215330 (M14782) pre-neck appendage protein	1
ľ	1		hylococcus			[Bacteriophage phi-29]	1
601	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	aure	us plasmid pS194]		>gi 225367 prf 1301270G gene	
591	X06627		ence	0.19	137927	12 [Bacteriophage phi-29]	ļ
	I		usculus gene for			12 [Bactertophage phi-29]	2.3
592	X61597		krein-binding	- 1		(AE000675) cobalamin	l
372	A01397	prote	in	0.19	2982874	synthesis related protein CobW	, ,
	ı	Dien	ostelium			, some control protein CODW	1.7
	I		ideum protein	i		1	
	l	synth	esis elongation	- 1			
	Ĭ	factor	1-alpha (tef2)				
593	AF016242	gene	nartial ede	0.10		PUTATIVE RNA-DIRECTED	
		Vene	partial cds zuelan equine	0.19	133659	RNA POLYMERASE	1.4
		encep	halitis virus	- 1			
- 1		strain	1327	I		1	
I			rotein gene.	I		1	ľ
- 1			cds > ::	i i		1	i
_]		gbAF	004460 AF004				Í
- 1			enezuelan	a di di			i
- 1		equine	encephalitis	· 1		1	
			train 1385	Í		j	1
		polypro	otein gene,	ł		(1125068)t	Į
94	AF004447	partial	cds	0.19	4096173	(U25968) early embryogenesis protein [Oryza sativa]	
						INHIBIN BETA B CHAIN	1.3
		Human	elastin (ELN)	1		PRECURSOR inhibin precursor	
ł			xon I, clones			- bovine >gi 563753 (U16241)	ſ
95			5 and HELC-			betaB inhibin/activin precursor	i
		6. Homo s	aniama hiar	0.19	1170523	[Bos taurus]	12
- 1	l:	riomo s deacety	apiens histone			PROBABLE TRANSPORT	1.3
ł			ase 3 3) gene,		•	PROTEIN CY21C12.11	}
6		Complet	T. 1			>gi 2078066 gnl PID e315171	- 1
	337030 10	Jupier	e cus	0.19	3024881	(Z95210) betP	0.83

-	Near	est Nei	ghbor (BlastN vs.	Genbank)	Nearest Ne	eighbor (BlastX vs. Non-Redundant F	
SEQ	1					73. Non-Regundant F	roteins)
ID	ACCESS	ON	DESCRIPTION	P VALU	E ACCESSION	N DESCRIPTION	
-	 					FERREDOXIN-DEPENDENT	P VALI
[ł	- 1				GLUTAMATE SYNTHASE I	
1	ľ	- 1		1 .	I	(FD-GOGAT)	
l .		ľ		ł	1	>gi 2126524 pir S60228	ĺ
]	f	- 1		1		glutamate synthase (ferredoxin)	1
1		D		j	Í	(EC 1.4.7.1) gltB -	1
			nelanogaster	ł	1	Synechocystis sp. (PCC 6803)	1
597	M69053		ium-activated K+	,	J	>gi 515938 (X80485) glutamate	ł
	14107033		nnel subunit tyostelium	0.19	1707984	synthase	0.80
			ibasis plasmid				0.00
ŀ			1, complete	1		İ	ŀ
598	AF07627		mid sequence	1		(U00008) yejA [Escherichia	f
		pias	ind sequence	0.19.	453986	coli]	0.79
- 1		Mou	se MCNP gene	ſ			
- 1		for C	-type natriuretic		ł	1	
- 1		pepti	de, complete cds		<u>'</u>	(AE001092) acetyl-CoA	
599	D28873		n1, exon2)	0.19	2650444	synthetase (acs-1)	
		1,		0.19	2650444	[Archaeoglobus fulgidus]	0.63
- 1		Oxyt	richa nova				
			onuclear actin II			1	
600	U06071	gene.	complete cds.	0.19	1584024	complement control protein	
		Home	sapiens CLP		1384024	[Botryllus schlosseri]	0.48
601	L54057	mRN	A. partial cds.	0.19	3036883	(AL022374) putative ABC transporter	
ı		1			0030003	(AC004877) sco-spondin-mucin-	0.46
500	1/00		dius cDNA for	ď		like; similar to P98167 uncertain	
502	X89806	COLI	.2alpha gene	0.19	3638957	[Homo sapiens]	
J			eoglobus			(220mo suprens)	0.41
		fulgid	us section 3 of	j	•	1	
603	AE001104		the complete	j		(Y11739) transcription factor	
55 '	AE001104	genom		0.19	2315192	[Homo sapiens]	0.35
			norvegicus atellite	1		D-MeAsp	0.33
04	U54501	1	1		•	receptor:ISOTYPE=epsilon3	
	03.301	scquei	ce D0Mco22	0.19	228951	[Mus musculus]	0.32
ı		ĺ		1			
		Human		}		(AF096371) contains similarity	
1			mavirus type			to Rattus norvegicus cyclin G-	
)5	X74468	15 gend	omic DNA	010	260522-	associated kinase (SW:P97874)	J
		20 80110	DITA	0.19	3695390	[Arabidopsis thaliana]	0.28
1		Human	Gps1 (GPS1)	1		(AJ002527) glucitol-6-	
6 1			complete cds	0.19	2592650	phosphate dehydrogenase	ļ
		Human	gene for	J.17	2582659	[Clostridium beijerinckii]	0.27
		interleu	kin 3 receptor	ļ		(A F00050 ()	
_ [ľ	alpha su	bunit, exon	1		(AF008596) alpha1,3-	l l
7 I		10		0.19	2522368	fucosyltransferase [Helicobacter	1
					2322308	pylori].	0.16

-		st Neighbor (BlastN vs.	Genbank)	Nearest Nei	ghbor (BlastX vs. Non-Redundant F	roteins)
	Q ACCESSION	DN DESCRIPTION	P VALUE	1		Toteins)
			T VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens		 		
- 1		pituitary specific	1	·	· ·	
- 1	1	homeodomain protei	n	Ī		İ
- 1	i	(PROP1) gene, exon	i	l	(X03541) tels ==== 1	
60	8 AF041141		0.19	37403	(X03541) trk gene product (aa 1 641) [Homo sapiens]	
- 1	İ	Discopyge ommata			o-ty [Homo saptens]	0.091
- 1	1	Ca2+ channel alpha 1	·	1		[
60	7 1253	subunit gene		Į.		
00	L12531	sequence.	0.19	3618274	(AJ223219) hypothetical protein	0.069
		Yellow fever virus clone HONG9	İ	, .		0.003
- 1	ł	1				
610	AF052445	polyprotein gene, complete cds	1 0,0		(U15928) KH-domain putative	
	12 032 113	B.anthracis sap gene	0.19	1932822	RNA binding protein	0.001
- 1	1	encoding S-layer	J j			
611	Z36946	protein	0.19	172241	(L06487) ZIPI protein	
		Homo sapiens full	0.15	173241	[Saccharomyces cerevisiae]	2e-04
	ľ	length insert cDNA			(AC005400) have all as	f
612	AF087984	clone YW29A12	0.19	3786014	(AC005499) hypothetical protein [Arabidopsis thaliana]	
1	1	Archaeoglobus			protein (Adabidopsis thaliana)	1e-06
j	1	fulgidus section 97 of	Į.			
613	45001010	172 of the complete	ł		(AF060248) unknown	1
013	AE001010	genome	0.19	3135493	[Arabidopsis thaliana]	7e-08
ı	ı		1			70 00
1	1	Trichosporon	Į.		1	i
i	i	cutaneum carbamoyi	1		1	1
1	ł	phosphate synthetase	Į.			ſ
Ι.	l	large subunit (argA)	1		(U41278) F33G12.3 gene	1
614	L08965	gene, partial cds.	0.19	1086901	product [Caenorhabditis	İ
		Rattus norvegicus	<u> </u>	1080901	elegans]	2e-08
[A2b-adenosine			ļ. I	ſ
	·	receptor mRNA,		,	(AE000773) acetoin utilization	1
615	M91466	complete cds.	0.19	2984320		6- 00
					protein [Aquifex aeolicus] (AL032643) similar to	6e-09
1 1		ľ	1		Uncharacterized protein family	j
	ı		i		UPF0034, Double-stranded	ľ
	į				RNA binding motif; cDNA EST	į į
1			Ī		yk489b3.5 comes from this	- 1
	- 1.	S.lividans groEL2	1		gene; cDNA EST yk439g7.5	
616	7/0 70-	ene groet2	0.10		comes from this gene	
		Circ	0.19	3925277	[Caenorhabditis elegans]	7e-10
	ls	Schizosaccharomyces	ı		(U97016) similar to drosophila	
		combe scd2 (scd2)	1		RIc1 gene product ribosomal	·
617		ene, complete cds.	0.19		protein L4 (YML4)	
				1730349	(NID:g459259)	3e-14

	None					
	Iveare	est Neighbor (BlastN vs.	Genbank)	Nearest Nei	ghbor (BlastX vs. Non-Redundant F	
SEQ	1				-E-1001 (E-1001-Redundant)	Toteins)
ID	ACCESSI	ON DESCRIPTION	P VALUE	ACCESSION		P VALUE
	· · · · · ·	California			(U97016) similar to drosophila	T
ı			*		RIc1 gene product ribosomal	
518	1112530		1	1	protein L4 (YML4)	1
	012339	gene, complete cas.	0.19	1938549	(NID:g459259)	9e-15
					gene; cDNA EST EMBL:D33710 comes from this gene; cDNA EST EMBL:D34467 comes from this gene; cDNA EST EMBL:D35005 comes from this gene; cDNA EST EMBL:D37535 comes from this gene; >gi 3878710 gnl PID e1348373	
	760207	Human DNA sequence from cosmid U25D11, between markers DXS366 and DXS87		·	EST EMBL:D33710 comes from this gene; cDNA EST EMBL:D34467 comes from this gene; cDNA EST EMBL:D35005 comes from this gene; cDNA EST	
' -	208327		0.19	3875774	gene;	6e-15
0	U66525	discoideum ORFveg114 mRNA, complete cds	0.19	3540281	(AF056116) All-1 related	
	U25830	Newcastle disease virus isolate Herts/33 matrix protein mRNA, complete cds	0.19	2228750	(U93868) RNA polymerase III	2e-17
	U89407	BALB/c delta- aminolevulinic acid dehydratase (Lv) mRNA, partial cds	0.19	1825764	(U88314) C46H11.11 gene product [Caenorhabditis	3e-25
A	F095598	Bison bison athabascae microsatellite BBJ 2	0.18	<none></none>		NONE>
A		~-	0.18	<none></none>		NONE>
	9 O	9 Z68327 U89407 AF095598	ACCESSION DESCRIPTION Schizosaccharomyce pombe scd2 (scd2) gene, complete cds. Human DNA sequence from cosmid U25D11, between markers DXS366 and DXS87 on chromosome X. Dictyostelium discoideum ORFveg114 mRNA, complete cds Newcastle disease virus isolate Herts/33 matrix protein mRNA, complete cds Newcastle disease virus isolate Herts/33 matrix protein mRNA, complete cds Mus musculus strain BALB/c delta-aminolevulinic acid dehydratase (Lv) mRNA, partial cds Bison bison athabascae microsatellite BBJ 2 Strongylocentrotus purpuratus SRC8	ACCESSION DESCRIPTION P VALUE Schizosaccharomyces pombe scd2 (scd2) gene, complete cds. Human DNA sequence from cosmid U25D11, between markers DXS366 and DXS87 on chromosome X. Dictyostelium discoideum ORFveg114 mRNA, Complete cds Newcastle disease virus isolate Herts/33 matrix protein mRNA, complete cds U25830 Newcastle disease virus isolate Herts/33 matrix protein mRNA, complete cds O.19 Newcastle disease virus isolate Herts/33 matrix protein mRNA, complete cds O.19 Newcastle disease virus isolate Herts/33 matrix protein mRNA, complete cds O.19 Stronglocentrotus purpuratus SRC8 Strongylocentrotus purpuratus SRC8	ACCESSION DESCRIPTION P VALUE ACCESSION	D ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION

\vdash	Ne:	rest	Neighbor (BlastN vs	. Genbank)	7	Nearest N.	eighbor (BlassV N	
SE	EQ		1			5 62 631 141	eighbor (BlastX vs. Non-Redundan	(Proteins
	D ACCESS	NOI	DESCRIPTION	P VAL	UE	ACCESSIO	N DESCRIPTION	P VAL
\vdash			Abit i to					IF VAL
1	j.		Arabidopsis thalian	a				
62	25 U6953		AtKAP alpha mRN	A.			1	
-	00933		complete cds Bovine DNA for	0.18		<none></none>	<none></none>	1,000
1	ł			1			GIONES	<non< td=""></non<>
	- [prostaglandin	1			- -	
62	6 D8904	. 1	F2alpha receptor.	j	- 1			
	20004		partial cds Dictyostelium	0.18		<none></none>	<none></none>	<non< td=""></non<>
ĺ	1		discoideum tRNA-	i	1			KINOIN
1	ł			1	- 1			
627	M2457	, [`	Glu-GAA gene, clon yGluGAA7.	i i			j	
	3,42437		D.melanogaster ovo	0.18		<none></none>	<none></none>	<non!< td=""></non!<>
	1	l'a	gene required for	1	- 1			12140141
	1	٤	emale germ line					1
628	X59772		levelopment		J			-
	1337,72		Plasmodium	0.18		<none></none>	<none></none>	<none< td=""></none<>
	j		alciparum DNA ***	1				1 21011
	1	s	EQUENCING IN	j.	- 1		1	ł
	ł	P	ROGRESS ***	1	- 1			
	J		om contig 3-104,	I	1		1	
629	AL01020		omplete sequence	1	i			
	1		lethanococcus	0.18	- -	<none></none>	<none></none>	<none< td=""></none<>
	i		nnaschii section 117					1
	I	of	150 of the				1	
630	U67575		mplete genome	0.10			inositol 1,4,5-triphosphate	İ
		C	nenorhabditis	0.18	4_	111839	receptor 2 - rat	8.5
			gans cosmid					
631	U28730		10B2	0.18	ł	170760	(AE000232) orf, hypothetical	•
		\top		0.18	+	1787604	protein [Escherichia coli]	8.3
- 1		L.1	actis pepF1 &		1		(AF079110) glycosomal malate	
532	X99798		F2 genes	81.0	l	2400004	dehydrogenase [Trypanosoma	}
- 1		\top		0.10	+-	3406624	brucei]	8.1
- 1		1	.		1		PROBABLE NUCLEAR	
			nio rerio band 4.1-		i .		ANTIGEN herpesvirus 1 (strain	
			protein 4 (nbl4)		ı		Kaplan) >gi 334072 (M34651)	
33	AF025306	mR	NA, complete cds	0.18	l	465445	ORF-3 protein [Pseudorabies	
		1			$\vdash \vdash$	70,743	virus]	7.9
1		Mu	s musculus				1	
1		lipo	xygenase (alox)	j			(781368) hamada i	
34	AF059251	mRi	NA, complete cds	0.18		1655667	(Z81368) hypothetical protein Rv2393	
ا ۽			omesticus CTCF				3-methyl-2-oxobutanoate	6.6
5	Z22605	prote	ein mRNA.	0.18		481864	dehydrogeness	
1		l				.51004	dehydrogenase	6.6
ł			o sapiens mRNA					
.			CIAA0514	l			(781464) prodicts 4	
6	AB011086	prote	in, complete cds	81.0			(Z81464) predicted using Genefinder	
			• •			2.0	Generalizet	6.4

05/13	Near	est Neighbor (BlastN v	s. Genbank)	Nearest Nai	ghbor (Block V N	
SEQ	2			- TOWN STATE	ghbor (BlastX vs. Non-Redundant P	roteins)
Э	ACCESSI		N P VALUE	ACCESSION	DESCRIPTION	
	 	Caenorhabditis		T		PVALL
	j	elegans cosmid				
	ł	C07A4, complete	I			
	I	sequence		1	(AJ011681) retinoblastoma-	ĺ
637	770505	[Caenorhabditis		l .	related protein [Chenopodium	
037	Z78536	elegans]	0.18	3702121	[rubrum]	
	1				(Z81094) Weak similarity to 65	6.4
	ł		j	i	KDA heat shock protein	
	l	24.4	1		(TR:G602231); cDNA EST	
	ł	Methanococcus	_	ł	EMBL:D71705 comes from this	
		jannaschii section 7:	2	1	gene; cDNA EST	
638	U67530	of 150 of the			EMBL:D74382 comes from this	
	00/330	complete genome	0.18.	3877946	Igene [Caenorhabditis elegano]	6.3
			1		(Z69634) cDNA EST	0.3
ı			1		EMBL:D71510 comes from this	
- 1		j	į.		gene; cDNA EST	
- 1					EMBL:C08449 comes from this	
			·[]		gene; cDNA EST yk266b12.3	
· 1		Influenza	1 1		comes from this gene; cDNA	
1		A/Duck/England/1/62			EST yk266b12.5 comes from	
I		(H4N6) nucleoprotein			this gene; cDNA EST	
39	M63781	mRNA, complete cds			yk461h7.3 comes from this	
\Box			0.18	3873663	gene; cDNA	6.2
		Oryctolagus	1 1			
·	•	cuniculus integrin	1		1	
		beta-8 subunit	1 1		1	į
- 1		mRNA, complete cds.	1 1		1	
		> :: gb I44828 I44828		•	i	
		Sequence 3 from		j		Į.
ю	M73781	patent US 5635601	0.18	1362129	major allergen OLE17 -	
. 1	****	D.melanogaster Rop			common olive (AB011527) MEGF1 [Rattus	5.8
1 /	X67219	gene .	0.18			
					norvegicus] [PROTEIN-PII]	4.8
- 1		Homo sapiens beta-			URIDYLYLTRANSFERASE	j
2 / 4		arrestin 2 mRNA,	1	1.	vinelandii >gi 39257 (X59610)	ı
' 	AF106941	complete cds	0.18	548353	uridylyl transferase	_ 1
1					and the designation of the second	3.7
		Danio rerio	1	 ,	potential IGF binding protein	l
		huntingtin (HD) mRNA, complete cds	ŀ	lí	chickens, Peptide Partial, 77 aa,	j
3 A						

	Ne:	rest Neighbor (E	lastN vs. C	Genbank)	Nearest Ne	eighbor (BlastX vs. Non-Redundant	
1	Q	1				Aginor (Blaset Vs. Non-Redundant	Proteins)
	D ACCESS	SION DESCR	IPTION	PVALUE	ACCESSION		P VAL
				ļ		(Z68314) predicted using	1. 1
1	- 1			l	1	Genefinder; cDNA EST	+
1	1	1		•	1	EMBL:M75775 comes from the	is
ł	ľ	1			i .	gene; cDNA EST	1.
ı	1	1			ł	EMBL:M89255 comes from th	is
1	1	ı			1 .	gene; cDNA EST	- [
1	1	Homo sapie	ns mRNA		1	EMBL:M89127 comes from the	is
_,,	. [for KIAA09	02			gene; cDNA EST	
644	AB0207		plete cds	81.0	3875570	EMBL:T00141 comes from this	3
	1	HIV-1 isola	e patient			gene; cDNA EST EMBL:T	2.1
	1	3 country U	SA pol		٠,	-	
645	AF09688	polyprotein	(pol)	٠.		j	İ
	71.09088		cds	0.18	3250696	(AL024486) putative protein	1
	1	Pyrocoelia m (clone pB-Pr	пуако	7		patative protein	1.7
	ł	luciferase m	DNA	ľ	•	•	j
646	L39928	complete cds		0.10		(AC003974) unknown protein	
		- Joinpiete Cus		0.18	2914702	[Arabidopsis thaliana]	0.73
	j	Human		1			0.75
	j	carcinoembry	onic			l l	
		nonspecific	ì	- 1			
		crossreacting	antigen	j			
547	34155	(CEA; NCA)		- 1		PECITI ATONYON	
34/	M17082	exons 1 and 2		0.18	1351833	REGULATORY PROTEIN ABAA	
I		1				RNA-binding protein rnpD -	0.72
- 1		17		ľ		Arabidopsis thaliana (fragment)	
- 1		H.sapiens ITIF (exon 22) and	il gene	- 1		>gi 510240 (X61108) RNA	
48	X75318	gene	111H3			binding protein [Arabidopsis	
$\neg \tau$		ECIIC		0.18	629557	thaliana]	0.41
ı		Mus musculus	- 1				U 1
	•	apoptosis assoc	iated	· j		1	
- 1		tyrosine kinase	- 1	I	•	1	
		(AATYK) mRI	ĪΑ;	- 1	-	(1602220)	1
19	AF011908	complete cds		0.18	330442	(K03332) nuclear antigen 2	ı
1						[Epstein-Barr virus] ASPARTYL-TRNA	5e-04
-			- 1	1		SYNTHETASE aspartate	
-		Simian .	- 1		J	tRNA ligase (EC 6.1.1.12) -	
1		oimian immunodeficien		ı	į,	Escherichia coli coli]	j
1	ĺ	virus SIVagmVE	Ey	l	į:	>gi 1736513 gnl PID d1016401	l
- 1		envelope protein			lo	(D90829) AspartatetRNA	
)		gene, partial cds.		10	[1	igase (EC 6.1.1.12)	ĺ
T		Xenopus laevis		0.18		Ecohomick 111	6e-11
1	- 11	RanGTPase		1			
上		ectivating protein		.18	005714	X91258) pid:e198503	[
			<u>~</u>		995714	Saccharomyces cerevisiae]	2e-13

	Neare	est Neighbor (BlastN vs.	Genbank)	Nearest Nei	ghbor (BlastY us Non Boden)	
SEQ	2			The state of the s	ghbor (BlastX vs. Non-Redundant)	Proteins)
ID	ACCESSIO	ON DESCRIPTION	P VALUE	ACCESSION		P VALI
	 				(Z66511) similar to ribokinase	1
ł	Į		1		cDNA EST EMBL:D69553	
i	j	İ	ļ		comes from this gene; cDNA	}
İ	l				EST EMBL:D65938 comes	1
	1		1	ĺ	from this gene; cDNA EST	1
	1	B.oleracea gene for S	. [ł	yk280h9.3 comes from this	1
		receptor kinase-like	7	,	gene; cDNA EST yk280h9.5	1
652	Z18921	protein	0.18	200000	comes from this gene; cDNA	1
		S.cerevisiae STA2	U.18	3875535	EST yk223d11.3 come	le-19
653	M60650	gene, complete cds.	0.16	<none></none>		
			0.10	CNONES	<none></none>	<none< td=""></none<>
j		Eucalyptus globulus]]			
ı		NADP-isocitrate	j l			!
		dehydrogenase	1 1		(AF057298) ornithine	l
654	Lincolo	(EgICDH) mRNA,	1		decarboxylase antizyme 2 [Mus	İ
034	U80912	complete cds	0.16	3766172	musculus]	1
		So-hum.				4.2
.		Sambucus nigra		•		
- 1		ribosome inactivating protein precursor	· ·		1	
655	AF012899	mRNA, complete cds			hypothetical protein 4 - fowl	
	-11012077	military, complete cas	0.16	76749	adenovirus 1	4.0
- 1		Arabidopsis thaliana	į.			
- 1		cellulose synthase	i i			
	•	catalytic subunit (Ath-			İ	
		B) mRNA, complete	1		(A EOSSOO)	
556	AF027174	cds	0.16	3044086	(AF055904) unknown	
1				3077000	[Myxococcus xanthus]	0.60
ı	į	Glycine max sucrose	1		1	
57	A F02000	synthase (SS) mRNA,	f		1	
~/ 	AF030231	complete cds	0.078	<none></none>	<none></none>	-NIONE-
			T	•	cell wall glycoprotein, 75K,	<none></none>
ł		Woodshual: barres	1		precursor - diatom	
ł	į,	Woodchuck hepatitis virus (WHV),	- 1		(Cylindrotheca fusiformis)	
- 1	1.	complete genome,	ł		>gi 515363 (X80394) P75K	
8	M19183	clone WHV 59.	0.072		gene product [Cylindrotheca	
T		Ovine adenovirus	0.072	1076190	fusiformis]	6.3
- [jr	Va2 protein gene,	1	1		
		ONA polymerase	ł			ŀ
	g	ene, terminal protein	1		.	ſ
1		ene and 52.55 kDa	- 1	:		ſ
	P	rotein gene, partial	i	. [,	A E 06 12 44 \	ŀ
9 1		ds	0.072		AF061244) unknown	l
				3311143	Agrocybe aegerita]	6.2

	Neares	t Neighbor (BlastN vs.	Genbank)	Negreet Nois	hhor (Black V up No - D - 1 - 1	
SF	Q		1	cmcst tasis	hbor (BlastX vs. Non-Redundant P	roteins)
	ACCESSIO		P VALUE	ACCESSION	DESCRIPTION	P VALUE
<u> </u>		Caenorhabditis				1. 1742.02
	1	elegans cosmid				
		Y44A6B, complete		ł		1
İ	1	sequence		i]	1
1,,		[Caenorhabditis	1			1
66	0 AL021491	elegans]	0.070	<none></none>	<none></none>	<none></none>
	1	X.laevis Xotch	1			
66	1 1/22074	protein mRNA,		ļ	(Y09076) RAD3	1
100	1 M33874	complete cds. Mus musculus	0.070	1654096	[Schizosaccharomyces pombe]	0.23
		ZAN75 mRNA for	1			
-			ł	į .		İ
66	2 AB012725	zinc finger protein,	0.000		MITOCHONDRIAL	ľ
 "	110012123	complete cds Caenorhabditis	0.069.	1350800	RIBOSOMAL PROTEIN S5	2.0
- 1		elegans cosmid	1			
		Y44A6B, complete				
i		sequence	i i		1	
ı	1	[Caenorhabditis	1			
663	AL021491	elegans	0.068	<none></none>	NONE	
			0.000	410ML2	<none></none>	<none></none>
ł		H.sapiens CpG DNA,			(U55376) F16H11.2 gene	
ł		clone lel, reverse			product [Caenorhabditis	
664	Z60318	read cpglel.rla.	0.068	1280134	elegans]	2.6
1	1				PROBABLE SUCCINTL-	
	1				COA:3-KETOACID-	Ī
1					COENZYME A	ĺ
ı					TRANSFERASE PRECURSOR	ı
1					EMBL:Z14816 comes from this	ľ
İ	j		Į.		gene; cDNA EST	ı
1			ŀ		EMBL:Z14946 comes from this	1
1	1		J		gene; cDNA EST	
1	1	S.cerevisiae			EMBL:D69746 comes from this	1
		chromosome II	j		gene; cDNA EST yk219b6.3	į.
665	Z35973	reading frame ORF			comes from this gene; cDNA	ľ
1 303		YBR104w Streptomyces lividans	0.068	2493000	ES	0.68
1		rpsP, trmD, rplS,				
1		sipW, sipX, sipY,	ł.]	1
l		sipZ, mutT genes and	1		1	- 1
ĺ		open reading	1		(3/06710) 11	
666		rames	0.068	1925074	(X96713) collagen [Globodera	
		tanes	0.008	1235974	pallida]	4e-0-1
			- [(AC005164) match to ESTs	
]		j	ĺ	AA731149 (NID:g2140138),	
]		į		AA731149 (NID:g2140138), AA731908 (NID:g2752719),	
	· /	Anthonomus grandis	1		AA731908 (NID:g2732719), AA287837 (NID:g1933519),	j
		itellogenin gene	1		AA262811 (NID:g1898382),	
667		VTG), complete cds.	0.068		and AA825820 (NID:g2899132)	le-59
					(1110.82099132)	16-09

	Near	est Neighbor (BlastN vs	Genbank)	Nearest Na	ighbyr (Blact Y us NI - D	
SE	EQ.		T	incarest Ne	ighbor (BlastX vs. Non-Redundant	Proteins)
П	D ACCESSI	ON DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALU
-						TI VALU
66	8 3424161	Rat tachykinin (PPI	· 1			+
100	8 M34161	gene, exons 5 and 6	0.067	<none></none>	<none></none>	<none:< td=""></none:<>
	ı	Aspergillus niger zir				- CHOILE
- 1	1	finger protein (creA		i	1	1
66	9 L03811	gene, complete cds.				Ĭ
	200011	Human fibrinogen	0.067	<none></none>	<none></none>	<none:< td=""></none:<>
1		beta chain gene,	j	1 .		
	j	complete mRNA. >	}	1		Ĭ
- 1	1	gb I47706 I47706	j	I	1	1
1 .	I	Sequence 3 from	1	ł		Í
670	M64983	patent US 5639940	0.067			
		Nicotiana tabacum	0.067	<none></none>	<none></none>	<none></none>
1	1	Mg chelatase subunit	ĺ	İ		
1 .	1	(ChiH) mRNA,	1			
671	AF014051	partial cds	0.067	«NONE»		
			0.007	<none></none>	<none></none>	<none></none>
672	Y07540	H.sapiens sil gene	0.067	92331	glycoprotein GP330, renal - rat	
1			0.00.	92331	(fragments) 25 KD OOKINETE SURFACE	7.5
j	ł	1	1 1		ANTIGEN PRECURSOR	l
1	I	Rattus norvegicus	1 1		(PRS25) >gi 320962 pir A44966]
1	j	mRNA for 3'(2'),5'-	! !		25k ookinete surface antigen	l i
		bisphosphate	l i		precursor - Plasmodium	
673	AJ000347	nucleotidase	0.067	129238	reichenowi reichenowi]	
ſ	i				hypothetical protein MJ0750 -	7.4
i	1				Methanococcus jannaschii	
674	7.10070	Squid sodium channel	ı		>gi 1592304 (U67521)	
6/4	L19979	mRNA, complete cds.	0.067	2128473	ferredoxin-type protein	1.5
		Yeast tRNA-Glu(3)			7 P P S.C.II.	
675	X08050	gene and flanking	- 1		(X15081) MURF2 protein (AA	
0,5	A00030	regions	0.067	1334398	1-348)	0.65
			Í		HYPOTHETICAL 31.6 KD	<u> </u>
			ľ		PROTEIN CY49.14C	
		Human mRNA for	ŀ		>gi 1370241 gn1 PID e247089	·
1		IgM heavy chain			(Z73966) hypothetical protein	j
676	X17115	•	0.063		Rv2075c [Mycobacterium	- 1
		complete sequence	0.067	1731331	tuberculosis]	0.51
Į					ALPHA-2C-1 ADRENERGIC	
Į	l	' I	- 1	٠	RECEPTOR human >gi 178194	
l	ſ	Homo sapiens	j		(J03853) kidney alpha-2-	į
- 1		uncoupling protein 3	1	i	adrenergic receptor [Homo	
		(UCP3) gene, exon 1	· · · · · · · · · · · · · · · · · · ·	Ī	sapiens] >gi 1628638 (U72648)	[
677		and partial exon 2	0.067		alpha2-C4-adrenergic receptor	1
			0.007	112900	[Homo sapiens]	0.50

	Nearest	Neighbor (BlastN vs. C	ienbank)	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)				
SEQ						1		
ID	ACCESSION	DESCRIPTION	PVALUE	ACCESSION	DESCRIPTION	P VALUE		
	L	T T	Ī		DYNAMIN 3 (DYNAMIN,			
					TESTICULAR) rat			
	ł	Mouse class II MHC			>gi 391872 gnl PID d1003668			
		E-beta 2 (d) gene			(D14076) testicular dynamin			
678	X05319	exon 3	0.067	585074	[Rattus norvegicus]	3e-04		
		Candida albicans	1	i .	-			
679	A D004343	CaSLN1 gene,	0.067		(AC003007) Unknown gene			
0/9	AB006362	complete cds	0.067	. 3417296	product (partial) [Homo sapiens]	9e-56		
		African horse	•	i				
	•	sickness virus capsid						
	İ	VP3 (L3) mRNA,			1			
680	AF021236	complete cds	0.066	<none></none>	<none></none>	<none></none>		
		Helicobacter pylori,	, , _					
		strain J99 section 68						
		of 132 of the						
681	AE001507	complete genome	0.066	<none></none>	<none></none>	<none></none>		
		Caenorhabditis			·			
682	AF039717	elegans cosmid R13H8	0.066	-NONE				
002	AI-039717	Syncerus caffer	0.066	<none></none>	<none></none>	<none></none>		
		isolate Queen						
		Elizabeth Mweya 14						
		mitochondrial DNA						
683		control region	0.066	<none></none>	<none></none>	<none></none>		
		Homo sapiens full						
		length insert cDNA			(X97203) C1 protein [Beet curly			
684	AF087967	clone YU51G05	0.066	2982476	top virus]	9.5		
ŀ						1		
l		Baboon endogenous			(L37868) POU-domain	ľ		
		virus proviral long	1		transcription factor [Homo	ı		
685	L.	terminal repeat DNA.	0.066	972767	sapiens]	7.3		
1					[apicits]			
		Lycopersicon	Ì		[
ļ		esculentum class I	ŀ		i	1		
		knotted-like			(AC002131) Strong similarity to	ł		
i		homeodomain protein	ŀ		extensin-like protein gb Z34465	1		
۷٥٤		(LeT6) mRNA,	225		from Zea mays. [Arabidopsis			
686		complete cds Bensingtonia sp.	0.066	3157926	thaliana]	5.6		
- 1		OK255 gene for 18S	Į		·			
		RNA > ::				I		
]		bj AB001747 AB00	[[
- 1		1747 Bensingtonia	ŀ	•	(AF070064) cap 'n' collar	Į.		
- 1		sp. OK259 gene for	1		isoform C [Drosophila	į		
687		ISS rRNA	0.066	3859889	melanogaster]	0.38		

7. 7.	Nearest	Neighbor (BlastN vs. (Genbank)	Nearest Neigh	bor (BlastX vs. Non-Redundant P	roteins)
SEQ			1		Co. (Diabat vo. 1 con reconstant t	T
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	
	1	Helicobacter pylori,	TIVALUE	ACCESSION	DESCRIPTION	P VALUE
		strain J99 section 22	 			+
	1	of 132 of the				
688	AE001461	complete genome	0.065	<none></none>	<none></none>	<none></none>
		Chicken erythroid		4,0,,2,	- CHOILE	KNONES
l		transport proteins c1				
689	M30821	and c2	0.065	<none></none>	<none></none>	<none></none>
		Homo sapiens gene				
		for osteonidogen,	i i		1	
690	AB009802	intron 3	0.065	<none></none>	<none></none>	<none></none>
	ľ	Homo sapiens full				
691	A F00 < 0 < 0	length insert cDNA		' ,	·	1
991	AF086062	clone YZ06B11 Human mRNA for	0.065	<none></none>	<none></none>	<none></none>
١,		KIAA0371 gene,			SIGNAL SEQUENCE	ļ
692	AB002369	complete cds	0.065	2500884	BINDING PROTEIN binding	
92.		complete cus	0.005	2300884	protein [Synechococcus sp.]	5.5
		Cyclopodia sp. large				
		subunit ribosomal		_		i l
		RNA gene,		·		1
		mitochondrial gene				
		for mitochondrial				
		RNAs, partial			1	ĺĺ
		sequence > ::]	
		gb AF086866 AF086				l f
		866 Penicillidia sp. large subunit				
		ribosomal RNA gene,				
- !		mitochondrial gene	l l			
- 1		for mitochondrial	1			
		RNAs, partial			(AB012057)	
693		sequence	0.065	3721684	(AB012957) probable glycosyl transferase [Vibrio cholerae]	5.5
		sequence	0.005	3721084	[uansterase [vibito cholerae]	3.3
,		Bacteriophage BK5-T	Ī	•		
ľ		ORF410, 3' end pf	ĺ			ŀ
		cds, 20 ORFs.	1			
. [repressor protein, and	i			
		Cro repressor protein	i			
		genes, complete cds,	1		PEPTIDASE T	ł
		ORF70' gene, 5' end			(AMINOTRIPEPTIDASE)	
694	L44593	of cds.	0.065	1172067	influenzae Rd]	3.2
1	l,	Ciona intestinalis	- 1			
		MyoD-family protein	1	[j
		CiMDFa) mRNA,	į		(AL035353) contains EST]
695		complete cds	0.065	4218110	gb:F15281	2.5
		op.ctc cus	0.005	→210110	Kn.L13791	2.3

		rest	Veighbor (BlastN vs.	Genbank)	Nearest No	eighbor (BlastX vs. Non-Redundant	
	EQ D ACCESS	ION	DESCRIPTION	P VALU	1		
-					T	DESCRIPTION	P VALUE
			Homo sapiens mRN	A			
69	42000		for KIAA0911	1	1	MINOR CAPSID PROTEIN I	
1-03	6 AB0207		protein, complete cd	s 0.065	1722734	>gi 1020192 type 23]	l l
1	Í		Zea mays copia-like			B-J-020192 type 23]	1.9
1			retrotransposon Stl-	1		ſ	
69	7 AF08213		14 leader region.	1	1	(U89278) polyhomeotic 2	1
1	A1 08213		partial sequence R.norvegicus ZnBP	0.065	1877501	homolog [Homo sapiens]	1.1
1	1		gene for zinc binding	1			1.1
698	8 X64053		protein	1	1	}	1 .
	120,033	۳	rotem	0.065	464963	TRYPSIN PRECURSOR	0.36
1	1	1	Aus musculus		1		
		- 1	outyrophilin (BTN)] .	}		1 1
1	1		ene, promoter region	J	j		1 1
699	U67065	a	nd complete cds	0.065	2122250	hypothetical protein YPL263c -	1 1
				0.005	2132252	yeast	3e-10
l	1	R	at matrin F/G	ĺ		(AF041105) organic anion	
700	M64862	п	RNA, complete cds.	0.065	3420183	transporter protein 3 [Rattus	1 1
	· J		east (S.cerevisiae)		3120103	norvegicus]	4e-19
1	j		anscriptional				1 1
•	1		tivator of amino			1	1 1
	1		id-biosynthetic				1
701	Koooos		nes (GCN4) gene,			·]
701	K02205		mplete cds.	0.064	<none></none>	<none></none>	<none></none>
	I		aize mRNA for a				STONES
702	X58282		gh mobility group			1	1 1
	1130202		ono sapiens	0.064	<none></none>	<none></none>	<none></none>
	1		bclone 1_f3 from	- 1			
			H69) DNA	ľ			j
703	AC001545		uence	0.064		į į	
			mo sapiens	0.004	<none></none>	<none></none>	<none></none>
			A3B region				
704	AF023461		uence	0.064	<none></none>	1	ı
j		Cae	norhabditis	0.007	CNONES	<none></none>	<none></none>
		ele	gans cosmid	Į		1	
705	U50307	F43	H9.	0.064	<none></none>	31017	- 1
			ptococcus crista		THOMES	<none></none>	<none></none>
- 1		Hm	pA gene, partial	1			
- 1			putative	ŧ		(D83659) TPR protein pombe]	ł
j			esin/ABC	İ		>gi 2894282 gnl PID e1251103	- 1
ı			sport system	1		(AL021838) pre-mrna splicing	j
706			ein (scbA) gene,	1		factor. [Schizosaccharomyces]
~	U46542	com	plete cds	0.064	1209391	pombe)	9.2
	1	Δ	sticana DNIA				
07			sticana mRNA eutral peroxidase			(U60315) MC094R [Molluscum	- 1
		· • · · 11	~ ~ · · · · · · · · · · · · · · · · · ·	0.064	1492037	contagiosum virus subtype []	

	Near	st Neighbor (BlastN vs.	. Genbank)	Nearest Nai	ghhor /PlaceV N	
SEQ	2			Tremest Net	ghbor (BlastX vs. Non-Redundant P	roteins)
ID	ACCESSIO		P VALUE	ACCESSION	DESCRIPTION	B
	 	Human alpha-2-		1		PVALL
1	1	macroglobulin				
i	ľ	receptor/lipoprotein	1	Í		ĺ
1		receptor protein	ļ	ſ	rab15B protein - wheat	1
708		(A2MR/LRP) gene,	ł	1	>gi 21853 (X62476) rab protein	l
1/08	U06986	exons 39-41.	0.064	100800	[Triticum aestivum]	
	Í	Human CpG island			(U88325) suppressor of	5.3
709	D04	sequence, clone	1		cytokine signalling-1 (Mus	
/09	D85773	Q28B8	0.064	2245382	musculus]	
1 1					(AF096370) contains similarity	5.3
1	*		1 .		to a C. elegans hypothetical	
i i		1	1		protein F44G4.1 (GB:Z49910)	
1 1		1	1	, ,	and several yeast hypothetical	
}		Apis mellifera			proteins such as 35.1 KD	
		ligustica complete	1		protein in NAM8-GAR1	
		mitochondrial	1		intercerie (CR Pecce)	
710	L06178	genome	0.064	3695379	intergenic region (SP:P38805)	
				3073379	[Arabidopsis thaliana] HYPOTHETICAL 70.5 KD	3.2
- 1		1	i I		PROTEIN IN AGP3-DAK3	
- 1		1	1		INTERGENIC REGION	
- 1			1 1		ANTEROENIC REGION	
- 1			1 1		>gi 1084712 pir \$56201	
ł			1 1		probable membrane protein	
- 1		Triticum aestivum			YFL054c - yeast	
_ 1		mRNA for beta-			(Saccharomyces cerevisiae)	
711	Y16242	amylase	0.064	1175958	>gi 836701 gn1 PID d1009825	
- 1		Homo sapiens		1173936	(D50617) YFL054C	3.1
·		(subclone 2_a2 from	J		1	
- 1		PI H25) DNA	1		1,4500000	
712	L81779	sequence	0.064	3845169	(AE001391) phosphatase (acid	
- 1		C.reinhardtii psb1	0.007	3043109	phosphatase family)	0.81
1		mRNA for OEE1	1		T	
ı	1	protein of].		(M04535) ATD	i
•	1	photosystem [I	f	. •	(M94535) ATPase	I
		(oxygen-evolving	ł	ļ	[Saccharomyces cerevisiae]	1
713		enhancer protein)	0.064	171040	cerevisiae, Peptide, 377 aa]	į
ı				171040	[Saccharomyces cerevisiae]	0.054
	(3	Asapiens mRNA for	ľ	1.	(AE020261)	1
14	X06487	ocl2-Ig fusion gene	0.064	2420362	(AF020261) proline rich protein	ı
ı				2429362	[Santalum album]	0.016
ľ	ł		· 1	ĺ		
- 1		Aus musculus cyclin-	i		l	Į
- 1		ependent kinase	j	ľ	I	1
1		hibitor protein	1	L	A F000	ł
ſ	la	ol5(INK4b)) gene,	1	(AF082557) TRF1-interacting	1
15		on 2 and partial cds	0.064		inkyrin-related ADP-ribose	- 1
			3.004	3929221 p	olymerase [Homo sapiens]	e-10

	Neare	st Neighbor (BlastN vs. (Genbank)	Nearest Na	Pighhor (PlaceV vs. No. D.	
SEQ	1				eighbor (BlastX vs. Non-Redundant	Proteins)
ID	ACCESSIO	N DESCRIPTION	P VALUE	ACCESSION		
		Human T cell	1	ACCESSION	N DESCRIPTION	P VAL
		receptor alpha chain	 	 		T
716	U39099	mRNA, partial cds	0.063			
		- I partial cas	0.003	<none></none>	<none></none>	<non< td=""></non<>
	f	Clostridium	}	Į.		
		acetobutylicum KdpC	ļ	ŀ		ļ
		(kdpC) gene, partial	[ĺ		1
		cds, sensor histidine	1			
		kinase homolog	}	i	1	1
- 1		(kdpD) and response		•	i	1
		regulator homolog			1	į.
i		(kdpE) genes,			<u> </u>	1
717	U39673	complete cds	0.063	-NONE] .
T		Human DNA	0.003	<none></none>	<none></none>	<none< td=""></none<>
- 1		sequence from clone				
		140L1 on	1		1	1
- 1		chromosome 22q13.1	í		ł	
- 1		13.31, complete	ı		(1105073) 7	1
		sequence [Homo	1		(U95973) Serine	ł
718	AL022317	sapiens]	0.063	1931640	carboxypeptidase isolog	1
- 1				1731040	[Arabidopsis thaliana]	5.2
		Spiroplasma citri orfa			1	
1		and orff genes, partial	- 1		1	
- 1		cds, orfb, orfc, and	1		1	
		orfe genes and	- 1		1	
		Spiroplasma virus	J		1 '	
ı	1	SpV1-derived ORF1				
	i	and ORF3 genes.	- 1		ľ	
	<u> </u>	complete cds, and			(AF070704) envelope	
19		SpVI-derived ORF14	į		glycoprotein [Human	
'	U28972	gene, partial cds.	0.063	4091939	immunodeficiency virus type 1]	5.0
- 1		Mus musculus limk	7		(AC004877) sco-spondin-mucin-	5.2
0		inase (limk) mRNA,	1		like; similar to P98167 uncertain	
-		omplete cds	0.063	3638957	[Homo sapiens]	5 1
		Iomo sapiens				5.1
	<u> </u>	poprotein receptor-	Į.		1	
1		elated protein	j			
ı l A		LRP1), exons 39, 40,			(AE000276) orf, hypothetical	
1-		asmodium	0.063	1788123	protein [Escherichia coli]	4.0
1		lciparum	1			7.0
1		romosome 2,	- 1	ľ	. 1	
1	161	ction 67 of 73 of	i		ŀ	
1			1	ĺ	1	- 1
AI	~ ~ ~	e complete		ľ		ļ
• • • •	Section Ise	quence	0.063	2244849	(Z97337) hypothetical protein	4.0

	\vdash	Ne:	irest	Neighbor (BlastN v	s. Genbank)		Nearest N	eigh	hor (BlastY us Non Bada)		
		EQ							bor (BlastX vs. Non-Redundant)	Proteins)	
	<u> </u>	D ACCESS	NOI		P VALU	Æ	ACCESSIO	N	DESCRIPTION		
	-			Streptococcus		7		11	(Z70203) cDNA EST	P VAI	ַט
		1		pneumoniae methy					EMBL:D72339 comes from the	+	
	1	l		transferase gene	f	- 1			gene; cDNA EST	S	
	1 72	23 L2932	_	cluster, complete	- 1	ł			EMBL:D75197 comes from thi	_	
	<u> </u>	L2932	3	sequence	0.063		3874022		gene (Chenorhabditic alamana)	I .	
		ı	ĺ		1				(2/3105) predicted using	2.3	_
	1			H.sapiens mRNA	1	- 1			Genefinder; cDNA EST		
	1	ł		encoding Rev-	1	- 1	•		EMBL:T01277 comes from this	;	
	1	1		ErbAalpha > ::	1	- 1			gene; cDNA EST		
	1	1	le	mb X72632 HSRE	v!	- 1			EMBL:T01796 comes from this	: [
	İ	j		RB2 H.sapiens		I			gene; cDNA EST	1	
	1	1	ļr	nRNA encoding Re-	v-l		••		EMBL:D32545 comes from this		
		. 1	ĮE	rbAalpha (internal		1			gene; cDNA EST	İ	
	724	X72631	f	ragment)	0.063		3979878	- 1	EMBL:D33060 comes from this	İ	
	1	·1				+	2777076	\dashv	gene; cDNA EST EMBL:D (AF025467) contains similarity	1.7	
	ł	1		luman initiation	1				to drosophila DNA-binding	i	
	725	1117060	fa	ictor eIF-5A gene,	1			Į,	protein K10 (NID:g8148)		
ı	723	U17969		omplete cds.	0.063		2429509	- li	Caenorhabditis elegans	١,,	-
ļ		ł		rchaeoglobus Igidus section 107		Τ		7		1.4	4
-		ł	0,5	172 of the	l	1		- 1			- 1
l	726	AE001000		mplete genome	0.000	1	,		AF082486) nef protein [Human		- 1
ſ				p[40]=svp-related	0.063	╀	3462802	i	mmunodeficiency virus type 1]	0.35	- 1
1		1		clear	1	ı					٦
1				eptor/retinoid	ĺ	1			j		1
l			sig	naling modulator	[1		10	159734)		I
l	207			brafishes, mRNA.		l			U58734) weak similarity to nkyrin G [Caenorhabditis		1
ŀ	727	S80986	38	76 nt]	0.063		1326288	اما	egans]		1
l			1					pr	oline-rich proteoglycan 2	0.093	4
l			ı					рг	ecursor, parotid - rat		Ł
1			lu _o	ma annius 7 (0			•	>8	gi 310200 (L17318) proline-		1
	728	AF109134		mo sapiens 7-60 NA, complete cds				ric	th proteoglycan [Rattus		1
Т		100154	11100	MA, complete cas	0.063		· 1083764	no	rvegicus]	0.001	1
	ſ		Hur	nan mRNA for	İ						1
	ı			A0276 gene,	ſ			(A	L021816) SPBC24E9.03c,		
	729	D87466		ial cds	0.063		2879865		known, len:251aa		
	J				3:003		20/9803	USC	chizosaccharomyces pombe]	6e-05	1
				no sapiens mRNA	I				1		1
7	₂₀	A DO 10		CIAA0726	i			(Δ1	E053455) tetrogram This con		1
	30	AB018269	prote	ein, complete cds	0.063		2995865	IH.	F053455) tetraspan TM4SF		ı
								HY	POTHETICAL 47.6 KD	2e-16	
			Cric	vulus ania	i			PRO	OTEIN C16C10.5 IN		l
	- [etulus griseus	f				ROMOSOME III		
	- 1			chrome P-450	ſ				3874383 gnl PID e1344077	į	ĺ
7:	31	D86954	2A14	complete cds	0.063			type	(RING finger)		l I
				ompicie cus	0.063		2496896	[Cae	enorhabditis elegans]	le-22	

C=		arest Neighbo	or (BlastN vs. C	enbank)		Nearest 1	Neighh	or (BlastX vs. Non-Redundar	
SEC	- 1		CRIPTION	P VALU	Æ	ACCESSIO			
<u> </u>		Plasmo				TICCE331(DESCRIPTION	P VAI
1	1	falcipa	um DNA ***		_				
ł	1	SEQUE	ENCING IN		- 1		- 1		
	1		ESS ***		- 1		- 1		- 1
732	4.50.00	from co	ntig 4-58,		ı		- [i
732	AL0102		e sequence	0.062	ı	<none></none>	. 1	NONE	
	ł	Mycopi					$\neg \neg$	<none></none>	<non< td=""></non<>
	1	gallisep			ı				1
	İ	haemag					- 1		Į
733	U9071	precurso 4 complete			1		ı		
	9,507.		piens clone	0.062		<none></none>	[<none></none>	NONT
	ł		NA-binding		· ·				<noni< td=""></noni<>
	[protein S	OX21	٠.					1
		(SOX21)		•	1		- 1		1
734	AF10704	4 complete		0.062	1	A101	1		1
		Caenorha	bditis	0.002	+	<none></none>		<none></none>	NONE
		elegans R			1				
- 1		ribonucle	oprotein		1				1
226	•	autoantige	n mRNA,		1			E000607	j
735	L41729	complete	cds	0.062	1	2983060	I (A	E000687) putative protein	
- 1		1			1		PC	quifex aeolicus]	8.6
- 1		1	1		1			RINE/THREONINE-	1
- 1		Caenorhab	ـ نينهـ		1		PR	OTEIN KINASE D1044.3	
ı		elegans co			ĺ		IN	CHROMOSOME III	l
		Y7A9D, co			ı		>gi	495684 (U00065) contains	į.
		sequence	ompiete		1		JEG	F-like repeats; highly similar	1
•		[Caenorhal	viitie				to 2	C84.1; 3' exons similar to	1
36	Z99287	elegans]	1	0.062	١.		pro	ein kinase (Caenorhabditis	i
		1		0.062	1	176542	eleg	ans]	5.8
- 1		Homo sapie	ns mRNA	Ĭ					
		for KIAA00	514	ı			D.	A CUM LOT TO	
37	AB014514	protein, par	tial cds	0.062	Af	033395	UNA	A GYRASE SUBUNIT B	
	•	Human gerr	nline				Subu	nit [Myxococcus xanthus]	3.9
-		immunoglol	oulin light	1				ľ	
- 1		chain variab		- 1					
- 1		(lambda-IIIt		i			1		
8	L29165	subgroup) fr rheumatoid f	- 1				(Y12	014) RAD23 protein,	
\top		Schistosoma	actor. 0	.062	19	14685	isofo	rm II	1.3
1		japonicum C		1					1.3
I		clone pY6		ĺ			1	Í	ľ
-		paramyosin n	nRNA	1			1		į
	U09364	partial eds.		.062			MITC	CHONDRIAL	1
		Triticum aest	ivum U.	002	135	0800	RIBO	SOMAL PROTEIN S5	1.3
1	l	mRNA for be		ı		,	hypoti	hetical protein 1246 (uvrA	
1		amylase		062	70	834) - Micrococcus luteus	
				 -	19	UJ4	(fragm	ient)	0.59

	- Neare	st Neighbor (BlastN vs.	Genbank)	Negros No	The column at th	
SE			T T	IACTIES! IAGIE	hbor (BlastX vs. Non-Redundant F	roteins)
II	- 1	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
<u> </u>		Leishmania pifanoi			TROPOMYOSIN I (TMI)	1. VALUE
1	. 1	cysteine proteinase			(POLYPEPTIDE 49)	+
		(cys2) gene, complet	e	ļ	>gi 320989 pir A60607	ľ
74	1 M97695	cds.	0.062	1174754	tropomyosin - fluke	0.018
ľ					tropomyosin - fluke (US8755) coded for by C.	0.018
1	ľ				elegans cDNA yk34b1.5; coded	j
1	į.		1		for by C. elegans cDNA	1
	ı		1		yk13h10.5; coded for by C.	
ĺ			1		elegans cDNA yk46e8.5; coded	
1		Methanococcus	1 !		for by C. elegans cDNA	i l
	1	jannaschii section 68			yk46d5.5; coded for by C.	
1		of 150 of the	1	• •	elegans cDNA yk43c2.5; coded	
742	U67526	1	0.050	10000	for by C. elegans cDNA	1
<u> </u>	007320	Caenorhabditis	0.062	1330345	yk46e8	le-40
1		elegans cosmid	l . I			
	1	W09D12, complete	i . I			
		sequence	i I			! [
ļ		[Caenorhabditis	1		1	í í
743	Z78414	elegans]	0.061	<none></none>	<none></none>	200
1		Mus musculus gene		40	KINOINES	<none></none>
1	ł	encoding filensin,	ľ		(AE000651) H. pylori predicted	
744	Y13606	exons 6, 7	0.061	2314715	coding region HP1527	4.9
	1				HYPOTHETICAL 35.5 KD	
	1				PROTEIN IN TRANSPOSON	1
l	i				TN4556 >gi 80759 pir JQ0431	
ļ	ı	E	i		hypothetical 35.5K protein -	ſ
745	J04374	Eggplant mosaic virus genome.	226		Streptomyces fradiae transposon	1
	304374	Marine obligately	0.061	141449	Tn4556	3.8
1	į.	oligotrophic			1	ŀ
]	bacterium POO-10	j		ļ I	
1	İ	DNA for 16S.			ļ i	1
	ľ	ribosomal RNA,	1	•	(AB000307) transcarboxylase-	1
746	AB022200	partial sequence	0.061	3983593	beta	22
		Rat mRNA for zinc				2.2
		finger protein AT-	į.		(L46815) DNA binding protein	ļ
747	X54250	BP2, partial cds	0.061	1377886	Rc [Mus musculus]	0.98
	1	M.musculus mRNA	7			- 3.70
748		of enhancer-trap-			(AE000748) putative protein	- 1
748		locus I	0.061	2983969	[Aquifex aeolicus]	0.57
		Mus musculus mRNA	- 1		.1	
749		for scrapie responsive protein 1	2001		(AC005223) 45643	
		H.sapiens mRNA for	0.061	4204265	[Arabidopsis thaliana]	5e-31
750		CD88 protein	0.060	ANONE		
	- 10203	e protein	0.060	<none></none>	<none></none>	<none></none>

	Nea	rest l	Neighbor (BlastN v	Genhank		T			
SEQ			, J. (J. (J.)	s. Genbank)		Nearest N	Veigh	bor (BlastX vs. Non-Redundar	t Proteins)
ID	ACCESS	ION	DESCRIPTION	P VAI	UE	ACCESSIO			7
- -	 _					. recession	NIA.	DESCRIPTION	P VAL
1 75.			Human clone 2374:	5					
751	U7926		mRNA, complete c	ds 0.06	0	<none></none>		1	
j	l		Plasmodium			VIVOIVES.		<none></none>	<non< td=""></non<>
752	V07.45	. I	falciparum 11-1 ger	ne i				1	
132	X0745		part I	0.060	0	<none></none>		21017	
			Rattus norvegicus		\neg			<none></none>	<non< td=""></non<>
			protein tyrosine	1	- 1			1	- 1
		الم	phosphatase delta	j	- 1			ĺ	
753	U57502	١	gene, catalytic	1				(AF044915) polar tube proteir	.
	037302		lomain, partial cds. A. fascicularis gene	0.060		3452285		PTP55 precursor	
		f	or apolipoprotein C	1 .		• •			0.28
754	_ X68359		or aponipoprotein C.		- 1			SHUTTLE CRAFT PROTEIN	.
			seudomonas braB	0.060	-+	730843		>gi 487400	2e-04
ı			ene for branched		- [20.03
		ct	nain amino acid		- 1		- 1		
			ansport carrier (LIV]			- 1		1
755	X51634	II		0.059	-	1925622	- 19	(U85718) CCML [Pseudomona	ıs
1		T		0.057	┰	1835622		outida GB-1]	8.1
ı		- 1			1		- 1		
- 1		Go	ossypium hirsutum	ł	.		- 1		1
- 1		co	tton fiber expressed		1				1
756	AF072405		otein 2 (CFE2)		1		la	lkaline phosphatase, 145K -	
-	AL-072403	m.	NA, complete cds	0.059		423766	S	ynechococcus sp.	1
		Sar	mbucus nigra		Γ		+	y memococcus sp.	4.7
		ribe	osome inactivating		1		- 1		
i		Dro	tein precursor		ı		- 1		
57	AF012899	mR	NA. complete cds	0.054	1		(A	AF034859) juvenile hormone	
		Rati	tus norvegicus	0.056	╄-	2662481	re	sistance protein	3.3
		hom	ner-1c mRNA,		1		I^-		
58 A	LF093268		plete cds	0.054	1	£430 :=	1	·	l
1		Hyd	ra N-COL 2	0.034	├-	547847	LE	CTIN PRECURSOR	7.0
		mRI	NA for mini-		I	•			
9	X61046	colla	igen, partial cds	0.053	ĺ	<none></none>	1		
		Arab	oidopsis thaliana		 	ZITOITE>	+-	<none></none>	<none></none>
1		mRN	NA for					·	
0 A			anthin cleavage		Ī		1	1	İ
- A	J005813	enzyı	me	0.052	!	<none></none>		-NONE-	
1	ł	J = 0 = =	lo				+	<none></none>	<none></none>
1			dimension	j			GA	METOGENESIS	
			dization . osatellite	ł			EXI	PRESSED PROTEIN GEG-	J
			M) [Beta	1			154	>gi 2137331 pir I48361	1
1			ris=sugar beets,	ł			gene	GEG-154 protein - mouse	- 1
s	79843	jeno. .aišai	mic, 537 nt]				>gil:	550123 (X71642)	1
	10	501101	mc, 337 ntj	0.025		1730145	pid:	2550123 [Mus musculus]	2e-16

-	Near	est Neighbor (BlastN vs.	Genbank)	Nearest Main	bbox (DLV	
SEQ	l			. rearest Iverg	hbor (BlastX vs. Non-Redundant	Proteins)
<u>D</u>	ACCESSI	ON DESCRIPTION	P VALUE	A COFFEE TO	ļ	
		Mouse mRNA for	T VALUE	ACCESSION	DESCRIPTION	P VAL
		GATA-2 protein,		 		
762	AB00009	6 complete cds	0.023			
			0.023	<none></none>	<none></none>	<none< td=""></none<>
		H.sapiens CpG DNA			ZINC FINGER PROTEIN 142	
		clone 67h7, forward		1	(KIAA0236) to Human zinc	1
763	Z62366	read cpg67h7.ft1a.	0.023	3123312	finger protein(ZNF142) [Homo	1
- 1		Human	9.000	3123312	[sapiens]	5.9
J		transmembrane	1		hymothesis 1 care	
		glycoprotein (CD53)	1		hypothetical 67K protein -	1
764		gene, exons 2 through	1 .		Mycobacterium fortuitum	1
764	L11670	8.	0.023	80636	plasmid pAL5000 >gi 149986	
					(M60875) ORF2	3.4
1		Sulculus diversicolor	•			ļ
		DNA for IDO-like	1 1		(AF061267) inner membrane	ļ
765	D92004	myoglobin, complete	1 1		component HtxE [Pseudomonas]
	D83984	cds S.tuberosum mRNA	0.023	3114665	stutzeri]	
- 1		for inorganic				3.4
- 1		phosphate	1			
766	X98890	transporter, StPT1			(X02155) thyroglobulin [Bos	
		transporter, StP11	0.023	683532	taurus)	1.1
		Dissostichus mawsoni				
		preprotrypsin gene,	1			
67	U58835	complete cds	0.022	2102777]	
ĺ		Glomus versiforme	0.022	<none></none>	<none></none>	<none></none>
		chitin synthase gene	1	}		
68	AJ009630	(clone Gvchs3)	0.022	<none></none>	1	
- 1			+	CHOILES	<none></none>	<none></none>
.	70.40	Human glucagon	1		· T	
59	J04040	mRNA, complete cds.	0.022	<none></none>	-NONT	
0	V74000	L.esculentum Asr3			<none></none>	NONE>
` -	X74908	gene	0.022	<none></none>	<none></none>]
- [Shigella dysenteriae			- GAOINES	NONE>
		O-antigen	i		. 1	I
- 1		oolysaccharide	J	1		- 1
-		piosynthesis rfbX, O-	1	I		i
],	intigen polymerase	ſ	i	ļ	- 1
	17	rfc), rhamnosyl	ł	1	1	[
	·	ranferase I and II	İ	ľ		j
1	16	rfbR and rfbQ) and	l		[- 1
	ri	bD genes, complete	ł	1		- 1
L		ds.	0.000			
			0.022	<none></none>	<none></none>	NONE>

D ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION ACCESSION DESCRIPTION ACCESSION DESCRIPTION ACCESSION DESCRIPTION ACCESSION DESCRIPTION ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE		Ne:	rest Neighbor (BlastN v	s. Genbank)	Nearest No	eighbor (BlastX vs. Non-Redundar	t Proteins
Mus musculus Inositol Inosi		-		1		L 1335E VS. 14611-Reduildali	(Froteins)
Mus musculus	<u> </u> -	ACCESS		PVALUE	ACCESSIO	N DESCRIPTION	
Polyphosphate 5	-				T	250ckii Holy	PVALL
Phosphatase II (INPP5P) mRNA, complete cds	j	1					
AF040094 Complete cds	- 1	ı		1		1	ľ
AF040094 complete cds	- 1	1		ľ	1		1
H.sapiens HLA-DMB gene	1 7	72 4 50400		1	ı	1	1
773 X76776		2 AF0400	- 1-0picte cus	0.022	<none></none>	<none></none>	
Helicobacter pylori, strain J99 section 82 of 132 of the	77	3 V7677	- 1	1B		THE STATE OF THE S	<none:< td=""></none:<>
Strain J99 section 82	<u> </u>	A/0//		0.022	<none></none>	<none></none>	NONE
AE001521 Of 132 of the Complete genome O.022 NONE> NONE> NONE> NONE>	- 1	i				4.0.12	<none:< td=""></none:<>
AE001521 complete genome 0.022 NONE> NONE> NONE>	- 1	1		2 }	ł	•	
A.longa rbcL, rpl5, rps8, rpl36, rps14, rps2, trnl,trnF, trnC and rpoB (partial) genes > :: emb X75651 ALRIBP A.longa plastid genes for ribosomal proteins, tRNAs, RNA polymerase subunit beta and rubisco large subunit 0.022 NONE> N	77	4 AF00153				1	ľ
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T78 Z96622 SPTEL002, read SPTEL00002.seq 0.022 191333 (J05503) carbamoyl-phosphate synthetase (E.C.6.3.5.5) 9.8			H.sapiens telomeric	i			1 1
778 Z96622 5PTELOO002.seq 0.022 191333 (105303) carbamoyl-phosphate synthetase (E.C.6.3.5.5) 9.8 Sulculus diversicolor DNA for IDO-like myoglobin, complete cds probable membrane protein YDR018c - yeast 9.7 H.sapiens flow-sorted chromosome 6 HindIII fragment (AB022786) N-acetyl-beta-D-			DNA sequence, clone	i			; i
Sulculus diversicolor DNA for IDO-like myoglobin, complete cds H.sapiens flow-sorted chromosome 6 HindIII fragment O.022 191333 synthetase (E.C.6.3.5.5) probable membrane protein YDR018c - yeast (AB022786) N-acetyl-beta-D-	770	2044		1		(105503) carbamoul shoots	1 1
Sulculus diversicolor DNA for IDO-like myoglobin, complete cds H.sapiens flow-sorted chromosome 6 HindIII fragment (AB022786) N-acetyl-beta-D-	//8	Z96622	5PTELOO002.seq	0.022	191333	Synthetice (E.C.6.2.5.5)	
DNA for IDO-like myoglobin, complete cds 0.022 1078509 probable membrane protein YDR018c - yeast 9.7 H.sapiens flow-sorted chromosome 6 HindIII fragment (AB022786) N-acetyl-beta-D-	I		la			Symmetase (E.C.0.3.3.3)	9.8
myoglobin, complete cds 0.022 1078509 probable membrane protein YDR018c - yeast 9.7 H.sapiens flow-sorted chromosome 6 (AB022786) N-acetyl-beta-D-	- 1						ľ
779 D83984 cds 0.022 1078509 Probable membrane protein H.sapiens flow-sorted chromosome 6 (AB022786) N-acetyl-beta-D-	- [1			1
H.sapiens flow-sorted Chromosome 6 (AB022786) N-acetyl-beta-D-	770	D02004		j		probable membrane protein	, ,
chromosome 6 HindIII fragment (AB022786) N-acetyl-beta-D-	113			0.022	1078509	YDR018c - venst	0.7
HindIII fragment (AB022786) N-acetyl-beta-D-					-	Jeast	9.1
I Irindili Iragment.	j			ł	j	(AB022786) N-acetyl-heta-D	- 1
780 277052 ISSG 1990 ISSG	780	777052		1		glucosaminidase (Enterobacter	1
780 277952 SC6pA4A3 0.022 4204206 sp. 7.5		211932	SCOPA4A3	0.022			7.5

	Neare	est Neighbor (BlastN vs	. Genbank)	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEQ	? [·		Total Vs. Non-Redundant	roteins	
ID	ACCESSIO	DESCRIPTION	P VALUE	ACCESSIO	DE00====	1	
		Xenopus laevis		1.10023310	DN DESCRIPTION	P VA	
	1	mitochondrial DNA			Doi: 60		
781	M10217	complete genome.	0.022	2145763	B2168_C2_205 protein -		
	1			21437,03	Mycobacterium leprae	7.	
	j		ł		PROBABLE HELICASE		
	İ]		j	MOTI Motlp is a probable	1	
		Page 111	1	1	helicase essential for vegetative	. 1	
	•	Pea chloropiast		<u> </u>	growth on rich glucose medium	1	
		glyceraldehyde-3- phosphate	Í	ļ.	at 30 degree C: Swiss-Prot		
		dehydrogenase	1	1	Accession number P32333;	1	
ĺ	1	(Gpb1) gene,	1	ł	similar to S. cerevisiae RAD26	1	
782	M55147	complete cds.	0.000	· .	gene product: Swiss-Prot	1 .	
		Acholeplasma virus	0.022	417308	Accession number P40352	4.2	
- 1		MV-L1 DNA for			(AB008757) subunit II of	1	
ı		complete circular	1		c(o/b)3-type cytochrome c	1	
783	X58839	genome	0.022	3273189	oxidase [Bacillus	1	
- 1				3273109	stearothermophilus] VITELLOGENIN I	4.1	
ı			i i		PRECURSOR (YOLK		
			i i	•	PROTEIN 1)		
		ļ.,	1 1		>gi 72270 pir VJFF1		
- 1		Mouse c-myb	1		vitellogenin I precursor		
84	M26185	oncogene, exon 1 and			unnamed protein product		
~ 	W120183	exon 2 (partial).	0.022	138592	[Drosophila melanogaster]	2.5	
		Streptomyces albus	j			2.5	
	:	valine dehydrogenase	i				
1		(Vdh) gene, complete	1		(AF003145) B0414.8 gene		
35	AF061195	cds	0.022	2000776	product (Caenorhabditis		
- 1			0.022	2088768	elegans]	0.86	
	j	Homo sapiens alpha	I		EARLY GROWTH RESPONSE PROTEIN 1 fish		
		1,2-mannosidase IB	1				
6 /		gene, exon 9	0.022	1352361	>gi 531456 (U12895) egr l [Danio rerio] rerio]		
1		S.cerevisiae			[2-morerio] teno]	0.36	
J		chromosome XIV	1		PUTATIVE TUMOR		
7	Z71500	eading frame ORF			SUPPRESSOR LUCA 15		
		1122246	0.022	1708875	[sapiens]	0.16	
1	ŀ	lerpes simplex virus	1				
1		pe 2 genomic DNA	ļ		1		
1	fo	or 0.74-0.84 region,	1		kapa		
1		omplete cds	0.022	3132276	(AB0114S6) short ORF [TT		
1	Z	ea mays T		3132210	virus]	0.13	
		toplasm male	1				
1		erility restorer	į		(AL031035) putative aldehyde		
1.		ctor 2 (rf2) mRNA,	1		dehydrogenase [Streptomyces		
1	J43082 cc	mplete cds	0.022	3319720	land never a	001:	
			39		1	0.011	

	\Box	Nearest Neighbor (BlastN vs. Genbank)			Neares M	ai-th and are	
S	EQ				racmest N	eighbor (BlastX vs. Non-Redunda	nt Proteins)
-	DA	CCESSI		PVALUE	ACCESSIO	N DESCRIPTION	
-			H.sapiens simple		T	- Joeka Holy	P VALU
1	<u> </u>		tandem repeat DNA	1			
	90	X86913		0.021	<none></none>	-NO.	1
1	- 1		Mus musculus		1	<none></none>	<none:< td=""></none:<>
1	.		Pontin52 mRNA.		I		
79	<u>, </u>	AF100694	complete cds	0.021	<none></none>		1
			Nannostomus sp. large subunit rRNA gene, mitochondrial gene encoding mitochondrial rRNA		CNONES	<none></none>	<none:< td=""></none:<>
79:	2 1	U34016	partial sequence.	· 1		1	1 .
	7		Yeast mitochondrial	0.021	<none></none>	<none></none>	<none></none>
			genes for 15S rRNA				
793	3 3	X00845	and tRNA-Trp			· ·	1
			Homo sapiens gene	0.021	<none></none>	<none></none>	<none></none>
	ı		for CC chemokine	1			1.0
	ı		PARC precursor.			i	1
794	AE	3012113	complete cds	0.00.		į.	1 .
			Daucus carota	0.021	<none></none>	<none></none>	<none></none>
795	,	62395	globulin-like protein (Gea8) gene, complete cds				4.10.12
	╁	02393	complete cas	0.021	<none></none>	<none></none>	<none></none>
796	М	22718	P.falciparum actin II gene, complete cds.	0.021		(AF004835) tyrocidine synthetase 3 [Brevibacillus	KNONE
			Arabidopsis thaliana	0.021	2623773	brevis]	8.8
	i		glutamyl-tRNA	1		(AJ006631) cysteine-rich	1
79 7	L U2	27118	reductase	000	3546	secretory protein-1 [Equus	1 1
			H.sapiens CLN3	0.021	3549885	[caballus]	8.8
798	X9		gene, complete CDS	0.021	0.40	(S52010) orf1 5' of EpoR [mice	
			B, volimpicie CD3	0.021	262249	Peptide, 85 aal [Mus sp.]	8.7
		ŀ	Homo sapiens TRAIL	ı		SUCCINYL-	1
- 1			receptor 2 mRNA.	1	•	COA:COENZYME A	
799	AF0		complete cds	am.		TRANSFERASE transferase) 1
\neg			opicte cus	0.021	729048	[Clostridium kluvveril	8.7
- 1		- 1		j		LIPOPOLYSACCHARIDE 1,2-	
1		Į,	Tuman DNA	1		N-	1
- 1			equence from PAC	1		ACETYLGLUCOSAMINETR	1
- 1			79115, BRCA2 gene	i		ANSFERASE >gi 466761	1
- 1		lr.	egion chromosome			(U00039) rfaK [Escherichia	i
ĺ			3q12-13 contains	1		coli] >gi 1790053 (AE000440)	i
1			ctase-phlorizin	1		probably hexose transferase:	i
00	Z92		ydrolase (LCT)	0.00.	_	lipopolysaccharide core	- 1
		[11]	Grorase (LC1)	0.021	585820	biosynthesis	5.3

CE	ivear	est Neighbor (BlastN vs	. Genbank)	Nearest Ne	eighbor (BlastX vs. Non-Redundant P	
SEC	-		P VALUE	1		
\vdash		dopamine D2				P VAL
1	1	receptor [human,			(Y08029) NAD(P)(+)arginine	 -
801	S58588	brain, Genomic, 379	1	1	ADP-ribosyltransferase]
	030300	nt, segment 4 of 5] Rat nerve growth	0.021	2677620	[Oryctolagus cuniculus]	5.1
	f	factor-inducible	į.			3.1
		protein (VGF) gene,	l	1		ĺ
802	M60522	complete cds.	0.021		(AF030050) replication factor C	
			0.021	4103934	[Rattus norvegicus]	3.1
	J	Gallus gallus	1			
	ł	neuregulin beta-la	ł		(4-50.05.55.55	
803	AF045654	mRNA, complete cds	0.021	·· 2746829	(AF040647) No definition line	
				2140829	found [Caenorhabditis elegans]	3.0
	I	1	· ·	•	(Z82056) T26H5.8	
804			1		[Caenorhabditis elegans]	
804	M69023	Human globin gene.	0.021	3880259	>gi 3880787 gnl PID e1350288 (AL032620) T26H5.8	
					(AL032020) 126H3.8	2.4
		H.sapiens CpG DNA,	·l		(U80845) similar to family 1 of	
805	Z65960	clone 69d2, reverse	1		G-protein coupled receptors	
	203900	read cpg69d2.rt1b.	0.021	1707245	[Caenorhabditis elegans]	0.70
- 1			!!!		CORE ANTIGEN	0.79
- 1		A.oligospora gene	ł		>gi 73601 pir NKVLC2 core	
806	X97073	encoding lectin	2.22.		antigen - woodchuck hepatitis	
		D. melanogaster	0.021	116949	virus 2 >gi 336135	0.47
		mRNA for gene				
- 1		containing opa	1		1	
307	X56491	repetitive element	0.021	2042750	HOMEOBOX PROTEIN DLX-	
		Homo sapiens	0.021	2842750	7 >gi 1620520	0.16
- 1		(subclone I_f6 from	ł			
<u></u>		PI H31) DNA	- 1		IIII ALTI CY ASS TOTAL	l
08	L78760	sequence	0.021	113671	!!!! ALU CLASS F WARNING ENTRY !!!!	
.]					CYSTEINE SYNTHASE A (O-	0.15
1	ľ			1	ACETYLSERINE	
- 1)	ł	1		SULFHYDRYLASE A) (O-	
- [1		,]		ACETYLSERINE (THIOL)-	
- 1			1	}	LYASE A) (CSASE A)	1
ŀ	- 1		I		>gi 68323 pir SYEBAC cysteine	ł
- 1	1	1	ſ	Į.	synthase (EC 4.2.99.8) A -	1
- 1	1,	Tomo sapiens	ļ]:	Salmonella typhimurium	ł
	li.	KIAA0404 mRNA,	ı] :	>gi 153935 (M21450) cysK	1
9 A	B007864	Partial cds	0.02	Į.	protein [Salmonella	- 1
		Aycobacterium	0.021	118144 t	typhimurium]	0.12
		uberculosis H37Rv	1	[
. 1	C	omplete genome;	1	1.		
) <u>A</u>		gment 22/162	0.021		AL021932) hypothetical	- 1
				2909314 p	protein Rv0439c 7	e-10

	Neares	t Neighbor (BlastN vs. (Genbank)	Nearest Neio	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEC			T		/ / / / / / / / / / / / / / / / / / /	ioteins)		
В	- 1	N DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE		
-	 	Hypocrea jecorina	 					
ł		mannose-1-phosphate	.					
1	Į.	guanylyitransferase	1		(AL031538) mannose-1-	ł		
1	İ	(MPGI) mRNA,	1	ĺ	phosphate guanyltransferase	İ		
811	U89991	complete cds	0.021	3581924	[Schizosaccharomyces pombe]	6e-20		
	1	Sugar beet mitochondrial	1					
1	1	minicircle pO						
812	X00641	sequence	0.020	<none></none>	NONE			
		D.melanogaster	0.020	CHOILES	<none></none>	<none></none>		
1	ľ	mRNA for hdc	ŀ					
813	Z50097	protein.	0.020	<none></none>	<none></none>	<none></none>		
		Phoebis sennae large						
İ		subunit ribosomal						
	1	RNA gene, partial			1 .			
1		sequence; tRNA-Val						
	J	gene, complete]					
		sequence; and small subunit ribosomal	ì					
		RNA gene, partial						
		sequence,	•					
1		mitochondrial genes	ſ		j·	İ		
		for mitochondrial	1	*				
814	AF044866	RNAs	0.020	<none></none>	<none></none>	<none></none>		
		Sambucus nigra						
		hevein-like protein	1					
815	AF074386	mRNA, complete cds	0.020	<none></none>	<none></none>	<none></none>		
					370.72	CITOINE		
		Arabidopsis thaliana						
		cellulose synthase catalytic subunit (Ath-			1 .	. 1		
		B) mRNA, complete	.	•		Ì		
816	AF027174	cds	0.020	<none></none>	<none></none>	<none></none>		
	1	Plasmodium			3,0112	VIVOIVES		
		falciparum			[İ		
ļ		chromosome 2, section 42 of 73 of						
		the complete			(AF003342) bunched gene			
817		sequence	0.020	2196776	product [Drosophila melanogaster]	8.4		
				3170,70	inclanoguster)	0.4		
ł		Sambucus nigra				i		
818		nevein-like protein	0.000		histidine-rich protein -]		
310	14 0/+30/ [I	nRNA, complete cds	0.020	627071	Plasmodium lophurae	2.8		

WO 01/02568

	Nearest	Neighbor (BlastN vs. C	ionbook)	No.		
SEQ		THE PROPERTY OF THE PROPERTY O	Jenoank)	Nearest Neig	hbor (BlastX vs. Non-Redundant P	roteins)
· ·	· ·		1			
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
_	 					
1		Hylobates hoolock				1
1		mitochondrial DNA	l	1	(D10043) ORF [Acetobacter	ł
819	Y13304	for cyth gene, Horace	0.020	285580	pasteurianus]	2.1
1	Í				(U80439) coded for by C.	
]			1		elegans cDNA yk7c8.5; coded	}
					for by C. elegans cDNA	i l
1				İ	yk133b3.5; coded for by C.	ŀ
1					elegans cDNA yk65a4.5; coded	<u> </u>
		1	!		for by C. elegans cDNA	ļ (
1 1		ĺ			yk7c8.3; coded for by C.	
1 1		77			elegans cDNA CEESQ66F;	:
820	Z66539	H sapiens creatine			coded for by C. elegans cDNA	
820	200339	transporter gene	0.020	1703594	yk65a4.3;	0.98
ĺ		Homo sapiens alpha			EARLY GROWTH	
		1.2-mannosidase IB			RESPONSE PROTEIN I fish	ľ
821	AF053622	gene, exon 9	0.000	1250051	>gi 531456 (U12895) egr1	İ
<u> </u>	A 053022	gene, exon 9	0.020	1352361	[Danio rerio] rerio]	0.72
					PROTEIN IN SBCB-HISL	1
		1	ı		INTERGENIC REGION	
			i		>gi 405956 (U00009)	1
1			f		ORF_ID:0349#4; similar to	
' I			ì		[SwissProt Accession Number	- 1
		•	ı		P33015] [Escherichia coli]	ł
	1		ſ		>gi 1736693 gnl PID d1016570	ı
	1		1		Number P33015] [Escherichia	
]:	Human MHC class II	ł		coli] >gi 1788323 (AE000292)	'
j	Į:	HLA-DRw53-beta	1		putative transport system	
	4	(DR4,w4) gene,	į		permease protein [Escherichia	1
822		xons 2,3,4,5,6.	0.020	465569	coli	0.43
П	Ţī	Human MHC class II			COENZYME POO	0.43
Į	1	HLA-DRw53-beta	I		SYNTHESIS PROTEIN F	ļ
]		DR4,w4) gene,	. [synthesis F - Pseudomonas	
823	M20555 e	xons 2,3,4,5,6.	0.020	1709751	fluorescens >gi 929802	0.42

	ive	arest f	Veighbor (BlastN v	s. Genbank)		Nearest	Neigh	bor (BlastX vs. Non-Redundant I)
SE	-	SION	DESCRIPTION	N P VAL	UE	ACCESSI		DESCRIPTION	
<u> </u>						1002551	011	TOTAL ICAL 12.3 KD	P VAL
1	i	I			1			PROTEIN ZK637.2 IN	
l	1	- 1		1				CHROMOSOME III	
l	1]		1	ı			>gi 102507 pir S15787	1
[1	- 1		ł	- 1			hypothetical protein 1 (cosmid	1
	·]	- 1		1	- 1			ZK637) - Caenorhabditis	i
	1	- 1		1	ł		-	elegans Genefinder; cDNA EST	
	1			1	- 1			yk217b5.3 comes from this	1
	1			j	- 1			gene; cDNA EST yk217b5.5	ł
	J.	- 1		1	- 1			comes from this gene; cDNA	ļ
	ł	- 1		- 1	- 1		i	EST yk340g12.3 comes from	
	i	L.	_	ł	1	٠.		this gene; cDNA EST	ł
	l		lomo sapiens mRN		j			yk340g12.5 comes from this	[
824	A 10060		or putative SMC-li	ke	- 1			gene; cDNA EST yk428c5.5	1
	AJ00501) bi	otein, partial	0.020	L	267449		co	
	l	_T .	accaria bicolor						le-12
			yoxal malate	1					
			nthase protein	1			ļ		V.
825	AF03409		RNA, complete cd		1		- le	(U41538) No definition line	
	12 05 10 7		us musculus	s 0.020		1109847	lf	found [Caenorhabditis elegans]	le-22
			ntin52 mRNA,	j	1		16	OUS RIBOSOMAL PROTEIN	10-22
326	AF10069		mplete cds	1 2212	1.		ļī	28 protein L28 [Rattus	
\neg			ttus norvegicus	0.019	+	132836	n	orvegicus]	5.7
- 1			ner-1c mRNA,	l			- 1		
27	AF093268		nplete cds	0.019	1	0.00.	C	Z99109) similar to DNA	
- 1		Mu	s musculus	0.019	╁┈	2633401	e	xonuclease	4.5
- 1		Por	tin52 mRNA,	ĺ	İ				
28	AF100694		plete cds	0.019	1	2492604	M	IULTIDRUG RESISTANCE	
- 1					1-	2492004		ROTEIN CDR2 albicans]	4.4
1				ł	1			LUCOSYLTRANSFERASE	
		1		1	1		ĺċ	17C9.07	
•		1			1			:i 1314159 gn1 PID e241760	
}		1		•	l		ίZ	73099) SPAC17C9.07,	
	•	J					pu	tative glucosyl transferase len:	
- 1			nanococcus		l		50	1, similar to	
			aschii section 80	ļ			sv	V:ALG8_YEAST P40351	
9	U67538	ſ	0 of the				glu	cosyltransferase ALG8	
1	20,330		olete genome an periodic	0.019		1723566	por	mbe]	2.7
1			ophan protein 2	1			T		
1			2) gene, exons	Í			1	l	- 1
	U56088	3 to 1		0010			coll	lagen alpha I(II) chain -	- 1
		1		0.019		2144804	bov	•	0.040
I		Samb	ucus nigra	- 1			1		
1			me inactivating	j				1	ľ
1			n precursor				(U9	1682) vitelline membrane	- 1
	U76524		A. complete cds	810.0		1017025		ein homolog [Aedes	. [
			J	0.010		1916976	aegy	/ptil	7.2

	Nearest	Neighbor (BlastN vs. (Genbank)	Nearest Neig	hbor (BlastX vs. Non-Redundant Pr	rotoina\
SEQ			T	- Tourest Heig	itoor (Blasta Vs. Non-Reddindam Fi	(ciens)
ID	ACCESSION	DESCRIPTION				[
	TACCESSIOI	DESCRIPTION	PVALUE	ACCESSION	DESCRIPTION	P VALUE
 	 	Onobrychis viciifolia				
1	l		ŀ		(Z48799) ZP3 [Cyprinus carpio]	
	ļ.	chalcone synthase			>gi 777724 (L41637) egg	
832	A F026260	(CHS) mRNA,			membrane protein [Cyprinus	
832	AF026258	complete cds	0.018	763076	carpiol	5.2
1	<u>.</u>	Xenopus laevis XL-	1	1	ŀ	
]	·	INCENP (XL-]	i	į	
833	U95094	INCENP) mRNA,	0.000		(AJ005438) beta adrenoreceptor	
833	093094	complete cds C.jejuni VSI DNA >	0.009	3955011	В	0.60
İ .					ļ	
1 1		emb A39603 A39603	1	٠,		
1		Sequence 2 from	į			
		Patent WO9417205 >	٠.			
1		:: gb I76090 I76090	1			,
		Sequence 2 from				
834	X71603	patent US 5691138	0.008	AIONES	, vo. =	
	1271005	patent 03 3091136	0.008	<none></none>	<none> HEAD FIBER PROTEIN</none>	<none></none>
					(LATE PROTEIN GP8.5)	
					>gi 75846 pir WMBP8H gene	
		Rattus norvegicus			8.5 protein - phage PZA	- 1
i í		homer-1c mRNA,			>gi 216057 (M11813) head	
835	AF093268	complete cds	0.008	138116	fiber protein	
			0.000	130110	SUPEROXIDE DISMUTASE	8.1
1					(FE) 1.15.1.1) (Fe) -	1
1 1		Bovine herpesvirus			Pseudomonas aeruginosa	i i
836	X91751	type 1 UL7 gene	0.008	1711436	>gil409767	5.9
		<u> </u>			<u> </u>	J.9
		Arabidopsis thaliana	1			i
l		1-aminocyclopropane-	1		1	
		1-carboxylate	j		1	
[synthase (ACS2)	i		(Z48229) orf1 gene product	İ
837		gene, complete cds.	0.008	683698	[Saccharomyces cerevisiae]	1e-06
	1	Methanococcus				
- 1		annaschii section 7	ľ		1	1
-		of 150 of the	1		(Z68493) predicted using	
838		complete genome	0.008	3874664	Genefinder	le-07
.,,	1	B.taurus mRNA for			1-aminocyclopropane-1-	
839	X72388	îlensin	0.008	100174	carboxylate synthase	7e-09
J	1		1	· · · · · · · · · · · · · · · · · · ·		
]		Human Cdk-inhibitor			1	l
040		57KIP2 (KIP2)			(U93868) RNA polymerase III	
840		nRNA, complete cds.	0.008	2228750	subunit [Homo sapiens]	2e-18
1		Cenopus laevis LIM	1			
		lass homeodomain			1	
841	L42546 p	rotein	0.007	<none></none>	<none></none>	<none></none>

	Nearest	Neighbor (BlastN vs. G	enbank)	Negreet Naighb	or (BlastX vs. Non-Redundant P	roteins)
SEQ	carest		JJu.,	racarest racigno	O (Diaser vs. 11011-redundant 1	T T
D	ACCESSION	<u> </u>	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens				
		ribosomal protein s4				
Į .		X isoform gene,				1
842	AF041428	complete cds	0.007	<none></none>	<none></none>	<none></none>
1		Secale cereale omega				
1 _		secalin gene.				ł
843	AF000227	complete cds	0.007	<none></none>	<none></none>	<none></none>
		Human MHC (HLA)				ł
		DRB intron 1 DNA,				
844	D86254	partial sequence	0.007	<none></none>	<none></none>	<none></none>
Į i		c.				
		Sambucus nigra				
		ribosome inactivating				1
845	A F010000	protein precursor	0.007	NONE	NONE	1,70
843	AF012899	mRNA, complete cds M.musculus gene for	0.007	<none></none>	<none></none>	<none></none>
846	Y07738	vimentin	0.007	<none></none>	<none></none>	NONES
1070	10/736	Arabidopsis thaliana	0.007	CHOILES	ZNONES	<none></none>
į l		mRNA for	İ			1
		neoxanthin cleavage				
847	AJ005813	enzyme	0.007	<none></none>	<none></none>	<none></none>
 	73003813	Homo sapiens alpha-	0.007	CHOILE	410NE	CIVOINE>
		tectorin (TECTA)		ļ		
848	AF055119	gene, exon 6	0.007	<none></none>	<none></none>	<none></none>
		<u>g</u>				13.3.3.3.3.3.3.3.3.3.3.3.3.3.3.3.3.3.3.
1 1		Zucchini 1-	I	•		Ì
ĺ		aminocyclopropane-1	ł			
849	M61195	carboxylate synthase	0.007	<none></none>	<none></none>	<none></none>
		Homo sapiens DSG3				
		gene, partial intron	J	. [
		and partial exon 6,	§		·	
850		140 bp	0.007	<none></none>	<none></none>	<none></none>
	1	M.voltae vhuD,				
ļ		vhuG, vhuA, vhuU &	ľ	1	•	
851		vhuB genes	0.007	<none></none>	<none></none>	<none></none>
		Brassica rapa mRNA				1 1
		for SLG45, complete				l
852	AB012105	cds	0.007	<none></none>	<none></none>	<none></none>
ľ		telomere:	ļ	i		ļ
j	ı		i	İ		
		(minichromosome,	J	İ]
i		repeats}	1			
853		[Trypanosoma brucei.	0.007	NONE	AIONES	NOTES
رده	S43882	Genomic, 1170 nt]	0.007	<none></none>	<none></none>	<none></none>

199.5	Nearest	Neighbor (BlastN vs. G	ienbank)	Nearest Neigh	bor (BlastX vs. Non-Redundant Pr	oteins)
SEO		T	1		T TOTAL TOTAL CONTROL OF THE CONTROL	Olellis)
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1	1	Geomydoecus nadleri		1		
i		mitochondrial			1	
964		cytochrome oxidase I			1	
854	L32674	gene, partial cds.	0.007	<none></none>	<none></none>	<none></none>
		Caenorhabditis elegans cosmid		,	1	
855	U58732	F48D6.	0.007	ANONIC-	11017	
1000	038732	F40D0.	0.007	<none></none>	<none></none>	<none></none>
1		Sambucus nigra			1	
1	İ	ribosome inactivating				
ì		protein precursor		* ,		
856	U76524	mRNA, complete cds	0.007	<none></none>	<none></none>	<none></none>
					HYPOTHETICAL 121.1 KD	
				•	PROTEIN IN BIO3-HXT17	
1 1		H.sapiens mRNA for			INTERGENIC REGION	
		MDR3 P-			PRECURSOR YNR067c - yeast	
857	Z35284	glycoprotein	0.007	1730696	(Saccharomyces cerevisiae)	9.5
1 1		U			1	
		Human sno oncogene mRNA for snoA			(7724202)	
858	X15217	protein, ski-related	0.007	902455	(U24203) membrane protein	0.0
050	RIJEIT	protein, ski-related	0.007	902433	[Escherichia coli]	8.8
		Arabidopsis thaliana				
		cellulose synthase				1
		catalytic subunit (Ath-				
1 1		A) mRNA, complete	•		(Y09454) ORF3 (Lactobacillus	1
859	AF027173	cds	0.007	1684636	casei bacteriophage A2]	8.3
] [
		Sambucus nigra			ļ i	- 1
		ribosome inactivating]	- 1
860		protein precursor			(Z48795)·R05H5.7	
800	AF012899	mRNA, complete cds	0.007	3878803	[Caenorhabditis elegans]	8.3
		membrane protein	I			
		scavenger receptor				
' I		homolog (clone 18,				
. I		intron and flanking	:		l	ŀ
·]		exons 14 and 15}	ı			
ŀ		[sheep, lymph node,	ĺ			i
J		lymphocytes,	į			
	. [6	Genomic, 308 nt,	į	·	(L08174) ORF2	ł
861	S76317	segment 2 of 2]	0.007	294747	[Romanomermis culicivorax]	7.4

Pedicularis verticillata chloroplast DNA, intergenic region between trnT(UGU) and trnL(UAA)S'exon 0.007 2555187 Pimpla nipponical chloroplast DNA, intergenic region between trnT(UGU) and trnL(UAA)S'exon 0.007 2555187 Pimpla nipponical chloroplast DNA, intergenic region between trnT(UGU) and trnL(UAA)S'exon 0.007 2555187 Pimpla nipponical chloroplast DNA, intergenic region between trnT(UGU) and trnL(UAA)S'exon 0.007 115978 ACTIVATION ANTIGEN 6.5 CDNA EST EMBL.035637 Comes from this gene; cDNA EST yk397b2.3 comes from this gene; cDNA		: :÷.	Neares	st Neighbor (BlastN vs	. Genbank)	Negreet No	ighbox (PlaneY)	
D ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION P VALUE		SEC				ivearest ive	Ignoor (BlastX Vs. Non-Redundant F	roteins)
Pedicularis verticillata Chloroplast DNA, intergenic region Chicken mRNA for aldehyde Chicken mRNA for aldehyde Chicken mRNA for aldehyde Chicken mRNA for aldehyde Chicken mRNA for aldehyde Chicken mRNA for aldehyde Chicken mRNA for aldehyde Chicken mRNA for aldehyde Chicken mRNA for aldehyde Chicken mRNA for aldehyde Chicken mRNA for aldehyde Chicken mRNA for aldehyde Chicken mRNA for Chicken mRNA			· .	N DESCRIPTION	P VALUE	ACCESSION	N DESCRIPTION	P VALUE
Verticillata Chloroplast DNA, intergenic region between trnT(UGU) 1.50		<u> </u>	 -	Padigulacia				
Chloroplast DNA intergenic region the product of the product		l	ľ	i i	1	ļ		
Secondary Seco		1	1		1	ł		1
Detween tmT(UGU) and tmL(UAA)Sexon 0.007 2555187 (AF026789) vitellogenin [Impgla nipponica] 6.9			I		j	1		J
According to the complete of		•	1			ļ	1	1
Chicken mRNA for aldehyde dehydrogenase		862	D88084					1
Chicken mRNA for aldehyde Chicken mRNA for aldehyde Chicken mRNA for aldehyde Chicken mRNA for aldehydrogenase Chicken mRNA for aldehydrogenase Chicken mRNA for aldehydrogenase Chicken mRNA for allowed Chicken mRNA for al			200004	Talid dilL(OAA)3 exc	on 0.007	2555187	[Pimpla nipponica]	6.9
Activation Anticem Activation Anticem Activation Anticem Activation Anticem Activation Anticem Activation Anticem Activation Anticem Activation Anticem Activation Anticem Activation Anticem Activation Anticem Activation Anticem Activation Anticem Activation Anticem Activation Activation Activ			i	Chicken mRNA for		l		
Activation Antigen 6.5			ł		1			
According to the content of the co		863	X58869	•	0.007	116070		
CDMA EST EMBL-D35637	ı			- Conjuingeniase	0.007	113978	ACTIVATION ANTIGEN	. 6.5
Comes from this gene; cDNA EST yk322a3.5 comes from this gene; cDNA EST yk3397b2.5 comes from this gene; cDNA EST yk348b11.5 comes from this gene; cDNA EST yk348b11.5 comes from this gene; cDNA EST yk348b11.5 comes from this gene; cDNA EST yk348b11.5 comes from this gene; cDNA EST yk397b2.3 comes from this gene; cDNA EST yk397b2.3 comes from this gene; cDNA EST yk322a3.5 comes from this gene; cDNA EST yk322a3.5 comes from this gene; cDNA EST yk327b2.5 comes from this gene; cDNA EST yk348b11.5 comes from this gene; cDNA EST yk348b11.5 comes from this gene; cDNA EST yk348b11.5 comes from this gene; cDNA EST yk348b11.5 comes from this gene; cDNA EST yk348b11.5 comes from this gene; cDNA EST yk348b11.5 comes from this gene; cDNA EST yk348b11.5 comes from this gene; cDNA EST yk348b11.5 comes from this gene; cDNA EST yk348b11.5 comes from this gene; cDNA EST yk348b11.5 comes from this gene; cDNA EST yk348b11.5 comes from this gene; cDNA EST yk348b11.5 comes from this gene; cDNA EST yk348b11.5 comes from this gene; cDNA EST yk348b11.5 comes from this gene; cDNA EST yk348b11.5 comes from this gene; cDNA EST yk348b11.5 comes from this gene; cDNA EST yk397b2.5 comes from this gene; cDNA EST yk397b2.5 comes from this gene; cDNA EST yk397b2.5 comes from this gene; cDNA EST yk397b2.5 comes from this gene; cDNA EST yk397b2.5 comes from this gene; cDNA EST yk397b2.5 comes from this gene; cDNA EST yk397b2.5 comes from this gene; cDNA EST yk397b2.5 comes from this gene; cDNA EST yk397b2.5 comes from this gene; cDNA EST yk397b2.5 comes from this gene; cDNA EST yk397b2.5 comes from this gene; cDNA EST yk397b2.5 comes from this gene; cDNA EST yk397b2.5 comes from this gene; cDNA EST yk397b2.5 comes from this gene; cDNA EST yk397b2.5 comes from this gene; cDNA EST yk397b2.5 comes from this gene; cDNA EST yk397b2.5 comes from this gene; cDNA comes from this gene; cDNA comes from this gene; cDNA comes	-		l				cDNA EST EMBL:D35637	
EST yk322a3.5 comes from this gene; cDNA EST yk397b2.5 comes from this gene; cDNA EST yk397b2.5 comes from this gene; cDNA EST yk348b11.5 comes from this gene; cDNA EST yk397b2.3 comes from this gene; cDNA EST yk397b2.3 comes from this gene; cDNA EST yk397b2.3 comes from this gene; cDNA EST yk397b2.5 comes from this gene; cDNA EST yk397b2.3 comes from this gene; cDNA EST yk397b2.3 comes from this gene; cDNA EST yk397b2.3 comes from this gene; cDNA EST yk397b2.3 comes from this gene; cDNA EST yk397b2.3 comes from this gene; cDNA EST yk397b2.3 comes 5.1 (AF010403) ALR (Homo aprilement) ALR (Homo aprilement) All (Homo aprilemen	- [1	''			
Seene: cDNA EST yk397b2.5 comes from this gene; cDNA EST yk348b11.5 comes from this gene; cDNA EST yk397b2.3 comes from this gene; cDNA EST yk397b2.5 comes from this gene; cDNA EST yk397b2.5	1		1	1			EST yk322a3.5 comes from this	1
Comes from this gene; cDNA EST yk348b11.5 comes from this gene; cDNA EST yk397b2.3 comes from this gene; cDNA EST yk397b2.3 comes from this gene; cDNA EST yk397b2.5 comes from this gene; cDNA EST yk322a3.5 comes from this gene; cDNA EST yk322a3.5 comes from this gene; cDNA EST yk348b11.5 comes from this gene; cDNA EST	-		ĺ				gene; cDNA EST vk397b2.5] .
EST yk348b11.5 comes from this gene; cDNA EST yk3y7b2.3 comes from this gene; cDNA EST yk3y7b2.3 comes from this gene; cDNA EST yk3y37b2.3 comes from this gene; cDNA EST yk3y37b2.5 comes from this gene; cDNA EST yk3y37b2.5 comes from this gene; cDNA EST yk3y37b2.5 comes from this gene; cDNA EST yk3y37b2.5 comes from this gene; cDNA EST yk3y7b2.3 comes from this gene; cDNA EST yk3y37b2.3 comes from this gene; cDNA EST yk3y37b2.3 comes from this gene; cDNA EST yk3y37b2.3 comes from this gene; cDNA EST yk3y37b2.3 comes from this gene; cDNA EST yk3y37b2.3 comes from this gene; cDNA EST yk3y37b2.3 comes from this gene; cDNA EST yk3y37b2.3 comes from this gene; cDNA EST yk348b11.5 comes from this gene; cDNA EST yk397b2.3 comes from this gene; cDNA EST yk397b2.3 comes from this gene; cDNA EST yk397b2.3 comes from this gene; cDNA EST yk397b2.3 comes from this gene; cDNA EST yk397b2.3 comes from this gene;							comes from this gene; cDNA	
this gene; cDNA EST yk397b2.3 comes fr >gij3880965[gnl]PID[e1350578 comes from this gene; cDNA EST yk322a3.5 comes from this gene; cDNA EST yk397b2.5 comes from this gene; cDNA EST yk3297b2.5 comes from this gene; cDNA EST yk397b2.5 comes from this gene; cDNA EST yk397b2.5 comes from this gene; cDNA EST yk348b11.5 comes from this gene; cDNA EST yk397b2.3 comes 5.1 865 X68793 H.Sapiens gene for antithrombin III 0.007 2358285 sapiens] Danio rerio mRNA for opioid receptor homologue 0.007 2507509 colis Streptomyces albus valine dehydrogenase (Vdh) gene. complete cds (AF003145) B0414.8 gene product (Caenorhabditis elegans) 1.9 Arabidopsis thaliana mRNA for neoxanthin cleavage neceptor homologue 0.007 2088768 elegans) 1.9 Arabidopsis thaliana mRNA for neoxanthin cleavage razyme 0.007 2110105	1							
Streptomyces albus valine dehydrogenase (Vdh) gene. complete cds O.007 2088768 O.007	1			·	1 1			
comes from this gene; cDNA EST yk3223.5 comes from this gene; cDNA EST yk397b2.5 comes from this gene; cDNA EST yk397b2.5 comes from this gene; cDNA EST yk397b2.5 comes from this gene; cDNA EST yk348b11.5 comes from this gene; cDNA EST yk397b2.3 comes from this gene; cDNA EST yk397b2.3 comes 5.1 H.Sapiens gene for antithrombin III 0.007 2358285 ABOUT THE TICAL 29.8 KD PROTEIN IN HOLB-PTSG INTERGENIC REGION Sgil1787342 (AE000210) orf, hypothetical protein [Escherichia coli] protein in holB 3'region . [Escherichia coli] 1.9 Streptomyces albus valine dehydrogenase (Vdh) gene. complete cds AF061195 Arabidopsis thaliana mRNA for neoxanthin cleavage R88 AJ005813 AD05813 CAPOUR AST yk392b.5 COMES From this gene; cDNA EST yk348b11.5 comes from this gene; cDNA EST yk348b11	1			Í				
comes from this gene; cDNA EST yk3223.5 comes from this gene; cDNA EST yk397b2.5 comes from this gene; cDNA EST yk397b2.5 comes from this gene; cDNA EST yk397b2.5 comes from this gene; cDNA EST yk348b11.5 comes from this gene; cDNA EST yk397b2.3 comes from this gene; cDNA EST yk397b2.3 comes 5.1 H.Sapiens gene for antithrombin III 0.007 2358285 ABOUT THE TICAL 29.8 KD PROTEIN IN HOLB-PTSG INTERGENIC REGION Sgil1787342 (AE000210) orf, hypothetical protein [Escherichia coli] protein in holB 3'region . [Escherichia coli] 1.9 Streptomyces albus valine dehydrogenase (Vdh) gene. complete cds AF061195 Arabidopsis thaliana mRNA for neoxanthin cleavage R88 AJ005813 AD05813 CAPOUR AST yk392b.5 COMES From this gene; cDNA EST yk348b11.5 comes from this gene; cDNA EST yk348b11	1				1			
Homo sapiens mRNA for GS3786, complete cds 0.007 3879589 yk392.3.5 comes from this gene; cDNA EST yk397b2.5 comes from this gene; cDNA EST yk397b2.5 comes from this gene; cDNA EST yk348b11.5 comes from this gene; cDNA EST yk397b2.3 comes 5.1 865 X68793 H. Sapiens gene for antithrombin III 0.007 2358285 sapiens] 3.8 BAJ001596 Danio rerio mRNA for opioid receptor homologue 0.007 2507509 CAFOLOGIA (AF003145) B0414.8 gene product (Caenorhabditis elegans) 1.9 Streptomyces albus valine dehydrogenase (Vdh) gene, complete cds 0.007 2088768 elegans] 1.9 Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme 0.007 1710105	1			I	1 1		comes from this gene; cDNA	
Homo sapiens mRNA for GS3786, complete cds	l			i	1 1		EST yk322a3.5 comes from this	
Homo sapiens mRNA for GS3786, complete cds				· .	1		gene; cDNA EST yk397b2.5	1
B64		j			1			1
864 D87120 Ich GS3786, complete cds	İ	ľ					EST yk348b11.5 comes from	1
H.sapiens gene for antithrombin III 0.007 2358285 (AF010403) ALR [Homo sapiens] 3.8 Bacterian Service of Se		864	D97130	•			this gene; cDNA EST	1
865 X68793 antithrombin III 0.007 2358285 sapiens] 3.8 Danio rerio mRNA for opioid receptor homologue 0.007 2507509 250	H		D8/120		0.007	3879589		5.1
866 AJ001596 Danio rerio mRNA for opioid receptor homologue 0.007 2507509 CAF003145) B0414.8 gene product [Caenorhabditis elegans] 1.9 Arabidopsis thaliana mRNA for neoxanthin cleavage 868 AJ005813 enzyme 0.007 1710105 Sapiens] 3.8 HYPOTHETICAL 29.8 KD PROTEIN IN HOLB-PTSG INTERGENIC REGION >gil1787342 (AE000210) orf, hypothetical protein in holB 3'region . [Escherichia coli] protein i	L	865	Y68702				(AF010403) ALR [Homo	
PROTEIN IN HOLB-PTSG INTERGENIC REGION >gi 1787342 (AE000210) orf, hypothetical protein [Escherichia coli] protein in holB 3'region . [Escherichia coli] protein coll selection and selection and selection a	卜		1600793	anduromon III	0.007	2358285	sapiens]	3.8
Danio rerio mRNA for opioid receptor homologue Danio rerio marketa for opioid receptor homologue Danio rerio marketa for opioid receptor homologue Danio rerio marketa for opioi	ı	- 1					HYPOTHETICAL 29.8 KD	
Danio rerio mRNA for opioid receptor homologue 866 AJ001596 Danio rerio mRNA for opioid receptor homologue Streptomyces albus valine dehydrogenase (Vdh) gene. complete cds AF061195 Cds Arabidopsis thaliana mRNA for neoxanthin cleavage 868 AJ005813 enzyme Danio rerio mRNA for hypothetical protein [Escherichia coli] protein in holB 3'region . [Escherichia coli] protein in holB 3'regi	1	. [1			
B66 AJ001596 Danio rerio mRNA for opioid receptor homologue 0.007 2507509 Coli] 1.9 Streptomyces albus valine dehydrogenase (Vdh) gene. complete cds 0.007 2088768 (AF003145) B0414.8 gene product [Caenorhabditis elegans] 1.9 Arabidopsis thaliana mRNA for neoxanthin cleavage 868 AJ005813 enzyme 0.007 1710105			}					. 1
Banio rerio mRNA for opioid receptor homologue 0.007 2507509 [Escherichia coli] protein in holB 3'region . [Escherichia coli] protein in holD 3'region . [Escherichia coli] protein in holD 3'region . [Escherichia coli] protein in holD 3'region . [Escher	1	1					>gil1/8/342 (AE000210) orf,	1.
866 AJ001596 for opioid receptor homologue 0.007 2507509 [Escherichia coli] protein in holB 3'region . [Escherichia coli] 1.9 Streptomyces albus valine dehydrogenase (Vdh) gene. complete cds 0.007 2088768 [Escherichia coli] 1.9 AF061195 cds 0.007 2088768 [Escherichia coli] protein in holB 3'region . [Escherichia coli] protein in holB 3'region . [Escherichia coli] 1.9 [AF003145] B0414.8 gene product [Caenorhabditis elegans] 1.9 Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme 0.007 [Escherichia coli] protein in holB 3'region . [Escherichia coli] protein in holB 3'region . [Escherichia coli] protein in holB 3'region . [Escherichia coli] protein in holB 3'region . [Escherichia coli] 1.9	1	- 1	ľ	Danio rerio mRNA	i			1
866 AJ001596 homologue 0.007 2507509 coli] 1.9 Streptomyces albus valine dehydrogenase (Vdh) gene. complete cds 0.007 2088768 elegans] 1.9 Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme 0.007 1710105	l	1			Ī			į
Streptomyces albus valine dehydrogenase (Vdh) gene. complete cds AF061195 Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme 868 AJ005813 Streptomyces albus valine dehydrogenase (VAF003145) B0414.8 gene product [Caenorhabditis elegans] UDP-N-ACETYLGLUCOSAMINE 2-EPIMERASE UDP-N-acetylglucosamine 2-epimerase	_8	366			0.007	2507509		
valine dehydrogenase (Vdh) gene. complete cds AF061195 Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme 868 AJ005813 Valine dehydrogenase (AF003145) B0414.8 gene product [Caenorhabditis elegans] UDP-N-ACETYLGLUCOSAMINE 2-EPIMERASE UDP-N-acetylglucosamine 2-epimerase		T				2307309	COIT	1.9
867 AF061195 (Vdh) gene. complete cds 0.007 2088768 product [Caenorhabditis elegans] 1.9 Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme 0.007 1710105 (Planethabete description of the complete cds of the complete product [Caenorhabditis elegans] 1.9		I			j		1	į
867 AF061195 cds 0.007 2088768 product [Caenorhabditis elegans] 1.9 Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme 0.007 1710105 product [Caenorhabditis elegans] 1.9					1		(AF003145) B0414 8 gene	
Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme 0.007 2088768 elegans] 1.9 Arabidopsis thaliana mRNA for EPIMERASE UDP-N-acetylglucosamine 2-epimerase	_			Vdh) gene. complete	1			i
Arabidopsis thaliana mRNA for EPIMERASE UDP-N-neoxanthin cleavage acetylglucosamine 2-epimerase	8	67	AF061195 c	ds	0.007	2088768	[·	, ,
Arabidopsis thaliana mRNA for EPIMERASE UDP-N-neoxanthin cleavage acetylglucosamine 2-epimerase			T					1.9
mRNA for neoxanthin cleavage acetylglucosamine 2-epimerase acetylglucosamine 2-epimerase]		1	.]
868 AJ005813 enzyme 0.007 l710105 acetylglucosamine 2-epimerase					1			- 1
000 A3003013 Enzyme 0.007 171010= Im	Q.	٥٥ ا		_	ł			l
	_0(00	MJUUS813 Je	nzyme	0.007	1710105		1.7

ŀ	<u>::</u>		Neighbor (BlastN vs. (Genbank)	Nearest Neigl	hbor (BlastX vs. Non-Redundant Pi	roteins)
	SEQ	ľ		1			
Ĺ	ID	ACCESSIO	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
			Zebrafish retinoic	1		T	T VALUE
ı			acid receptor alpha				
	869	L03398	2.A	0.007	2239219	(Z97210) hypothetical protein	0.77
- 1		İ	Human mRNA for				<u> </u>
-			KIAA0150 gene,			(Z14014) Pistil extensin like]
ŀ	870	D63484	partial cds	0.007	19917	protein, partial CDS only	0.61
1			Maize glyceraldehyde				
-	Į		3-phosphate	1			İ
-1	i		dehydrogenase, 3'			mucin, tracheobronchial - dog	[
L	871	M31483	end.	0.007	543068	>gi 402558	0.15
Γ					3.3000	Zg1 402536	0.45
1			Lycopersicon		•	ALPHA-2B ADRENERGIC	
1	ı	•	esculentum cytosolic			RECEPTOR adrenoceptor	
-	ı		class II small heat			[Cavia porcellus]	
1			shock protein HCT2			>gi 1587159 prf 2206293B	
1	872	A.F.000.115	(HSP17.4) mRNA,			adrenoceptor alpha2B [Cavia	i
┝	8/2	AF090115	complete cds	0.007	2494941	porcellus]	0.42
	ı		Helianthus tuberosus	i		(550.110)	
1			lectin 1 mRNA.	1		(\$79410) nuclear localization •	f
1	873	AF064029	complete cds	0.007	1110587	signals Peptide, 140 aa] [Mus	224
Г				0.007	1110367	CUTINASE TRANSCRIPTION	0.26
			i	ľ		FACTOR I ALPHA	
	j					>gi 1262912 (U51671) cutinase	i
Ι.			H.sapiens PAL2A	j		transcription factor I [Fusarium	
\vdash	374	X88931	деле	0.007	1706176	solani f. sp. pisi]	0.21
1	1		-DAD alahaii	1			
1	ł		zRAR alpha =retinoic acid receptor alpha	1]	
ı	ı		(zebrafish, embryos,	1			1
18	75		mRNA, 1773 nt]	0.007	2220210		
			111111111111111111111111111111111111111	0.007	2239219	(Z97210) hypothetical protein	0.11
1	1	1.	Petromyzon marinus				1
ı	- 1		plasma albumin	I		OCTAPEPTIDE-REPEAT	
8	76	M74193	mRNA, complete cds.	0.007	730888	PROTEIN T2	0.011
			Saccharomyces			110.211.12	0.011
			cerevisiae Spp41p	1			I
	,, l		SPP41) gene,	- 1		(AL033126) 65G3.k	
8	77	U03673	complete cds.	0.007	3820885	[Drosophila melanogaster]	0.001
		i.	Homo sapiens mRNA	1			
			or Laminin-5 beta3	1	İ	2007	
81	78		hain, complete cds	0.007		(X96713) collagen [Globodera	
			mann. complete cus	0.007	1235974	pallidal	3e-06

	· · Near	est Neighbor (BlastN vs.	Genbank)	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SE	0		T T	iveriest iveig	hbor (BlastX vs. Non-Redundant)	Proteins)	
1	ACCESSION		P VALUE	ACCESSION	DESCRIPTION	P VALUE	
-		Caenorhabditis				I VALUE	
- 1	ł	elegans putative				 	
ł	j	transcription factor		l			
- 1	1	MAB-3 (mab-3)	ŀ		(AF095741) unknown [Rattus		
87	9 AF02238		0.007	3747107	norvegicus]	5.00	
		Acanthamoeba		27.7.37	ilor vegicus)	5e-09	
- 1	1	castellanii	1	j		i i	
ı	l l	transformation-	1		1	i i	
	ł	sensitive protein	ł				
- 1		homolog mRNA,	i i		(U89984) transformation-		
88	U89984	complete cds	0.007	1890281		1 1	
1			3,337	. 1030201	sensitive protein homolog	2e-09	
ļ	ľ	1			rabGAP domains; cDNA EST]]	
1		1	i i		EMBL:D34945 comes from this	.] [
1		İ	1		gene; cDNA EST		
	1		1		EMBL: D27313 comes from this	i i	
	1]		gene; cDNA EST	1	
1	1				EMBL:D34829 comes from this	1	
1			1		gene; cDNA EST	1 1	
1	i	1	1		EMBL:D27312 comes from this	1	
J	Į.		i I		gene; cDNA Probable	1	
Į			1 1		rabGAP domains; cDNA EST	1	
ĺ	i					1	
1	1				EMBL:D34945 comes from this	i I	
1	I				gene; cDNA EST]	
1					EMBL:D27313 comes from this		
1	í	l			gene; cDNA EST	1	
ĺ	1	Homo sapiens mRNA			EMBL:D34829 comes from this	1	
i	l	for KIAA0882			gene; cDNA EST	ı	
881	AB020689	protein, partial cds	0.007	222222	EMBL:D27312 comes from this	ł	
· .	1-02000	Mus musculus	0.007	3880809	gene; cDNA	1e-23	
l		Pontin52 mRNA,	1]		
882	AF100694	complete cds	0.006	2102-		1	
		complete cus	0.006	<none></none>	<none></none>	<none></none>	
		Arabidopsis thaliana	1				
		cellulose synthase	1			ĺ	
		catalytic subunit (Ath-	1			j	
		A) mRNA, complete				1	
883	AF027173	cds	0.006			i	
	11102/1/3	cus	0.006	<none></none>	<none></none>	<none></none>	
	ĺ	Sambucus nigra	I				
		ribosome inactivating	1	,		ļ	
ı		protein precursor	j	į		ŀ	
884	U76524	• •	0.006		f	1	
	0,0324	mRNA, complete cds	0.006	<none></none>	<none></none>	<none></none>	

<u> </u>	Neare	st Neighbor (BlastN vs	. Genbank)	Nearest Ne	ighbor (BlastX vs. Non-Redundan	Descri
SE	Q.			1	Ignoof (Blasex vs. Non-Redundan	(Proteins)
II	ACCESSIO	ON DESCRIPTION	PVALUE	ACCESSION	DESCRIPTION	P VALU
_		- C				
l	ľ	Sambucus nigra	1 .			
ĺ	Í	ribosome inactivatir protein precursor	ng	1		
88	5 U76524	mRNA. complete co		ļ		
	070324	Arabidopsis thaliana		<none></none>	<none></none>	<none></none>
	i	mRNA for	`	l		
		neoxanthin cleavage	1			
886	AJ005813		0.006	NOVE	!	
		Brassica rapa mRNA	0.000	<none></none>	<none></none>	<none></none>
		for SRK45, complete		ł		
887	AB012106	cds	0.006	<none></none>		1
		Rattus norvegicus	3.000	<140NE>	<none></none>	<none></none>
_	1	ceruloplasmin gene,	1		[
888	M80529	exon I and 5' flank	0.006	<none></none>	31037	ł
	1				<none></none>	<none></none>
	1	Arabidopsis thaliana			hypothetical protein 6 -	1
	I	cellulose synthase			Chlamydomonas reinhardtii	.
	1	catalytic subunit (Ath	-		transposon	1
889	4.500	A) mRNA, complete	1 1		>gi 1360717 gnl PID e33461	1
207	AF027173	cds	0.006	99408	reinhardtii]	9.6
	ſ					9.0
		Sambucus nigra lectin	1			1 1
890	U76523	precursor mRNA,			(AF039110) polyprotein	1 1
	070323	complete cds Rattus norvegicus	0.006	4039024	[Rubella virus]	9.3
	1	homer-Ic mRNA,		•		
391	AF093268	complete cds	0.006	1.000-	(M94428) merozoite surface	1 1
		complete eas	0.006	160533	antigen 1 [Plasmodium vivax]	7.5
		Brassica rapa mRNA			/ -	
- 1		for SRK45, complete	ı		(AF093984) envelope	1 1
92	AB012106	cds	0.006	4019458	glycoprotein [Human	1 1
		Arabidopsis thaliana	- 0.000	4019438	immunodeficiency virus type 1]	7.0
ĺ		mRNA for	j		(U91682) vitelline membrane	1 1
_		neoxanthin cleavage	I		protein homolog [Aedes	1 1
93	AJ005813	enzyme	0.006	1916976	aegypti]	
- 1					promastigote surface antigen-2	6.8
-	l.		· 1		(clone 4.6) - Leishmania major	j 1
1		Rattus norvegicus	l		(fragment) >gi 9583 (X57135)	
4		homer-1c mRNA,	1		surface antigen P2 [Leishmania	ľ
- I	AF093268	Complete cds Rattus norvegicus	0.006	102059	major]	2.4
╁		SHIP SOFTWARE I		-		<u></u>
7			1			
7	[t	nomer-1c mRNA,			(AF067204) transcription factor	
5	AF093268 c	nomer-1c mRNA, complete cds	0.006	3171241	(AF067204) transcription factor BF-1 [Danio rerio]	1.0
7	AF093268 c	nomer-1c mRNA,	0.006	3171241 <none></none>		1.0

		earesi	Neighbor (BlastN vs	. Genbank)	Nearest Ne	ghbor (BlastX vs. Non-Redundant	Dente
	EQ					Blasta vs. Non-Redundant	Proteins)
-	D ACCES	SSIO	DESCRIPTION	P VALU	E ACCESSION	DESCRIPTION	P VAL
			Arabidopsis thalian				
1	j		cellulose synthase	4			
ì	- 1		catalytic subunit (A			1	1
	·		B) mRNA, complete	LI-7	l l		İ
89	7 AF027	174	cds	0.003			1
				0.003	<none></none>	<none></none>	<non< td=""></non<>
1	1		Borrelia burgdorferi				
1	- 1		(section 34 of 70) of			(41011056) 655	
898	8 AE001	148	the complete genome	0.003	4160388	(AJ011856) ORF Q0255	1
l	1				1100300	[Saccharomyces cerevisiae]	7.6
	1		Arabidopsis thaliana		1	ł	
ı	ł		cellulose synthase		1	NUCLEAR ENVELOPE PORE	. [
	1		catalytic subunit (At	1-	1	MEMBRANE PROTEIN POM	1
899	AF0271		A) mRNA, complete	1	Ī	121 (PORE MEMBRANE	
023	A.F02/1	/3	cds	0.003	1709213	PROTEIN OF 121 KD) (P145)	١ , ,
	1	- 1	Lycopersicon			121 120) (1 143)	1.5
	1		esculentum class II	1		1 (l
	1		small heat shock	1	ł	1	
	1		protein Le-HSP17.6	ł	<u> </u>		1
900	U7239		mRNA, complete cds	0.000			
			Mus musculus	0.002	<none></none>	<none></none>	<none:< td=""></none:<>
	i		Pontin52 mRNA,	1			
901	AF10069		complete cds	0.002	ALONE	1	
	1	C	hlamydomonas	0.002	<none></none>	<none></none>	<none></none>
	I		einhardtii light			1	
	į	h	arvesting complex II				
	ļ	p	rotein precursor	j]	
902			Lhcb3) mRNA,	i			
902	AF10463		omplete cds	0.002	<none></none>	<none></none>	NONE
ı	,		lus musculus			CHOILE	<none></none>
903	AF100694		ontin52 mRNA,	i			
	74 100094		omplete cds	0.002	<none></none>	<none></none>	<none></none>
- 1		f _C	rassica rapa mRNA	- 1			
004	AB012106	5 cd	r SRK45, complete	200-			
			ıman non-histone	0.002	<none></none>	<none></none>	<none></none>
- 1			romosomal protein	1			
J		H	MG-14 gene,			. 1	
05	M21339		mplete cds.	0.002	-NONE-	1	
				0.002	<none></none>	<none> <</none>	NONE>
.]		Sar	mbucus nigra	1	ŀ		
		rib	osome inactivating	ſ	1		
,		pro	tein precursor	j			J
06	AF012899	mR	NA, complete cds	0.002	<none></none>	NONE	
						<none> <</none>	NONE>

	1,04	est Neighbor (BlastN v	s. Genbank)	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SE	- 1			,	VS. Non-Redunda	ant Proteins)	
ID	ACCESS	ON DESCRIPTION	PVALUE	ACCESSION	D.700-	- 1 .	
<u> </u>		Human h-lys gene	for	ACCESSION	DESCRIPTION	P VAL	
1		lysozyme (upstrear	n	 			
907	X57103	region)	0.002	<none></none>			
	1			NOINES -	<none></none>	<non< td=""></non<>	
	1	Sambucus nigra	1	l		1	
908	A 507.00	hevein-like protein	1]	1		
300	AF07438		ds 0.002	<none></none>	<none></none>		
	1	Human CD4			KNONES	<noni< td=""></noni<>	
909	U01066	promoter, partial	1			1	
	001000	sequence. Barley mRNA	0.002	<none></none>	<none></none>	<none< td=""></none<>	
910	L28094	sequence.		.,		KNONE	
		Homo sapiens DNA	0.002	<none></none>	<none></none>	<none< td=""></none<>	
	ſ	from chromosome 1				110111	
	ł	cosmid f19399 (-17				- 1	
	1	kb EcoRI restriction			1	ł	
911	AD000833	fragment)	0.002	ANONE		İ	
			0.002	<none></none>	<none></none>	<none< td=""></none<>	
		Homo sapiens TRHR	:				
ا ء.ء		gene promoter and	1	ł		1	
912	AJ011701	exons 1-2, partial	0.002	<none></none>	-NONE	1	
- 1		Mus musculus			<none></none>	<none:< td=""></none:<>	
913	AF100694	Pontin52 mRNA,	1 1	}		1	
	71 100094	complete cds	0.002	<none></none>	<none></none>	NONE>	
- 1		Homo sapiens retinol	1 1			THORES	
1		dehydrogenase gene,]				
14	AF037062	complete cds	0.000			1	
$\neg \tau$		Rattus norvegicus	0.002	_ <none></none>	<none></none>	<none></none>	
- 1		homer-1c mRNA,		ŀ			
15	AF093268	complete cds	0.002	<none></none>			
		Methanococcus		CHOINE>	<none></none>	<none></none>	
- 1		jannaschii section 150				1	
,,	11/2/22	of 150 of the		1	•	1.	
16	U67608	complete genome	0.002	<none></none>	<none></none>	1	
-		A mahida mai sa sa sa			CHOINES	<none></none>	
1	ĺ	Arabidopsis thaliana	ł			1 1	
		cellulose synthase	1		•		
	Ţ	catalytic subunit (Ath-A) mRNA, complete	[}		1 1	
7 / 1		eds RNA, complete	2 227			1 1	
		H.sapiens DNA for	0.002	<none></none>	<none></none>	<none></none>	
1		repeat region (ABM.	ļ			1	
8	71/004	C82)	0.002			1 1	
T^{-}		Brassica rapa mRNA	0.002	<none></none>	<none></none>	<none></none>	
1		or SRK45, complete	ı				
) A		ds	0.002	NONE		1	
			3.002	<none></none>	<none></none>	<none></none>	

	Nearest	Neighbor (BlastN vs. G	ienbank)	Nearest Neigh	bor (BlastX vs. Non-Redundant P	roteins)
SEQ						
ID	ACCESSION	DESCRIPTION	PVALUE	ACCESSION	DESCRIPTION	P VALUE
		X.laevis mRNA for	 			I VALUE
920	Z85983	NOVA protein	0.002	<none></none>	<none></none>	<none></none>
		i vo v v protein	0.002	NO.TES	- CHOILE	KNONES
1 1		Arabidopsis thaliana				
]]		cellulose synthase	ļ	•	1	
		catalytic subunit (Ath-				1
		A) mRNA, complete	1			1
921	AF027173	cds	0.002	<none></none>	<none></none>	<none></none>
i I		medium-chain acyl-			1	
) }		CoA dehydrogenase				
i 1		{exon 10, intron 10}		• •		I
		[human, Genomic,			·	1
922	S61977	1407 nt]	0.002	<none></none>	<none></none>	<none></none>
i 1		Arabidopsis thaliana mRNA for				į i
		neoxanthin cleavage		·		
923	AJ005813	enzyme	0.002	<none></none>	NONE	<none></none>
723	H3003613	Brassica rapa mRNA	0.002	CNONES	<none></none>	<none></none>
		for SLG45, complete] [
924	AB012105	cds	0.002	<none></none>	<none></none>	<none></none>
		Brassica rapa mRNA	0.002	GIOILES	4.0.12	NONE?
ŀ		for SRK45, complete				
925	AB012106	cds	0.002	<none></none>	<none></none>	<none></none>
		Arabidopsis thaliana				i ,
		cellulose synthase catalytic subunit (Ath-			İ	
						ĺ
926		A) mRNA, complete cds	0.002	AMONE	NONE	NONTE
720		H.sapiens DNA for	0.002	<none></none>	<none> (AE001337) Yop C/Gen</none>	<none></none>
		dopamine D2			Secretion Protein D [Chlamydia	
927		receptor gene	0.002	3329125	trachomatis]	9.5
					HYPOTHETICAL ITZ.T KD	
1		ĺ	J		PROTEIN C06G4.1 IN	
- 1	[Į.		CHROMOSOME III	
1			ŀ		>gi 630524 pir S44748	
- 1					C06G4.1 protein -	ŀ
1	1				Caenorhabditis elegans	
A. 4	<i>:</i>	İ			>gi 409292 (L25598) homology	
	· [.	,	ĺ		with vigilin; coded for by C.	
3	i i	Mus musculus	1		elegans cDNA	
928		Pontin52 mRNA,	0.003		GenBank:M88954 (CEL 12C9);	
928		complete cds Human skeletal	0.002	465762	putative [Caenorhabditis	8.9
ĺ	j	nuscle ryanodine	1		co-repressor protein - mouse	ł
929		eceptor gene	0.002	2137221	>gi 642619	6.9
/- /	0707/0 1	ecchioi gene	0.002	213/221	>Rilo+=013	0.9

, ===:	Nearest	Neighbor (BlastN vs. (Genhank)	Negros Nai-	hhar (BLV N D)	
SEQ		- Grandor (Brastin Vs.)	J. J. J. J. J. J. J. J. J. J. J. J. J. J	ivearest iveig	hbor (BlastX vs. Non-Redundant P	roteins)
ID	ACCESSION	DESCRIPTION	P VALUE	ACCECCION	DESCRIPTION.	
-	Titeeboler	Mus musculus	I VALUE	ACCESSION	DESCRIPTION	P VALUE
	 	Pontin52 mRNA.		 	199	<u> </u>
930	AF100694	1	0.000	201501	(Z22520) membrane protein	
1 330	AF100094	Complete cds Mus musculus	0.002	806536	[Bacillus acidopullulyticus]	6.3
					·	}
931	45100604	Pontin52 mRNA,			(AL023844) Y48A6B.1	1.
931	AF100694	complete cds	0.002	3881055	[Caenorhabditis elegans]	5.8
		Lycopersicon	1			
	l	esculentum cytosolic	1	l	1	
1		class II small heat	ľ	J		l i
1	1	shock protein HCT2	1			
ĺ			l	· .		1
932	A E000116	(HSP17.4) mRNA,			(Z81097) K07A1.4	
932	AF090115	complete cds	0.002	3878330	[Caenorhabditis elegans]	4.8
		Rattus norvegicus				
933	A F002260	homer-lc mRNA,			REPLICATION PROTEIN EI	
933	AF093268	complete cds	0.002	137640	papillomavirus	4.0
Í.		Mus musculus	Ī	}		
024	A F010440	nuclear orphan		•	(U58757) similar to nucleotide	. [
934	AF019660	receptor RORgamma	0.002	1330365	pyrophosphatases	3.9
1		Mus musculus	ł		(U46951) ORF5; Method:	
935	A E 1 00 c 0 4	Pontin52 mRNA,			conceptual translation supplied	
933	AF100694	complete cds	0.002	1785972	by author	3.7
936	VOOSOO	Human gene for			(X56032) protease	
936	V00508	epsilon-globin.	0.002	1333804	[Ruminococcus flavefaciens]	3.5
		n . n		J	(AC005531) similar to mouse	
		Brassica rapa mRNA			homeodomain-interacting	
007	1.0000.00	for SLG45, complete			protein kinase 2; similar to	1
937	AB012105 -	cds	0.002	4153876	AF077659 (PID:g3702958)	3.0
					omithine carbamoyltransferase	1
		A sahidamaia shalissa	i i		(EC 2.1.3.3) - yeast	
		Arabidopsis thaliana			(Saccharomyces cerevisiae)	ŀ
		mRNA for	· .		>gi 929866 (X83502)	ì
938		neoxanthin cleavage			pid:e130025 [Saccharomyces	
926	AJ005813	enzyme	0.002	1070461	cerevisiae] >gi[1008256	2.8
- 1	ł	rod cGMP	ľ			
I			i		j i	ı
		phosphodiesterase	Į		1	ŀ
939		beta-subunit [human,	0.000		(AF083334) fibroin [Antheraea	
727	S41458	mRNA. 3231 nt]	0.002	3450883	pernyi]	1.6

_		_				
<u> </u>	Near	est Neighbor (BlastN vs.	Genbank)	Nearest Nei	ghbor (BlastX vs. Non-Redundant)	Protein
SE	Q		T	- Carest Men	Total (Blasta vs. Ivon-Redundant	rroteins)
Ln	ACCESSION	ON DESCRIPTION	P VALUE	ACCESSION	DECCE	
			T. VALUE	ACCESSION	DESCRIPTION	P VALUE
		Drosophila	 	 		-
- 1	· ·	melanogaster Gart locus with genes for		i		ł
ı	1		.1		1	1
ł	ł	GARS=phosphoribos	3			1
	1	ylamineglycine	i]	1.	
1		ligase,		1		1 .
		AIRS=phosphoribosy lformylglycinamidine		ĺ	İ	
ļ				ŧ		i
i		cyclo-ligase,	1	ł	ļ	1 1
	[GART=glycinamide ribotide		,		
	1	transformylase > ::		<i>'</i>	1	1
		gb J02527 DROGAR				
		T D.melanogaster				1
	1	Gart gene encoding	i		·	
	•	two polypeptides with	j			1 1
1	l l	GAR synthase, AIR	l i		·	1
	· J	synthase, and GAR	l 1]
1		transformylase	}			j k
	1	enzyme activities and	ŀ			
i	í	a pupal cuticle gene				}
l	i	nested within intron	ı			1 1
940	X06286	A of the Gart gene.	0.002	2662054	(ABODACE)	
-		Homo sapiens RNA	0.002	2002034	(AB004651) isocitrate lyase	1.5
	1	helicase p68	1			
ļ	1	(HUMP68) gene,	į		(AB008374) alpha 3 type I	
941	AF015812	complete cds	0.002	3641659	collagen	
	1				ZINC FINGER PROTEIN ZFP-	1.1
	i	H.sapiens HZF2	· I		37 (MALE GERM CELL	
		mRNA for zinc finger	- 1		SPECIFIC ZINC FINGER	1
942	X78925	protein	0.002	141624	PROTEIN)	1.0
	ŀ					
	Į	Sambucus nigra			(Z49071) weak similarity with	I
943	AF074386	hevein-like protein			mu-type opioid receptor (Swiss	1
	71 074380	mRNA, complete cds	0.002	3879997	Prot accession number (P33535)	1.0
		Human DNA	1			
		sequence from	Į.			ľ
		cosmid L241B9,	1	İ		- 1
		Huntington's Disease	- 1		.	-
		Region, chromosome	j		1	
		4p16.3 contains	1		1	1
		polymorphic VNTR	1		(AE076303) TCF book	
944	Z69639	pYNZ32.	0.002	3523162	(AF076292) TGF-beta/activin	
				2223102	signal transducer FAST-1p	0.81

-		est Neighbor (BlastN vs.	Genbank)	Nearest Nei	ghbor (BlastX vs. Non-Redundant P	rorainc)
9	€Q				The state of the s	T
I	D ACCESSI	ON DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	
				1 11002551014	DESCRIPTION	P VALUE
		Sambucus nigra				
	1	hevein-like protein	1	j	(AE000761) hypothetical	1
94	5 AF07438		ls 0.002	2984161	protein [Aquifex aeolicus]	0.00
		Rattus norvegicus			protein (Adultex aeolicus)	0.80
		homer-1c mRNA,	1	ļ	hypothetical protein B - chestnut	
94	6 AF09326		0.002	101830	blight fungus	0.72
1	1	Homo sapiens Ets-				0.72
	1	related transcription	1			1 1
94	7 AE01770	factor (ERT) mRNA	•	}	(M18071) prion protein [Mus	i I
1	7 AF01730	7 complete cds	0.002	. 200531	musculus]	0.72
		Drosophila	•			
		melanogaster Ovo-			Ĭ	1
	i ·	1028aa (ovo) mRNA	1		1	! !
94	U11383	complete cds.	0.002	2465207	(AF016045) OVO-like 1	ŀ
		John prote cus.	0.002	2465207	binding protein [Homo sapiens]	0.35
1	1.	Sambucus nigra			j i	
	1	ribosome inactivating				Ī
1	ľ	protein precursor	1 1		(U80846) No definition line	j
949	AF012899	mRNA, complete cds	0.002	3834294	found [Caenorhabditis elegans]	0.29
					(S68356) action potential	0.29
1	i i		1		broadening potassium	
	I	}	l i		channel=Shab [Aplysia, bag cell	- 1
1			i I		neurons, head ganglia, Peptide,	1
	1	Homo sapiens full	1 1		905 aa] [Aplysia]	
950	AF086315	length insert cDNA			>gi 743110 prf 2011375A K	
1	71 000313	clone ZD52F10	0.002	545067	channel [Aplysia californica]	0.15
	i	S.aureus genes				
	ł	encoding Sau96I	1			
ĺ	ł	DNA				1
ŀ	· ·	methyltransferase and			1	- 1
[ļ	Sau96I restriction	i		(AFOIRICE)	
951	X53096	endonuclease	0.002	2529575	(AF018164) kinesin-like protein 3C [Homo sapiens]	
		Brassica rapa mRNA		2327373	LA PROTEIN HOMOLOG (LA	11.0
		for SLG45, complete	İ		RIBONUCLEOPROTEIN) (LA	Í
952	AB012105	cds	0.002	729918	AUTOANTIGEN HOMOLOG)	0.092
		}			1021110110200)	0.092
			į.		TRICHOHYALIN	ŀ
		G.gallus RAR-			>gi 423321 pir A40691	1
953	V72072	gamma2 mRNA for			trichohyalin - sheep >gi 295941	
333	X73973	retinoic acid receptor	0.002	586122	(Z18361) trichohyalin	0.073
		rod cGMP	- 1			
		phosphodiesterase	1	ĺ	İ	I
		beta-subunit [human,	j			ļ.·
954	S41458	mRNA, 3231 nt]	0.002		(X90569) elastic titin [Homo	
			0.002	1017427	sapiens	0.013

_	Near	est Neighbor (BlastN v	s. Genbank)	Nearest No	ighbor (BlaceV vo. N	
SI	€Q			1.52.03.116	ighbor (BlastX vs. Non-Redundant	Proteins)
	D ACCESS	THE PROPERTY OF	PVALUE	ACCESSION	DESCRIPTION	P VALU
┢		D.melanogaster			(U88169) similar to	Tr AVER
1	ı	defective chorion-			molybdoterin biosynthesis	
95		fc125 (dec-1) gene	, [1	MOEB proteins [Caenorhabdit	<u>. </u>
1 73	5 M3588	7 complete cds.	0.002	1825606	elegans]	
1	1				locgans	0.008
1	İ	Laccaria bicolor		ł	.]	
1	1	glyoxai malate				1
1 ~		synthase protein	- 1	1	(U88167) D2092.2 gene produc	.]
95	6 AF03409		ds 0.002	1825593	[Caenorhabditis elegans]	1
1	I	Bactrocera dorsalis			[Cachornabditis elegans]	le-06
i		strain Tahiti			1	1
	ŀ	mitochondrial D-loc	op	٠,		1
	. 1	region, complete				1.
957	AF03392		9e-04	<none></none>	ALONE	1
l	1	Brassica rapa mRNA		4.0.11	<none></none>	<none></none>
		for SRK45, complete	e		1	
958	AB01210	cds	8e-04	<none></none>	NONT	1
	1			43.01.125	. <none></none>	<none></none>
		Homo sapiens DEAI	네 네			İ
	I	box protein (BAT1)	1 1			j
959	AF029062		8e-04	<none></none>	3,00,00	1
	İ	Human ataxin-2	1	N.O.N.	<none></none>	<none></none>
	1	related protein	1 1			
960	U70671	mRNA, partial cds	8e-04	<none></none>	NONE	
	[Dendrocopos		4.0.10	<none></none>	<none></none>
	ł	leucopterus clone 2	1 1			
	l	microsatellite HrU2	1 1		•	
961	AF051709	repeat region	8e-04	<none></none>	NOVE	
	ļ	Pea phy gene for		4.101122	<none></none>	<none></none>
	Į	phytochrome	1 1		1	ı
962	X14077	apoprotein	8e-04	<none></none>	1	
		Homo sapiens		1	<none></none>	<none></none>
		chromosome 21, P1] [(L27838) rhoptry protein	- 1
963	AC004497	clone LBNL#6	8e-04	457146	[Plasmodium yoelii]	·
ı		Homo sapiens			[[1 445HIOGIUM YOEHI]	9.6
		cartilage-derived C-	1	,	(A 101 1707) Took	ı
964	AF077344	type lectin	8e-04	3702123	(AJ011707) TraD protein [Escherichia coli]	
I				3.02123	(AJ004687) N-4 cytosine-	8.5
1		H.sapiens epb72 gene	f			j
65	X85117	exons 2.3.4,5,6,7	8e-04		specificmMethyltransferase	
- 1				20,0009	[Neisseria gonorrhoeae]	6.8
1		1	1	1	COPPER TRANSPORT	
I			J			
		Mus musculus	I		PROTEIN CTR1 transport	l l
	i	Pontin52 mRNA,	1		protein - yeast (Saccharomyces	- 1
66		complete cds	8e-04		cerevisiae) gene product	-
				107009	[Saccharomyces cerevisiae]	6.7

-	Neare	st Neighbor (BlastN vs. (Genbank)	Nearest Neig	hbor (BlastX vs. Non-Redundant I	
SEC					Vs. Non-Redundant I	roteins)
ID	ACCESSIC		P VALUE	ACCESSION	DESCRIPTION	Burr
<u> </u>	 	Homo sapiens			T T T T T T T T T T T T T T T T T T T	P VALU
1	ł	MLL/AF4			SMALL PROTEIN B	
1	ı	translocation	İ '	ĺ	HOMOLOG A43259, from E.	1
967	45001.400	breakpoint	ĺ	<u>[</u>	hirae [Mycoplasma	
907	AF031403	14 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	8e-04	2498926	pneumoniae)	6.6
j		Human (clone D13-2)	1			0.0
	ł	L-iditol-2	1		i	1
	1	dehydrogenase gene,	!		1	}
968	L29252	exon 4, exon 5, exon	1		(U63997) putative transposase	
200	129232	6 and exon 7.	8e-04	1488070	[Enterococcus faecium]	5.2
	l	Mouse N10 gene for		•.		1
969	X16995	a nuclear hormonal		•	(U47323) stromal cell protein	Í
	X10993	binding receptor	8e-04	1493833	[Mus musculus]	3.2
	ł	1	ł			
]	1	ſ		4-AMINOBUTYRATE	
	ĺ		i		AMINOTRANSFERASE	
	İ	1	1		TRANSAMINASE) (GABA	İ
			j		AMINOTRANSFERASE)	
		. [I		homolog - smut fungus	
		1	1		(Ustilago maydis) >gi 881562	
		Human interleukin-8	į.		Emericella nidulans gamma-	
J		receptor (IL8RB)	- 1		amino-n-butyrate transaminase	
970	M99412	gene, complete cds	8e-04	1346101	Swiss-Prot Accession Number	
		Human Down		1340[0]	P14010 [Ustilago maydis]	0.83
- 1		Syndrome region of	ſ		1	
		chromosome 21	i			
		genomic sequence,	1	,	(AE111003) Interpublica 2	
971	U37452	clone A31D6-1C5.	8e-04	4164069	(AF111093) latrophilin 3 splice variant bbah [Bos taurus]	224
- 1	ł				HYPOTHETICAL 13.0 KD	0.26
- 1	j		ſ		PROTEIN IN RAD26-GEF1	
- 1	1			ĺ	INTERGENIC REGION	ľ
	·				>gi 1077881 pir S57057	I
- 1	i		·]		probable membrane protein	
	l		1	}	YJR038c - yeast	[
	J.		1	J.	(Saccharomyces cerevisiae)	
- [Mus musculus		 ;	gi 1015688 (Z49538) ORF	ļ
72		Pontin52 mRNA,	. 1	Į,	YJR038c putative	·]
-		omplete cds	8e-04	1352877	Saccharomyces cerevisiae]	0.23
	1.	Rattus norvegicus				0.23
73		omer-1c mRNA,	!](AE000312) orf, hypothetical	1
	· 11 093208 C	omplete cds	8e-04	1788557 p	rotein [Escherichia coli]	0.19

	Nearest	Neighbor (BlastN vs. C	Genbank)	Nearest Neighbor (BlastX vs. Non-Redundant Protei		
SEQ				The state of the s	1001-Reddiddill F	i cicilis)
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
-			<u> </u>		HYPOTHETICAL 37.7 KD	
j					PROTEIN C18B11.06 IN	
1	1				CHROMOSOME I	
-	ı		<u> </u>		>gi 2130289 pir \$58305	
	1	H.vulgaris mRNA for	j l		hypothetical protein	
1		cAMP response			SPAC18B11.06 - fission yeast	1
	ì	element binding			hypothetical protein	ł
974	X83872	protein	8e-04	1175386	[Schizosaccharomyces pombe]	0.005
0.75		Rat simple sequence	1		(AF024502) No definition line	1
975	M32514	DNA, clone 5.	8e-04	2394492	found [Caenorhabditis elegans]	0.002
		Sambucus nigra	٠.			
1	1	hevein-like protein			(AB012223) ORF2 [Canis	
976	AF074386	mRNA, complete cds	8e-04	2981631	familiaris]	0.001
				2201031		0.001
Ì		H.sapiens DNA for	ĺ			
		endogenous retroviral	}		(Y12713) Pro-Pol-dUTPase	
977	X89211	like element	8e-04	2065210	polyprotein	3e-04
1					(AC002411) Strong similarity to	
		Human myosin-IC	1		myosin heavy chain gb Z34293	1 1
978	U14391	mRNA, complete cds.	. 8e-04	3142302	from A. thaliana. [Arabidopsis	
	01.351	Drosophila	. 86-04	3142302	thaliana]	4e-16
		melanogaster dead-	Í			
Ì		box protein	1			
•		D.melanogaster	1		·	
		DEAD-box gene,	ı		(AJ010475) RNA helicase	
979	L13612	complete CDS	8e-04	3776027	[Arabidopsis thaliana]	9e-24
		Sambucus nigra	1			
		hevein-like protein	ł]	}
980	AF074386	mRNA, complete cds	7e-04	<none></none>	<none></none>	<none></none>
		Mus musculus		4.01.12	CHOILE	CHOMES
	i	Pontin52 mRNA,	j			ł
981		complete cds	7e-04	<none></none>	<none></none>	<none></none>
		Rattus norvegicus				
982		homer-1c mRNA,	7- 01			ł
702	AF,093208	complete cds Human DNA	7e-04	<none></none>	<none></none>	<none></none>
		sequence from				1
		cosmid N120B6 on				1
		chromosome 22	1			ł
1	l·	Contains ESTs,				
		complete sequence	ĺ		1	Ì
983	Z73987	Homo sapiens]	7e-04	<none></none>	<none></none>	<none></none>

	Neares	Neighbor (BlastN vs. (Genhank)	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SE				INCEDEST INCE	gnbor (BlastX vs. Non-Redundant	Proteins)
IE	-	N DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUI
<u> </u>		Brassica rapa mRNA				1 VALUE
1		for SRK45, complete				
984	AB012106		7e-04	<none></none>	<none></none>	<none></none>
i		Rattus norvegicus				NIVOINE
		homer-lc mRNA,	i i			
985	AF093268	complete cds	7e-04	<none></none>	<none></none>	<none></none>
- 1	1	Arabidopsis thaliana				
1		cellulose synthase	ļ		- f	ľ
- i		catalytic subunit (Ath-	1			1
1	ľ	B) mRNA, complete			- 1	1
986	AF027174	cds	7e-04	<none></none>	24027	:
		Mus musculus	70-07	KHONES	<none></none>	<none></none>
1	1	Pontin52 mRNA,				
987	AF100694	complete cds	7e-04	<none></none>	NONE	1 ,,,,,,,,,
		Arabidopsis thaliana		- CHOILES	<none></none>	<none></none>
1	ļ .	mRNA for	i		1	1
1		neoxanthin cleavage			İ	1
988	AJ005813	enzyme	7e-04	<none></none>	<none></none>	<none></none>
1					3.101.22	TATOMES
İ	j	Helianthus tuberosus				
		lectin 1 mRNA,				
989	AF064029	complete cds	7e-04	<none></none>	<none></none>	<none></none>
	Í	Arabidopsis thaliana	f			
1		cellulose synthase	1			
1		catalytic subunit (Ath-	- 1			1
1		B) mRNA, complete				1 1
990		cds	7e-04	NOVE		1 1
	12 02/1/4	cus	<u>/e-04.</u>	<none></none>	<none></none>	<none></none>
1	j	Arabidopsis thaliana	1		1	i I
		cellulose synthase	1		1	i i
l		catalytic subunit (Ath-		,	1	1 1
ŀ		A) mRNA, complete				1 1
991	AF027173	cds	7e-04	<none></none>	<none></none>	<none></none>
						KNONL
	[1	Helianthus tuberosus	1			!
000		ectin 1 mRNA,	- 1			
992		complete cds	7e-04	<none></none>	. <none></none>	<none></none>
]		Vius musculus				
993		Pontin52 mRNA,			j	1
393	AF100694 c	complete cds	7e-04	<none></none>	<none></none>	<none></none>
	[,	Sambucus nigra	1			
		ibosome inactivating	i			l J
ł		rotein precursor	J			
994		RNA, complete cds	7e-04	777777	(AB014608) KIAA0708 protein	<u> </u>
		, complete cus	76-04	3327230	[Homo sapiens]	9.5

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEQ		Trengment (Billian 18. C	i choank)	ivearest iveign	Toor (BlastX vs. Non-Redundant Pr	oteins)	
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
<u> </u>							
İ	1	Sambucus nigra					
ŀ		ribosome inactivating					
995	1176504	protein precursor		i	(AB014608) KIAA0708 protein		
993	U76524	mRNA, complete cds	7e-04	3327230	[Homo sapiens]	9.3	
1		Sambucus nigra			(Z93380) predicted using		
1	Į.	hevein-like protein			Genefinder; similar to 7tm		
996	AF074387	mRNA, complete cds	7e-04	3876455	receptor protein [Caenorhabditis		
		india vin complete cas	70-04	3670433	elegans] hypothetical protein MJ1293 -	7.1	
1	j				Methanococcus jannaschii		
1		Sambucus nigra		٠,	>gi 1591931 (U67570) M.		
1	l	ribosome inactivating			jannaschii predicted coding		
1.		protein precursor	· ·		region MJ1293 [Methanococcus		
997	U76524	mRNA, complete cds	7e-04	2128771	jannaschii]	6.2	
	•						
i i	:	Human zinc finger	ľ		1 1		
998	U09412	protein ZNF134	2 04	100000	glutathione transferase (EC		
776	009412	mRNA, complete cds	7e-04	1083336	2.5.1.18) piA - mouse	5.4	
		Arabidopsis thaliana	I				
		cellulose synthase	ŀ		i i		
1 1		catalytic subunit (Ath-	1		(M17619) NADH		
	•	A) mRNA, complete	ı		dehydrogenase subunit ND4		
999	AF027173	cds	7c-04	473515	[Asterina pectinifera]	3.7	
		Sambucus nigra	I			Į	
í j		ribosome inactivating	İ		1	i	
1000		protein precursor mRNA, complete cds	7- 04	170 4007	(U79772) female sex protein		
1000		Mus musculus	7e-04	1724097	[Mercurialis annua]	3.3	
ŀ		Pontin52 mRNA.	- 1		(D40747) some one and asset 6	Ì	
1001		complete cds	7e-04	1197103	(D49747) core, env, and part of E2/NS1	22	
				1177103	unc-5 protein, long form -	3.2	
	I		ľ		Caenorhabditis elegans		
	ſ				>gi 258529 bbs 118648		
i					(S47168) UNC-	1	
ı	1		1		5=immunoglobulin and	}	
- 1	1		Ì		thrombospondin type I	j	
- 1	ł			ľ	transmembrane protein	ł	
- 1	l,	Aques NIO for	• 1		(alternatively spliced) aa]	1	
- 1		Mouse N10 gene for nuclear hormonal	ľ		[Caenorhabditis elegans]	}	
1002		inding receptor	70.04		>gi 2662596 (AF036698) C.	1	
	2110223	many receptor	7c-04	345372	elegans UNC-5 (NID:g25852)	2.7	

	Nearest	Neighbor (BlastN vs. C	ienbank)	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEC		1	T	iveatest tyeigh	ibor (BlastX vs. Non-Redundant P	roteins)	
ID	ACCESSION	DESCRIPTION .	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
<u> </u>	<u> </u>						
1	Ĭ	Sambucus nigra					
1	Ĭ	ribosome inactivating	f	}			
1.000		protein precursor			(AB022866) mobilization		
1003	U76524	mRNA, complete cds	7e-04	4204220	protein	2.5	
1	•	Rattus norvegicus					
1004	4 5003040	homer-1c mRNA,			(Y17116) fibrinogen-binding	ſ	
1004	AF093268	complete cds	7e-04	3201550	protein	2.4	
	ļ	Cart					
		Sambucus nigra			1	1	
1005	AF074386	hevein-like protein			(U45966) polyprotein [Hepatitis	1	
1003	AF0/4386	mRNA, complete cds	7e-04	1174264	G virus]	0.73	
1		Arabidopsis thaliana	•.				
1		cellulose synthase				ł	
1	l	catalytic subunit (Ath-				1	
1		A) mRNA, complete					
1006	AF027173	cds	7- 04	125200	TRANSCRIPTION FACTOR		
1000	11102/1/3	H.sapiens EWS gene,	7e-04	135308	JUN-D	0.065	
		intron 6.	1		IIII ALLI GUDEAN (N. 1. Co.		
1007	X98745	polymorphism	7e-04	728836	!!!! ALU SUBFAMILY SP		
		Arabidopsis thaliana	70-04	726630	WARNING ENTRY	0.001	
		mRNA for	ł				
		neoxanthin cleavage	- 1	•	j i		
1008	AJ005813	enzyme	7e-04	1633564	(U47924) C8 [Homo sapiens]	00.00	
				1033304	(047924) C8 [Hollo sapielis]	9e-09	
ı		Sambucus nigra	į.				
ł		hevein-like protein	ŀ		Ig epsilon chain C region form 3	j	
1009		mRNA, complete cds	6e-04	284171	- human	1.3	
ı		Brassica rapa mRNA			(AE001414) BRAHMA		
1		for SRK45, complete	ł	i	ortholog (DNA helicase	l	
1010		cds	6e-04	3845262	superfamily II)	0.25	
ĺ		Human DNA					
- 1	1	sequence from clone	1			j	
1	1	417C12 on	•				
1		chromosome Xp22.11					
1		22.2, complete	- 1				
, ,		equence [Homo	i		l l		
1011	AL034404 s	apiens)	3e-04	<none></none>	<none></none>	<none></none>	
- 1							
1012		Iomo sapiens (pp21)		l		- 1	
1012	M99701 r	nRNA, complete cds.	3e-04	<none></none>	<none></none>	<none></none>	

,							
<u> </u>		t Neighbor (BlastN vs.	Genbank)	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SE				T	- Committee of the contract of	roteins)	
П	ACCESSIO	N DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION		
				I HEELBOIGH	DESCRIPTION	PVALUE	
- 1		Ovis aries Merino		 			
- 1	1	breed DR beta-chair	า	ļ		}	
- [i	antigen binding					
ı	1	domain, MHC class			i	1	
101	3 1100000	DRB (Ovar-DRB24	· 1			1	
101	3. U00227	gene, partial cds.	3e-04	<none></none>	<none></none>	<none></none>	
- 1	ľ	Sambucus nigra	1	Í	·		
	1	hevein-like protein	1			1	
101	4 AF074387	mRNA, complete cd	3-04	310.5	İ		
	1 30,	inattivit, complete cu	s 3e-04	<none></none>	<none></none>	<none></none>	
- 1	1	Xenopus laevis	j		1		
1		mitotic			1	i i	
1	Í	phosphoprotein 90			(L19655) ORF [Tomato	1 1	
101	U95102	mRNA, complete cds	3e-04	999418	ringspot virus]		
1	ł	Brassica rapa mRNA			(AF011415) putative	8.3	
1,00		for SRK45, complete	·		pheromone receptor [Mus	.]	
1016	AB012106	cds	3e-04	2367460	musculus]	7.0	
	1 .					 '.\	
1	1	Mus musculus DNA	1 1		1	l f	
1017	AJ010737	for microsatellite 3kb upstream Ibp gene	1		(AF104411) neuronal-specific	1	
	1.2010757	apstream top gene	3e-04	4106549	septin 3 [Mus musculus]	5.5	
ſ			1 1		NADH-DEPENDENT FLAVIN		
1		Homo sapiens histone	1 1		OXIDOREDUCTASE acid-		
1	<u> </u> -	deacetylase 3 gene,	1 . 1		inducible - Eubacterium sp >gi 1381570 (U57489)		
l		exons 4, 5, 6, 7, 8, 9,	1	•	NADH:flavin oxidoreductase		
1018	AF053137	and 10	3e-04	416702	[Eubacterium sp. VPI 12708]		
					[Ludacterium sp. VFI 12708].	5.3	
1		Arabidopsis thaliana			1	1	
i i		cellulose synthase	1		!	1	
		catalytic subunit (Ath-	1		l	f	
1019		A) mRNA, complete			(Y08502) orf111d (Arabidopsis		
1015		cds Homo sapiens clone	3e-04	1785789	thaliana]	5.1	
		UWGC:y23x011					
	li li	from 6p21, complete	ľ			1	
		sequence [Homo	1		(D00017)	•	
1020		sapiens]	3e-04	550501	(D28917) polyprotein [Hepatitis	į.	
		Human IGF-I mRNA	- 30 07	558521	C virus]	1.1	
	f	or insulin-like	- 1		(AF118122) putative outer	- 1	
1021	X57025 g	rowth factor I	3e-04		membrane protein OmpU	0.65	
J					memorane protein Ompo	0.65	
1022	1755444	I.sapiens IL-IRa	l		(U40799) F42C5.7 gene product	j	
1022	X77090 g	ene.	3e-04	1065941	[Caenorhabditis elegans]	0.12	
	•						

117	Nearest Neighbor (BlastN vs. Genbank)		Nearest Neighbor (BlastX vs. Non-Redundant Proteins)				
SEQ		1.0.g.1001 (D18341 13. C	T T T	ivearest Neigi	rectiest (Vergnoor (DiastA vs. Non-Redundant Proteins)		
ID	ACCESSION		P VALUE	ACCESSION	DESCRIPTION	P VALUE	
ļ		Pseudorabies virus					
1	1	with upstream and			(AF040650) contains similarity		
1	l	downsteam			to sodium-potassium-chloride]	
1023	M34651	sequences.	3e-04	2746853	cotransport proteins	7e-05	
	į				PROBABLE ATP-		
1					DEPENDENT RNA		
ł	·	S.cerevisiae	į	İ	HELICASE HAS I		
1					>gi 626265 pir S47451	l	
	1	chromosome II reading frame ORF	!		hypothetical protein YMR290c	<i>l</i> 1	
1024	Z36011	YBR142w	7- 04	2500505	RNA helicase [Saccharomyces		
1024	2,30011	Dictyostelium	3e-04	2500537	cerevisiae]	4e-08	
1		discoideum 2034]	(17C4067) 27 1 C 1 1 1		
1025	AF020286	gene, partial cds	3e-04	1465024	(U64857) No definition line		
	12 020200	gene, partial cus	36-04	1465834	found [Caenorhabditis elegans]	6e-14	
		Chlamydomonas				i	
		reinhardtii dynein			İ	1	
	i	heavy chain alpha			(Z81077) predicted using		
		(ODA11) gene, exons			Genefinder; Similarity to Yeast]	
1026	L26049	2-15, and partial cds.	3e-04	3876775	protein 8248 (TR:G587531)	9e-15	
		Dictyostelium					
		discoideum 2034			(U64857) No definition line		
1027	AF020286	gene, partial cds	3e-04	1465834	found [Caenorhabditis elegans]	le-17	
l i					(269635) Similarity to Yeast		
			ſ		uridine kinase		
1 1					(SW:URKI_YEAST); cDNA		
			1		EST EMBL:Z14695 comes	ı	
1	ĺ				from this gene; cDNA EST CEMSE17F comes from this	Ì	
		i	1		gene; cDNA EST		
		·			EMBL:D67355 comes from this	ľ	
	ĺ	S.cerevisiae ACT3			gene; cDNA EST yk209h1.5	ļ	
1028	X79811	gene .	3e-04	3876090	comes from this ge	7e-31	
		•		3070070	comes from this ge	/e-31	
	į.	Arabidopsis thaliana					
j		cellulose synthase	j		ĺ	[
		catalytic subunit (Ath-	1			ł	
		A) mRNA, complete	Į		[j	
1029		ds	2e-04	<none></none>	NONE	<none></none>	
- 1		Human pancreatic					
- 1		phospholipase A-2	1	.	· 1]	
1030	1	PLA-2) gene, exons			1		
1030	M22970	to 3.	2e-04	<none></none>	<none></none>	<none></none>	

	Neares	t Neighbor (BlastN vs. (Genbank)	Nearest Nai	ghbor (BlastX vs. Non-Redundant	
SE				i vealest ive	Blastx vs. Non-Redundant	Proteins)
IE	- 1		P VALUE	ACCESSION	DESCRIPTION	P VALUE
L		Human DNA		T T		I VALUE
1		sequence from		 		
i	1	cosmid N2E9 on	1	1	<u>}</u>	Ĭ
1		chromosome 22.		ł		
1	·	Contains EST,		ł	1	-
	· I	complete sequence	I		1	1
103	1 Z68686	[Homo sapiens]	2e-04	<none></none>	<none></none>	
,		H.sapiens brca2 gene	 	4.10112	SIAOIAE>	<none></none>
1	i	exon 4 > ::		Ī		
[i	emb A62779 A62779	ł	i	1	
		Sequence 20 from		i	1	
1032	X95154	Patent WO9719110	2e-04	·· <none></none>	<none></none>	srase=
	1	Arabidopsis thaliana			ZNONES	<none></none>
i i		mRNA for				
1		neoxanthin cleavage				j i
1033	AJ005813	enzyme	2e-04	<none></none>	<none></none>	
1		Mus musculus		VI VOI VI	RNONES	<none></none>
1	İ	Pontin52 mRNA,				1 1
1034	AF100694	complete cds	2e-04	<none></none>	<none></none>	NONTE
I		Plasmodium			TYONES	<none></none>
ł	Î	falciparum				
1	1	chromosome 2,				i f
ł	l	section 52 of 73 of	j		1	1
1	ľ	the complete	1			1
1035	AE001415	sequence	2e-04	<none></none>	<none></none>	<none></none>
1	ł				1	CHOILE
[Lycopersicon]
l		esculentum cytosolic	ĺ		1	1 1
1		class II small heat	1			
İ	l i	shock protein HCT2	ſ		1] [
	ŀ	(HSP17.4) mRNA,	Į.			j
1036	AF090115	complete cds	2e-04	<none></none>	<none></none>	<none></none>
		Homo sapiens				N. VOLVEZ
		(subclone 6_d9 from		•	1	í í
,,,,,,		P1 H21) DNA				i i
1037		sequence	2e-04	<none></none>	<none></none>	<none></none>
		Rattus norvegicus				
1020		nomer-1c mRNA,	j		CD59 GLYCOPROTEIN	i i
1038	AF093268	complete cds	2e-04	2501523	PRECURSOR	7. i
ľ	l,	Sa_k	Г			
		Sambucus nigra	ļ			i i
		ibosome inactivating	1			1
1039		protein precursor			(Y13925) cathepsin L2 [Penaeus	1.
1009	U/0324 In	nRNA, complete cds	2e-04	2765360	vannamei]	6.8

	Nearest	Neighbor (BlastN vs. C	Genbank)	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEC						Totellisy	
ID	ACCESSION	DESCRIPTION	PVALUE	ACCESSION	DESCRIPTION	P VALUI	
-		<u> </u>			RNA POLYMERASE		
J		Arabidopsis thaliana			>gi 67126 pir RRXPLC RNA-	1	
1		cellulose synthase		Ĭ	directed RNA polymerase (EC	J	
1	I	catalytic subunit (Ath	1		2.7.7.48) - lymphocytic		
1040	A F002124	B) mRNA, complete		i	choriomeningitis virus (strain	ĺ	
1000	AF027174	cds	2e-04	133636	. Armstrong 53b) >gi 331369	5.2	
	Ī	Brassica rapa mRNA			(AF074613) type II secretion		
1041	AB012106	for SRK45, complete	2 04		protein (Escherichia coli		
104.	AB012100	cds	2e-04	3822155	O157:H7]	4.0	
1	i	Sambucus nigra					
ı	J	ribosome inactivating			į	1.	
ĺ		protein precursor				į	
1042	U76524	mRNA, complete cds	2e-04	1710105	REGULATORY PROTEIN E2	i	
	370327	Sus scrofa mRNA for	26-04	1718125	>gi 1020222 type 36]	0.38	
1	Ì	glucose transporte				1	
1043	X17058	protein	2e-04	3341906	(AB000503) miles to a	1	
		Homo sapiens	20 07	3341900	(AB009593) xylose transporter	2e-15	
ĺ	ľ	candidate tumor					
1044	AF008216	suppressor pp32r1	le-04	<none></none>	<none></none>	<none></none>	
		S.tuberosum mRNA			110112	CNONES	
ł		for inorganic			·		
		phosphate	ı		(U42580) a65L [Paramecium	1	
1045	X98890	transporter, StPT1	le-04	624126	bursaria Chlorella virus 1]	7.9	
		Charles on April 2	l				
1046	L14930	Glycine max (Rab7p)				j l	
1040	L14930	mRNA, complete cds. Mus musculus	9e-05	<none></none>	<none></none>	<none></none>	
		thromboxane A2	1			i I	
		receptor gene, exon 3,					
1047		partial	9e-05	<none></none>			
		M.musculus mRNA	96-03	KINOINES	<none></none>	<none></none>	
1048		for Brx gene, partial	9e-05	<none></none>	<none></none>	-NONTE-	
				- CHONES	ENONES	<none></none>	
ł	Į.	Polistes annularis			ĺ		
	ŀ	(clone pan48AAT)	ľ			· I	
1049	L10832	andem repeat region.	9e-05	<none></none>	<none></none>	<none></none>	
1	ĺ				(Z79758) CDNA EST	41.101.122	
- 1	1		1		EMBL:D28009 comes from this		
Ī			1		gene; cDNA EST	Į	
1			l l		EMBL:D28008 comes from this	ŀ	
- 1	1		J		gene; cDNA EST	j	
- 1	[EMBL:D32478 comes from this	j	
j	j	İ	1		gene; cDNA EST	1	
	l,	Ioma conicas alas	1		EMBL:D34508 comes from this	į	
		Iomo sapiens clone 4587 mRNA	i		gene; cDNA EST		
1050		equence	00.05		EMBL:D37581 comes from this		
		equence	9e-05	3880586	gene;	7.6	

	Nearest	earest Neighbor (BlastN vs. Genbank)		Negrest Neighbor (Black Vice No. D. J. J. D. J. D. J. D. D. J. D. D. D. D. D. D. D. D. D. D. D. D. D.			
SEQ		T		i vediesi iveig	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
-	 						
1		Sambucus nigra	l	1			
1	Í	ribosome inactivating			RHODOPSIN >gi 2290717		
1051	U76524	protein precursor			(AF000947) rhodopsin [Sepia	1	
1031	076324	mRNA, complete cds	9e-05	3024292	officinalis]	6.7	
ļ	ł	H.sapiens CpG DNA,	1		(AF064825) heparin/heparan		
Į	l	clone 34d6, forward			sulfate N-acetylglucosaminyl N-	1	
1052	Z58294	read cpg34d6.ft1a.	9e-05	2005406	deacetylase/N-sulfotransferase		
		Human mRNA for	36.03	3885496	[Bos taurus]	0.65	
	[KIAA0262 gene,			(766405) similar to alcund		
1053	D87451	complete cds	9e-05	· 3874739	(Z66495) similar to claustrin		
		Mus musculus cyclin-	70 00	3074739	like	0.004	
		dependent kinase	• •		(AL022598) hypothetical	1	
1054	L37092	homologue	9e-05	3080513	protein	40.00	
					j	4e-09	
		Sambucus nigra	ľ		İ		
	. 	hevein-like protein	1				
1055	AF074386	mRNA, complete cds	8e-05	<none></none>	<none></none>	<none></none>	
		A sobidonais abaliana	· 1				
		Arabidopsis thaliana cellulose synthase					
ĺ		catalytic subunit (Ath-	1				
		B) mRNA, complete	ł				
1056	J	cds	8e-05	<none></none>			
			30-03	CHONES	<none></none>	<none></none>	
ŀ	,	Sambucus nigra			l i	į.	
ł	J	hevein-like protein	i]		
1057	AF074386	mRNA, complete cds	8e-05	<none></none>	<none></none>	<none></none>	
- 1		Homo sapiens DNA			1.0.12	CHOINES	
- 1		from cosmid			1	j	
		clone:844, GT repeat	ı		1 1	1	
1058	D10102	sequence .	8e-05	<none></none>	<none></none>	<none></none>	
- 1	1	•			HYPOTHETICAL 80.4 KD		
- 1	1		l l		PROTEIN IN SMC3-MRPL8		
ł	ł		- 1		INTERGENIC REGION	ľ	
1	ļ		Ī		>gi 1078237 pir S56849	i	
- 1	l _r	ycopersicon	- 1		probable membrane protein	ł	
		sculentum class II	ł		YJL073w - yeast	į	
- 1		mall heat shock	- 1		(Saccharomyces cerevisiae) >gi 895898 (X88851)	i	
	1	rotein Le-HSP17.6	1			}	
059		RNA. complete cds	8e-05		hypothetical protein YJL073w [Saccharomyces cerevisiae]		
T				11,04/3	microtubule-associated protein,	6.0	
	H	I.sapiens XB gene .			110K tau - rat >gi 207158	[
		or tenascin-X, repeat	1		(M84156) big tau [Rattus		
060	X71934 X	III	8e-05		norvegicus]	3.7	
						J.1	

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEO			T T	,		Totellis/	
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
<u> </u>	<u> </u>						
1061	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	8e-05	4049682	(AF063866) ORF MSV092 hypothetical protein [Melanoplus sanguinipes entomopoxvirus]	2.1	
		Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA,			(AJ235271) unknown		
1062	AF090115	complete cds	8e-05	3861019	[Rickettsia prowazekii]	5e-14	
1063	A F207174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete					
1063	AF027174	cds Human lens	7e-05	<none></none>	<none></none>	<none></none>	
1064		membrane protein (mp19) gene, exon 11. B.napus gene for	7e-05	<none></none>	<none> hypothetical protein YPR 174c - yeast similarity to a nuclear</none>	<none></none>	
1065		LHC II Type III chlorophyll a/b binding protein	7e-05	2132314	lamin from C. elegans (PIR accession number S42257) [Saccharomyces cerevisiae]	8.9	
1066		Helianthus tuberosus lectin 1 mRNA, complete cds	7e-05	2979422	(AB006757) PCDH7 (BH- Pcdh)c [Homo sapiens]	5.7	
1067		Arabidopsis thaliana cellulose synthase catalytic subunit (Ath- A) mRNA, complete	7e-05	2493696	HYPOTHETICAL 21.5 KD PROTEIN (ORF 185) >gi 1480440 (U34204) ORF185; hypothetical 21.4 kD protein [Brassica oleracea]	5.7	
1068	I	Rattus norvegicus	7e-05	2501029	PROBABLE LEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR (LEUCINE TRNA LIGASE) (LEURS) KIAA0028 [Homo sapiens]	5.2	

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEQ				inearest ineignbor (Blasty Vs. Holl-Redundant Proteins)			
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
		Human DNA		T			
i		sequence from				 	
1		cosmid cN85E10 on	ľ	1		İ	
1		chromosome 22q11.2	ł]	
1069	Z68758	qter	3e-05	<none></none>	<none></none>	<none></none>	
ł		human Histone H3.3				44101125	
		pseudogene (CIR-		i			
1070	X60653	456)	3e-05	<none></none>	<none></none>	<none></none>	
	· .	Hanning Co.C. DNA					
ĺ	1	H.sapiens CpG DNA, clone 34d6, forward			GUANYLYL CYCLASE GC-E		
1071	Z58294		2.05	15045	PRECURSOR cyclase receptor		
10/1	230294	read cpg34d6.ft1a. Homo sapiens	3e-05	1706241	[Mus musculus]	9.6	
ŀ		mitochondrial outer					
		membrane protein		·			
	l	(Tom40) gene,			AMINE OXIDASE [FLAVIN-		
		nuclear gene			CONTAINING] B oxidase		
	f	encoding			(flavin-containing) (EC 1.4.3.4)		
		mitochondrial			B - human B [human, platelet,	•	
		protein, exons I			Peptide Partial, 520 aa] [Homo		
1072	AF043251	through 6	3e-05	113980	sapiens]	8.9	
			30 43	113300	sapiens	8.9	
			1	•		ļ	
		Chicken progesterone				1	
		receptor gene,	1			Į.	
		encoding forms A and	1		IG GAMMA LAMBDA	ŀ	
1073	M31104	B. exons 1 and 2.	3e-05	1170841	CHAIN V-II REGION	4.8	
		S	1			•	
	i	Sambucus nigra ribosome inactivating	Ī				
ı		-	- 1		ribosomal protein S3 -		
1074	AF012899	protein precursor	2.00	6.10.40.1	Chlamydomonas humicola		
		mRNA, complete cds Human vasopressin	3e-05	543684	chloroplast (fragment)	4.2	
l	. 1	receptor V2 gene,	İ		(1120615) C-01 1		
i075		complete cds.	3e-05	791207	(U20615) Gnot1 homeodomain		
		Rattus norvegicus	26-02	/9120/	protein [Gallus gallus]	1.8	
- 1		homer-1c mRNA.	į.		(AF033361) polyprotein	[
1076		complete cds	3e-05	3237340	[Hepatitis C virus]	0.94	
		Mus musculus		323,340	[Megantis C virus]	0.54	
- 1	ļī	Pontin52 mRNA,	- 1	i	(AL021813) hypothetical	i	
1077	AF100694	complete cds	3e-05	2879805	protein	0.001	
		Mus musculus					
j		Pontin52 mRNA,	1		(Z81555) predicted using	i i	
1078		complete cds	3e-05	3877951	Genefinder	3e-07	

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEC				and the second s			
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
ı		Lycopersicon					
1		esculentum cytosolic			1	1	
		class II small heat					
ı	i	shock protein HCT2	j		·		
1,070	45000115	(HSP17.4) mRNA,			•	1	
1079	AF090115	complete cds	2e-05	<none></none>	<none></none>	<none></none>	
i	1	Helianthus tuberosus		•		1	
1	l	lectin 1 mRNA.			(791120)		
1080	AF064029	complete cds	2e-05	3880197	(Z81132) predicted using Genefinder	1 . `	
		Homo sapiens full	20-05	, 3860197	Generinder	2.4	
1	i	length insert cDNA			!!!! ALU CLASS B WARNING		
1081	AF087989	clone YX29D10	2e-05	113667	ENTRY !!!!	1.8 .	
						1.0	
1		Helianthus tuberosus				1	
1	į	lectin I mRNA,		•	(L31967) mating type protein	J j	
1082	AF064029	complete cds	2e-05	474896	[Coprinus cinereus]	1.4	
		77	1				
1		Helianthus tuberosus	ŀ			1	
1083	AF064029	lectin 1 mRNA, complete cds	2- 05	2266000	(Y13274) M33 polycomb-like		
1005	AL 00-4029	Equus caballus UCD-	2e-05	2266988	protein [Mus musculus]	0.62	
1		E-CA-467	- 1				
1		dinucleotide repeat	i				
1		region, complete	I				
1084	U67415	sequence	1e-05	<none></none>	<none></none>	<none></none>	
		H.sapiens BGP gene					
]		for biliary	ľ				
l i		glycoprotein,	ľ			i	
1005		promoter region and			1		
1085	X67277	exon l	1e-05	<none></none>	<none></none>	<none></none>	
		H.sapiens epb72 gene			· .		
1086		exons 2,3.4,5,6,7	1e-05	<none></none>	NONTE	NONE	
		-1.01.0 ±1.2,±1,0,1	10-03	<110NE>	<none></none>	<none></none>	
	1:	Mus musculus	- 1		(Z29457) core region;		
	1:	suppressor of	Į.		pid:g443877 [Hepatitis C virus]	l	
1087		cytokine signalling-3	1e-05	443877	virus	3.9	
					(Z66498) similar to cuticle		
1	•		- 1		collagen; cDNA EST		
1000		Homo sapiens P2X7			EMBL:D75584 comes from this	1	
1088	Y12853	gene, exon 4-8	1e-05	3878726	gene	0.36	
j]	ł		(41025270) CLUTTING		
ŀ	1,	Borrelia burgdorferi			(AJ235270) GLUTAMYL-	j	
ĺ		section 26 of 70) of	J		IRNA AMIDOTRANSFERASE		
1089		he complete genome	1e-05	3860719	SUBUNIT A (gatA) [Rickettsia prowazekii]	45.15	
	<u></u>			3000/19	hinwasekiil	4e-15	

9.44	Nearest	Neighbor (BlastN vs. C	Genbank)	Nearest Neigh	nhor (BlastX vs. Non-Redundant P	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEC	,				The state of the s	Totellis)			
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE			
-	 	ļ,,							
1	1	Homo sapiens gamma adaptin gene, exon 2	1						
		and flanking intronic	1			İ			
1090	AJ224112	sequences	9e-06	NOVE		1			
	1,0224112	Homo sapiens DNA	96-00	<none></none>	<none></none>	<none></none>			
1		for repeat sequence			translation initiation factor IF-2	ŀ			
1091	AB000565	Alu	9e-06	72879	Escherichia coli				
		H.sapiens flow-sorted	30 00	12013	Eschericina con	5.1			
1	1	chromosome 6			1 .	1			
	i	HindIII fragment,			(M65164) 51C surface protein				
1092	Z 78985	SC6pA20B4	9e-06	·, 159975	[Paramecium tetraurelia]	4.8			
					50S RIBOSOMAL PROTEIN	7.0			
1	ļ	Thermotoga maritima	٠.		L2 maritima >gi 437926	İ			
1093	Z21677	DNA for spc operon	9e-06	585879	(Z21677) ribosomal protein L2	7e-14			
ļ									
l			Ĭ		DYNEIN BETA CHAIN,	İ			
l		Drosophila hydei	Ī		CILIARY sea urchin				
1004	15001101	Dhc7 (Threads)			(Anthocidaris crassispina) chain				
1094	AF031494	mRNA, complete cds	9e-06	729377	[Anthocidaris crassispina]	4e-18			
ł		Homo sapiens	-						
ľ		placental protein	1						
1095	AF051315	17a1 (PP17) mRNA, complete cds	4- 06	1101777					
1075	AI 051313	Homo sapiens	4e-06	<none></none>	<none></none>	<none></none>			
		(subclone 2_f4 from	1						
		BAC H107) DNA			(AE000952) ISA1214-6,				
1096		sequence	4e-06	2648304	putative transposase	6.2			
		H.sapiens mRNA for		2040304	puditive transposase	6.2			
		skeletal muscle-	Į.		(AB016726) calpain	I			
1097	X85030	specific calpain	4e-06	4239857	[Schistosoma japonicum]	0.006			
		Human polymorphic			(comotocoma japonicam)	0.000			
		arylamine N-	i			i			
1098		acetyltransferase	3e-06	<none></none>	<none></none>	<none></none>			
I		Rattus norvegicus							
ľ		mRNA for CDP-				i			
		diacylglycerol				j			
1099		synthase, complete			(Z70309) R 102.6				
1099		cds	3e-06	3879045	[Caenorhabditis elegans]	7.3			
I		H.sapiens flow-sorted		1	MERCURIC REDUCTASE				
Į		chromosome 6 HindIII fragment,	1		(HG(II) REDUCTASE)				
1100		SC6pA20B4	30.06		>gi 418744 pir S30168				
	210303	SCOPA2004	3e-06	266529	mercury(II) reductase	6.5			
- 1	ļ,	Homo sapiens mRNA			i				
		or Nedd8-activating	ľ		l	[
		nzyme hUba3,	1	Į.	(Z79697) F58H10.1	i			
1101		complete cds	3e-06		[Caenorhabditis elegans]	6.2			
				3011338	(Cachornaodinz elegans)	6.3			

	Nearest	Neighbor (BlastN vs. G	enhank)	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEQ				Mearest Neigh	1.021-051 (Verginoof (Diaable Vs. 14011-Reduitedalle F10		
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
<u> </u>		Homo sapiens				T	
1	İ	WSCR4 gene, exons			(Z80775) hypothetical protein	 	
1102	AF041056	3 and 4	3e-06	1568583	Rv0044c	1.9	
i	1	Mouse E(d) beta gene					
ı	ľ	5' flanking region and			(U72497) fatty acid amide		
1103	X00777	exon 1	3e-06	1680722	hydrolase [Rattus norvegicus]	0.008	
1		Human mRNA for					
		estrogen responsive			1	l i	
1 .	ŀ	finger protein,			(U09825) acid finger protein	1	
1104	D21205	complete cds	3e-06	563127	[Homo sapiens]	le-05	
		Human cosmid					
1105	Z47046	QLL2C9 from Xq28	1e-06	<none></none>	<none></none>	<none></none>	
1		Human MHC class III					
1106	L26261	HLA-RP1 gene.	le-06	<none></none>	<none></none>	<none></none>	
1		Rat 5S RNA gene,					
1107	M13402	clone 5S-2.	1e-06	<none></none>	<none></none>	<none></none>	
1,,,,,		H.sapiens gene for					
1108	X68793	antithrombin III	1e-06	<none></none>	<none></none>	<none></none>	
1 1		1			ZINC FINGER PROTEIN 33A		
1 1					(ZINC FINGER PROTEIN	}	
1 1		Homo sapiens	Ī		KOX31) (KIAA0065)	1	
1109	A F0006 40	Krueppel family zinc			(HA0946) Kruppel-related.	1	
1109	AF003540	finger protein	1e-06	2507553	[Homo sapiens]	0.098	
1 1		Homo sapiens					
		(subclone 10_d2 from P1 H21) DNA	Ī		<u> </u>	l j	
1110	L42096	1 ' 1			(U58762) T27F7.1 gene product		
1110	L+2090	sequence. Human DNA	1e-06	1330401	[Caenorhabditis elegans]	0.015	
l I		sequence from					
		cosmid cN116A5,				Ī	
		between markers		•			
		D22S280 and	j			1	
1 1		D22\$86 on	ļ			1	
		chromosome 22q12		•			
1111	Z69925	contains EST	9e-07	<none></none>	<none></none>	ANONT.	
	30773	tomanis 201	- 20-07	CIVONES	<none></none>	<none></none>	
		İ	. 1		(Z81109) predicted using		
	ĺ	ľ		·	Genefinder; similar to	1	
]	S. cerevisiae gene for	I		sodium/phosphate transporter;	ı	
		YmL33,	1	ľ	cDNA EST yk326f6.3 comes	- 1	
	ļ	mitochondrial	!		from this gene; cDNA EST	Ţ	
1		ribosomal proteins of	1		yk326f6.5 comes from this gene]	
1112		large subunit	9e-07		[Caenorhabditis elegans]	7.1	
					[Cac.ortiabortis cicgans]	7.1	

4.5	Nearest	Neighbor (BlastN vs. C	Sanhank)	T 77		
SEC	11001031	Treignoor (Blasus Vs. C	Jenoank)	Nearest Neig	hbor (BlastX vs. Non-Redundant Pr	oteins)
ID ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	
	1		T. VALUE	1 ACCESSION	(US8/SS) coded for by C.	P VALUE
	1		 		elegans cDNA yk34b1.5; coded	
1]			ł	for by C. elegans cDNA	į
	1	İ	l	i	ykl3hl0.5; coded for by C.	
					elegans cDNA yk46e8.5; coded	
1					for by C. elegans cDNA	ļ
ł		Sambucus nigra	ĺ	1	yk46d5.5; coded for by C.	
	ŀ	ribosome inactivating	1		elegans cDNA yk43c2.5; coded	
1		protein precursor		Ī	for by C. elegans cDNA	
1113	AF012899	mRNA, complete cds	9e-07	1330345	yk46e8	2e-29
				·		20-27
	i			'.	(U40945) coded for by C.	·
1	j		٠.	}	elegans cDNA yk74b9.3; coded	
1					for by C. elegans cDNA	
1	ĺ	i			yk74b9.5; similar to repeat of	
]					calcium channel alpha subunits;	i
1		Homo sapiens full			similar to tetracycline resistance	j
1		length insert cDNA			protein; similar to hypothetical	i
1114	AF086562	clone ZE16C03	4e-07	1072210	protein in HSP30-PMP1 region	
		0.00 ZEE 10005		1072210	(SP (Z46/95) similar to	3.9
1 1					transforming protein etc2;	1
i l					cDNA EST EMBL:D34137	· · · · · · · · · · · · · · · · · · ·
					comes from this gene; cDNA	1
			ľ		EST EMBL:D37172 comes	
			ĺ	•	from this gene; cDNA EST	
		Homo sapiens	ł	•	EMBL:D76266 comes from this	.]
1 1		interleukin 9 receptor			gene; cDNA EST	ł
ا , , , , , ا		IL9R pseudogene.	- 1		EMBL:D70493 comes from this	
1115	L39062	exons 1-9	4e-07	3879983	gene; cDNA	3.3
[[i]				
	1.	Human DNA	j		[Į.
•		sequence from	ľ			ì
		cosmid L96F8,	ŀ		·	1
		Huntington's Disease	1		}	- 1
		Region, chromosome	- 1		· •	
ľ		4p16.3 contains EST	1			
ı		and cDNA. > ::			i	- !
- 1	ŀ	mb Z69365 HSL96F	j	j		į
ļ		BA Human DNA	1	ļ		
]		sequence from			1	j
- 1		osmid L96F8,	İ		1	- 1
1		Iuntington's Disease	- 1			
		Region, chromosome	İ	1		. 1
1116		p16.3 contains EST			(AF022889) latent TGF beta	l
	209304 Ja	nd cDNA.	4e-07	3493176	binding protein [Mus musculus]	3.0

	Nearest	Neighbor (BlastN vs.	Genbank)	Negros Nais	hbor (BlastX vs. Non-Redundant P	
SEQ		The state of the s	1	ivearest iveig	nbor (Blasta, vs. Non-Redundant P	roteins)
ID	ACCESSION		P VALUE	ACCESSION	DESCRIPTION	P VALUE
<u> </u>	 	Human mRNA for				
1	1	KIAA0164 gene,			(AC005936) hypothetical	
1117	D79986	complete cds	4e-07	4038031	protein [Arabidopsis thaliana]	0.30
1	l	Human mRNA for				0.50
1	l _	KIAA0098 gene,		Į.		ľ
1118	D43950	partial cds	3e-07	<none></none>	.\ <none></none>	<none></none>
1	į				(AL032657) predicted using	1
1	i				Genefinder; similar to DnaJ	
1	ł		1		domain; Thioredoxin; cDNA	ı
I	J				EST yk433f3.5 comes from this	
					gene; cDNA EST	
1		Arabidopsis thaliana	i		EMBL:D32359 comes from this	
1	l	DnaJ homologue		<u> </u>	gene; cDNA EST	j j
1	. =====	(AU6) mRNA,		1	EMBL:D34721 comes from this	1
1119	AF037168	complete cds	3e-07	3881075	gene; cDNA EST yk433f3.3 c	3e-09
1		H.sapiens mRNA for			(U00043) similar to D.	
1120	X69838	G9a	3e-07	3873414	melanogaster trithorax protein	3e-29
]			
Ì		Homo sapiens mRNA			1	
ا ا		for KIAA0552	i		(U90880) hypothetical protein	
1121	AB011124	protein, complete cds	2e-07	2618749	2: predicted using XGrail	2.0
		Human cellular fms				
1120	******	proto-oncogene,			}	i i
1122	K03012	partial cds.	1e-07	<none></none>	<none></none>	<none></none>
		II DAYA	l j	•		
		Homo sapiens DNA,				
1123		microsatellite and Alu			!!!! ALU SUBFAMILY SQ	
1123	ABUIU193	repeat region	1e-07	728837	WARNING ENTRY	0.095
		Uomo soniasa	- 1		1	
1124		Homo sapiens	4 00		i	- 1
1127		psihHaA pseudogene Homo sapiens FLII	4e-08	<none></none>	<none></none>	<none></none>
- 1		gene for ERGB			1	1
ł		transcription fuctor.	Ī		. 1	
- 1		intron 4 and partial	ł	•	l	ł
1125		eds	40.00	720027	!!!! ALU SUBFAMILY SP	<u> </u>
		Homo sapiens ogg1	4e-08	728836	WARNING ENTRY	3.6
1126		gene. exons 1-7	40.00	112//0	!!!! ALU CLASS C WARNING	
		Homo sapiens	4e-08	113668	ENTRY !!!!	3e-05
ļ		subclone 1_c10 from	i			
- 1		21 H69) DNA	j			
1127		equence	3e-08	4225050	(41120701)	
1		oquerice	36-03	4225950	(AJ132701) centaurin gamma1B	1.8
1	la	Gallus gallus mRNA	1		(AC004537) similar to tumor	1
1		or high mobility	j	İ	suppressor p33ING1; similar to	į
1128		roup 1 protein	3e-08	2041055	AF044076 (PID:g2829208)	
		Iomo sapiens FGFR-	50-08	3041855	[Homo sapiens]	3e-31
1129		gene	le-08	NONE		
			10-00	<none></none>	<none></none>	<none></none>

<u> </u>	Near	rest N	Veighbor (BlastN v	. Genbank)	Nearest N	eighbor (BlastV N	
SEQ	İ				- i veurest iv	eighbor (BlastX vs. Non-Redundan	Proteins)
ID	ACCESS	ION	DESCRIPTION	P VALU	JE ACCESSIC	DESCRIPTION	P VALI
-			Managara				TVAL
1 .	ĺ		Mesocricetus aurat	us			 -
1 1	ĺ		serum amyloid P	- 1	i i		İ
1130	L22024		component gene,		1		1
	222027	` 	complete cds.	1e-08	<none></none>	<none></none>	<none< td=""></none<>
		Is	Sambucus nigra		1		
1 1		ļr	ibosome inactivatir	19	· I		1
} {		l _p	rotein precursor			į	ł
1131	AF01289		nRNA. complete co	ls 1e-08	ANONIT.		
, ,				10 00	<none></none>	<none></none>	<none< td=""></none<>
			luman mRNA for	j			,
			hospholipase C > ::		1		1
			b M37238 HUMPL		ł	1	
		1 -	Human			l l	
1132	V1.400.4		hospholipase C		1		
1132	X14034	m	RNA, complete cd	i. le-08	<none></none>	-\none>	<none:< td=""></none:<>
1			sapiens CpG DNA	1.			CHONE
1			one 152b10, rward read	i	1		ſ
1133	Z59381		g152b10.ft1a.	1	1		
	237301		omo sapiens	1e-08	<none></none>	<none></none>	<none></none>
		- 1	bclone 2_h3 from	1			
			H43) DNA	Į.	1	1	1
1134	L81839	•	quence	le-08	<none></none>		j
		T		10-08	<nune></nune>	<pre><none> HYPOTHETICAL PROTEIN</none></pre>	<none></none>
- 1				1	I	MJ1207 Methanococcus	
- 1		i		ŀ	Ĭ	jannaschii >gi 1591837	
ł					i	(U67562) protease synthase and	İ
ı		Hu	man GLA gene for		1	sporulation negative regulator	1
135	V14440		ha-D-galactosidase	.		Pail, putative [Methanococcus	
133	X14448	IA (EC 3.2.1.22)	le-08	3334427	jannaschii]	9.1
			nan DNA				9.1
			uence from clone F15 on	·		·	
- 1			omosome Xq25,			1	
- 1		Com	plete sequence			1	
136 A	L023774	(Ho	mo sapiens]	10.00		(U58330) probable copper-	
1			piens DNA	1e-08	1354935	transporting atpase	1.2
- 1			titive	- 1	•		
- 1		•	elomeric-like			1	1
37			ence (522 bp)	le-08	77257	hypothetical 70K protein -	ŀ
$\cdot T$		Hum	an HuD gene,	10-00	77356	eggplant mosaic virus	0.098
38 t		<u>5'</u> UT		5e-09	3387886	(AF070530) unknown [Homo	
					330/880	sapiens]	9.5

		st Neighbor (BlastN vs.	Genbank)	Nearest Neig	hbor (BlastX vs. Non-Redundant P	roteins)
SEQ		Ì			, ton-Redundant P	T T
ID	ACCESSIO		P VALUE	ACCESSION	DESCRIPTION	P VALU
	-	Human DNA				1. ************************************
	ł	sequence from				
	ļ	cosmid E86D10 on	ł	1		ł
	ł	chromosome 22.				· ·
	İ	contains ESTs,]	l		ł
1120	700.0.	exontrap, complete			!!!! ALU SUBFAMILY J	
1139	Z82181	sequence	5c-09	728831	WARNING ENTRY	8.4
	Ī	Mus musculus mRN	A)	4		- 0.4
	ł	for translation	1		İ	i
140	4 100 6 5 0 5	initiation factor eIF2	į .		(U22376) alternatively spliced	Ì
140	AJ006587	gamma X	5e-09	1872200	product using exon 13A	0.64
141	V11100	H.sapiens WNT8B	1	• •	(AF045646) contains similarity	0.04
141	Y11108	gene	4e-09	2854198	to collagens	4.0
ı		T				
j		Treponema pallidum	i i			
142	AE001223	section 39 of 87 of			CELL DIVISION PROTEIN	
	AE001223	the complete genome	4e-09	3334189	FTSY HOMOLOG	1.5
- 1						
ı			}]		fibroblast growth factor receptor	
I					Al precursor - African clawed	
- 1		Human cosmid	!		frog >gi 214894 (M55163)	
43	Z47046	QLL2C9 from Xq28	4 00		fibroblast growth factor receptor	
1	2,7010	Homo sapiens	4e-09	104045	[Xenopus laevis]	1.3
- 1		genomic DNA, 21q	f			
		region, clone:			l	
44	AG000746	T171Bm40	4e-09	112666	!!!! ALU CLASS A WARNING	
$\neg \vdash$			46-09	113666	ENTRY !!!!	0.33
			1		arginine rich domain, possesses	
- 1					weak similarity with the RNA	
I			ſ		binding domains from RNA	
ı	j		l		splicing factor U2AF 65 KD	
		1	ł		subunit; cDNA EST	
	<i>'</i>		· •	•	EMBL:D64658 comes from this	
- 1		·	1	•	gene; cDNA EST	
1	j		I		EMBL:D66829 comes f	
j	1		1		>gi 3878699 gnl PID e1351700	
	i		J		possesses weak similarity with	
	1	,			r with summing Mill	
	l		j	ſ	the RNA hinding domains from	
					the RNA binding domains from	i
					RNA splicing factor U2AF 65	
	I	fuman arginine-rich			RNA splicing factor U2AF 65 KD subunit; cDNA EST	
		Human arginine-rich			RNA splicing factor U2AF 65 KD subunit; cDNA EST EMBL:D64658 comes from this	
5	л М74002 г	nuclear protein	4e-09		RNA splicing factor U2AF 65 KD subunit; cDNA EST EMBL:D64658 comes from this gene; cDNA EST	2 61
5	л М74002 г		4e-09		RNA splicing factor U2AF 65 KD subunit; cDNA EST EMBL:D64658 comes from this	3e-06
5	M74002 r	nuclear protein	4e-09		RNA splicing factor U2AF 65 KD subunit; cDNA EST EMBL:D64658 comes from this gene; cDNA EST	3e-06
	M74002 r	nuclear protein nRNA, complete cds. Kenopus Iaevis XL-	4e-09	3875371	RNA splicing factor U2AF 65 KD subunit; cDNA EST EMBL:D64658 comes from this gene; cDNA EST	3e-06

	Neares	t Neighbor (BlastN vs. (Genhanki	No		
SEC	4	Telgiloor (Diasa) vs. v	Jenoank)	Nearest Neig	thbor (BlastX vs. Non-Redundant P	roteins)
SEC	- 1	N DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
ļ					UDP-	1
1147	U20554	Drosophila melanogaster UDP- glucose:glycoprotein glucosyltransferase mRNA, complete cds	2. 00	240000	GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (DUGT) glucosyltransferase - fruit fly (Drosophila sp.) glucosyltransferase precursor	
<u> </u>	020354	micrya, complete cus	2e-09	2499087	[Drosophila melanogaster]	4e-24
1148	Z56162	H.sapiens CpG DNA, clone 91c9, forward read cpg91c9.ft1a Mus musculus	le-09	<none></none>	<none></none>	<none></none>
	j	Pontin52 mRNA.			(1/25730) VCDI 1 5 1 D.4	
1149	AF100694	complete cds	1e-09	1002424	(U25739) YSPL-1 form 1 [Mus musculus]	
1150	M85276	Homo sapiens NKG5 gene, complete cds.	le-09	2315436	(AF016447) No definition line	8.9
		Human	1007	2313430	found [Caenorhabditis elegans]	8.3
1151	M94065	dihydroorotate dehydrogenase mRNA, 3' end.	1e-09	3892656	(AB014464) MGC-24v [Mus musculus]	6.2
1152	AJ131895	Homo sapiens genomic CAG repeat element, clone 60o2(250) Human DNA	5e-10	<none></none>	<none></none>	<none></none>
u.s.		sequence from cosmid E86D10 on chromosome 22. contains ESTs, exontrap, complete			!!!! ALU SUBFAMILY J	
1153		sequence	5e-10	728831	WARNING ENTRY	7.9
1154	AJ224442	Homo sapiens mRNA for putative methyltransferase Homo sapiens RET	5e-10	113667	!!!! ALU CLASS B WARNING ENTRY !!!!	0.15
1155		finger protein-like I antisense transcript, partial	5e-10	728834	!!!! ALU SUBFAMILY SB2 WARNING ENTRY	0.006
1156	AFIIIII6 r	Homo sapiens silencer of death domains (SODD) nRNA. complete cds	5e-10		(AF111116) silencer of death domains [Homo sapiens]	2e-08
1157	fi	domo sapiens mRNA or hypothetical protein	4e-10	<none></none>		<none></none>

		Neare:	st Neighbor (BlastN vs.	Genbank)	Nearest Neig	abbor (PlaceV V	
	SEC				- rearest riei	ghbor (BlastX vs. Non-Redundant	Proteins)
	ΙD	ACCESSIO		P VALUE	ACCESSION	DESCRIPTION	P VALUE
		 	Homo sapiens type I	I			1
	1160		integral membrane				
	1158	AF001298		4e-10	<none></none>	<none></none>	<none></none>
	1159	V.1205	H.sapiens mRNA for			(U34384) CheW [Borrelia	KNONES
ŀ	1139	Y11395	p40	2e-10	1000340	burgdorferi]	2.4
- 1		ı	Human non-coding	1]		
- 1			sequence upstream		I		
- 1	1160	U41096	from DOC-2 gene on			!!!! ALU SUBFAMILY SQ	l .
ŀ	1100	041096	chromosome 5	2e-10	728837	WARNING ENTRY	0.28
- 1		1	Sambucus nigra	ſ			
- 1		1	ribosome inactivating	1		1	ſ
- 1		ł	protein precursor		··	1	
- [1161	AF012899			1	1	
ŀ		AT 012899	mRNA, complete cds	6e-11	<none></none>	<none></none>	<none></none>
-1		•	chromosome II	j			
ſ			D.	1			1 1
	1162	Z36111	reading frame ORF YBR242w				}
H	1.02	230111	1 B K 24 2 W	6e-11	2213560	(Z97052) hypothetical protein	3e-27
1	ı					(Z80220) Similarity to yeast	1
1]		protein TREMBL ID E246895)	;]
1						cDNA EST EMBL:T00018	1 1
1			ļ			comes from this gene; cDNA	1 1
	f			1	•	EST EMBL:C13908 comes	1 1
1			Schizosaccharomyces			from this gene; cDNA EST	1 1
I	1		pombe mRNA, partial			EMBL:C11656 comes from this	: !
1	163	D89174	cds, clone: SY 1004	60.11	2020	gene; cDNA EST yk234a5.3	
Г	$\neg \uparrow$		Human DNA	6e-11	3879758	comes from this ge	4e-30
L			sequence from	i			
L	- 1		cosmid A1 on	ŀ		}	1 1
			chromosome 6	- 1		1	
	ı		contains ESTs.	1			1
l			HERV like retroviral	Ĭ		ł	1 [
11	164		sequence	5e-11	<none></none>		1 . 1
	Т				CHOILES	<none></none>	<none></none>
			Sambucus nigra				
	1	1	ribosome inactivating	- 1			i i
	ı		protein precursor	- 1		(AF106581)	
11	65		mRNA, complete cds	5e-11	3886065	(AF106581) contains similarity	
		l l	Human UbA52 gene			to C4-type zinc fingers	4.9
	1		oding for ubiquitin-	Ī			İ
		5	2 amino acid fusion	1		·	1
11	66		protein	2e-11	<none></none>	AIONE	
			Iomo sapiens full		SHOHES	<none></none>	<none></none>
	- [ļī.	ength insert cDNA	1	1.	apontosis inhihito - IAD I	Ţ
11	67		Ione ZD40G12	2e-11		apoptosis inhibitor IAP homolog	
	_					- human	3.8

F 1	Nearest	Neighbor (BlastN vs. C	ienbank)	Negrees Nois	hhar (Blass Var. No. B. L. J. B.	
SEQ		1.012.100. (2.1252. 1.73. (Jenearik,	ivearest iveig	hbor (BlastX vs. Non-Redundant Pr	roteins)
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	DVALIE
				cczosion	DESCRIPTION	P VALUE
		Homo sapiens mRNA	 		P53-BINDING PROTEIN	
1	I	for KIAA0771	1			į
1168	AB018314	protein, partial cds	2e-11	2024242	53BP2 Bbp/53BP2 [Homo	<u> </u>
		S.cerevisiae	26-11	3024343	sapiens] (AC004537) similar to tumor	2e-11
ļ		chromosome XV	1	j		
1	ļ	reading frame ORF		1	suppressor p33ING1; similar to	
1169	Z74972	YOR064c	2e-11	2041955	AF044076 (PID:g2829208)	
1.02	214772	Human DNA	26-11	3041855	[Homo sapiens]	2e-40
		sequence from				i
		cosmid E86D10 on				ł
1		chromosome 22.				
		contains ESTs.				
		exontrap, complete			1	
1170	Z82181	sequence	7- 12	2/01		
1170	202101	H.sapiens red cell	7e-12	<none></none>	<none></none>	<none></none>
		anion exchanger				
1		(EPB3, AE1, Band 3)				
1171	X77738				hypothetical protein - human	
11/1	A///36	gene, 3' region	7e-12	2135416	>gi 288145	0.012
		medium-chain acyl-			l i	
1 1		CoA dehydrogenase	j		· .	
1 1	i	{exon 10, intron 10}	•		1	
1 1			1		1	
1172		[human, Genomic, 1407 nt]			!!!! ALU CLASS A WARNING	
11/2		M.musculus DNA for	6e-12	113666	ENTRY !!!!	0.100
1173					(X83413) U88 [Human	
11/3		HC1 locus protein S=activated	6e-12	854065	herpesvirus 6]	2e-06
ľ	1.	·	1			
		protein C cofactor	ļ		1	
1174		rats, liver, mRNA,			(AF009243) proline-rich Gla	
11/4		3315 nt] Bovine OXT gene for	6e-12	2338292	protein 2 [Homo sapiens]	3e-10
' I			į		T	
1175		oxytocin, 5'			(L77967) small proline-rich	1
11/3	A384/4	noncoding region	2e-12	1296429	protein with paired repeat	4.1
	į,	Landau C. C. D.V.	ľ			-
ĺ		Lisapiens CpG DNA,		,		ľ
1176		ione 10h10, reverse			(AF030154) pVII [bovine	1
11/0	Z56314 г	ead cpg10h10.rt1a.	2e-12	2935221	adenovirus type 3]	2.8
ı	l.	Jameiana C. C. D.V.	ľ			
j		Landon CpG DNA,	. 1			
1177	_	lone 10h10, reverse			(AF037440) putative 26 kDa	i
1177	Z56314 r	ead cpg10h10.rt1a.	2e-12		protein [Edwardsiella ictaluri]	2.8
- 1	<u> </u>		j		BETA SCRUIN >gi 1015535	
	ľ	1 musculus h2-	ľ	i	(Z47541) beta scruin [Limulus	1
1178	Z19543 e	alponin cDNA	2e-12	2497945	polyphemus]	2e-0-
						

	Neares	t Neighbor (BlastN vs.	Genbank)	Nearest Nei	ghbor (BlastX vs. Non-Redundant	
SE				Theatest Iven	enoor (blastix vs. Non-Redundant	Proteins)
П	-		P VALUE	ACCESSION	DESCRIPTION	P VALUE
-		erythropoietin				+
1		receptor [human,	1			
1		placental, Genomic,	1	J	!!!! ALU SUBFAMILY SC	İ
117	9 S45332	8647 nt]	7e-13	728835	WARNING ENTRY	0.074
		Sambucus nigra ribosome inactivating				0.074
1		protein precursor	}		Ĭ	1
118	0 AF012899	mRNA, complete cds	2e-13	<none></none>	<none></none>	<none></none>
118	l AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds				ZINOINES
110	. HU12899	illikinA, complete cas	2e-13	<none></none>	<none></none>	<none></none>
1182	Z59509	H.sapiens CpG DNA, clone 15a1, reverse read cpg15a1.rt1a.	2e-13	3150251	(AL023634) hypothetical	0.66
1		Human CYP11B2				0.00
1	B.0	gene for steroid 18-			!!!! ALU SUBFAMILY SQ	
1183	D10170	hydroxylase	2e-13	728837	WARNING ENTRY	3e-05
1		Human MHC class I	•		LINE-1 REVERSE	30-03
11104	1165416	molecule (MICB)	1		TRANSCRIPTASE	i [
1184	U65416	gene, complete cds	2e-13	126295	HOMOLOG	6e-11
l	l	Mus musculus				
1185	A 10000031	IHABP gene,	3		hypothetical protein YPL186c -	1
1103	AJ006031	promoter	8e-14	2132223	yeast	1.1
ł		Human gamma-	- 1		(U34976) gamma-sarcoglycan	
1186	U34976	sarcoglycan mRNA,			[Homo sapiens] >gi 4239660	
1180	034976	complete cds	8e-14	1054903	sapiens]	0.034
		Rat mRNA for very- long-chain Acyl-CoA			ACYL-COA DEHYDROGENASE, VERY- LONG-CHAIN SPECIFIC (VLCAD) >gi 2388724 (AF017176) very-long-chain	·
1187		dehydrogenase,			acyl-CoA dehydrogenase [Mus	
1107	D30047	complete cds	8e-14	3183512	musculus]	8e-23
1188	· · ·	H.sapiens CpG DNA. clone 7g4, forward read cpg7g4.f1a.	бе-14	94205		
		чрагания.	26-14	86285	histone H1.01 - chicken	6.8
1189	U27196 r	Gallus gallus zinc inger protein (Fzf-1) nRNA, complete cds. African green	3e-14	2134436	zinc finger protein - chicken (fragment)	4e-10
		nonkey origin of	ľ			J
1190		eplication	2e-14	<none></none>	ANONE	
		· · · · · · · · · · · · · · · · · · ·		VII ONES	<none></none>	<none></none>

		Neares	st Neighbor (BlastN vs. (Genhank)	T M			
	SEC		(Diastiv Vs.)	Jenoank)	Nearest Neig	phbor (BlastX vs. Non-Redundant F	roteins)	
	ID	7		P VALUE	ACCESSION	DESCRIPTION	P VALUI	-
	<u> </u>	 	Mus musculus				T VALUE	=
	1191	AF100694	Pontin52 mRNA, complete cds	2e-14	4235641	(AF119040) NL0D [Lycopersicon esculentum]	0.65	1
	1192	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	1	3043728	(AB011174) KIAA0602 protein [Homo sapiens]		
	1193	AJ005866	Homo sapiens mRNA for putative Sqv-7- like protein, partial		4008517	(AJ005866) Sqv-7-like protein	0.28	
	1194	U32709	Haemophilus influenzae Rd section 24 of 163 of the complete genome	2e-14	3861056	(AJ235272) POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERA SE (pnp) [Rickettsia	0.004	
	1195	AF073485	Homo sapiens MHC class I-related protein MR I precursor (MR I) gene, partial cds	8e-15	728831	prowazekii] !!!! ALU SUBFAMILY J WARNING ENTRY	6e-28	
	1196	AF052135	Homo sapiens clone 23625 mRNA sequence	8e-15	4098124	(U73522) AMSH [Homo sapiens]	8e-14	
	1197	AF100694	Mus musculus Pontin52 mRNA, complete cds	3e-15	<none></none>	<none></none>	<none></none>	
	1198		Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	3e-15	113671	!!!! ALU CLASS F WARNING ENTRY !!!!	1.7	
1	199		S.cerevisiae chromosome XV reading frame ORF YOR196c	3e-15	·	(Z46381) similar to lipoic acid synthase; cDNA EST yk283b6.3 comes from this gene; cDNA EST yk283b6.5 comes from this gene; cDNA EST yk472f5.3 comes from this gene; cDNA EST yk472f5.5 comes from this		•
					20/02/0	gene; cDNA EST yk476e7.3	le-15	

-		t Neighbor (BlastN vs.	Genbank)	Nearest Neig	hbor (BlastX vs. Non-Redundant	Proteins)
SEC	ACCESSIO	N DESCRIPTION	P VALUE	1	DESCRIPTION	
<u> </u>				Ť T	(U42833) coded for by C.	P VALU
1200	X70052	S.cerevisiae sof1 gene	3e-15	1125754	elegans cDNA cm16f6; coded for by C. elegans cDNA CEESU63F; similar to S. cerevisiae SOF1 protein (SP:P33750) [Caenorhabditis elegans]	3e-29
1201	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	l	· · <none></none>		
					<none></none>	<none:< td=""></none:<>
1202	M92295	Gorilla gorilla gamma l and gamma-2 globin genes, complete cds.	le-15	284078	hypothetical protein 2 - human >gi 182220	7.4
1203	L34587	Homo sapiens RNA polymerase II elongation factor SIII, p15 subunit mRNA, complete cds. > :: gb AR022286 AR022 286 Sequence 7 from		·		
1205	L34387	patent US 5792634	9e-16	<none></none>	<none></none>	<none></none>
1204	D83649	Xenopus laevis mRNA for xSox7 protein, complete cds Homo sapiens PAC	8 e -16	2447043	(D83649) xSox7 protein [Xenopus laevis]	4e-06
1205	AC005190 s	clone DJ1152D16 from Xq23; complete sequence [Homo sapiens]	3e-16	<none></none>	<none></none>	<none></none>
1206	J03626 c	Human UMP synthase mRNA, complete cds.	3e-16	113667	!!!! ALU CLASS B WARNING ENTRY !!!!	0.65
1207	i	Human Alu family nterspersed repeat; lone BLUR11.	3e-16	728836	!!!! ALU SUBFAMILY SP WARNING ENTRY	4e-06
208	N	Mus musculus m- lumb (m-nb) mRNA. omplete cds	le-16	<none></none>	<none></none>	<none></none>

WO 01/02568

	Nearest	Neighbor (BlastN vs. G	enbank)	T No.	h (D1 V V V V V V V	
SEC		TACISHOOL (DIASA VS. O	Choank)	Nearest Neigh	nbor (BlastX vs. Non-Redundant P	roteins)
SEQ	•		i	ł		
F-110	ACCESSION	DESCRIPTION	PVALUE	ACCESSION	DESCRIPTION	P VALUE
	 	Human SWI/SNF				
i	ľ	1				
i	1	complex 60 KDa]		1
1209	1166610	subunit (BAF60c)			(U66619) SWI/SNF complex 60	
1209	U66619	mRNA, complete cds Drosophila	le-16	1549247	KDa subunit [Homo sapiens]	0.003
1	ĺ	melanogaster Rga and			+	I
1	l	Atu genes, complete			(2724.45)	i
1210	U75467	cds	1. 16	1660500	(U75467) Atu [Drosophila	l
1210	073407	cus	le-16	1658503	melanogaster]	5e-32
l		Human alternative		1		
ŀ	i	splicing factor		1 , .	1	
1211	M72709	mRNA, complete cds.	3e-17	<none></none>	<none></none>	ANONT:
		Human ferritin H		CHOILES	KNOWES	<none></none>
İ	ŀ	(FTHL13)	i			ì
1212	U26556	pseudogene.	3e-17	<none></none>	<none></none>	<none></none>
		Human gene for 2-		CITOTAL D	CNOINES	CHOINES
		oxoglutarate			(AF003386) F59E12.9 gene	
1	•	dehydrogenase.			product [Caenorhabditis	
1213	D32064	complete cds	3e-17	2088843	elegans]	0.12
					APAG PROTEIN	0.12
		Human (Papua New	ĺ		>gi 72927 pir BVECAG apaG	
		Guinean)			protein - Escherichia coli	
		Mitochondrial DNA	•	,	>gi 40918 (X04711) URF	
		control region,			hypothetical protein	
1214	M76364	sequence 131	3e-17	114009	[Escherichia coli]	0.006
		Homo sapiens				
		genomic sequence	1		1	
		from subtelomeric	1			
1215		region of			(U78948) MADS-box protein 2	
1213	AF017466	chromosome 4q	le-17	3947985	[Malus domestica]	4.1
	j	Homo sapiens			. 1	
J		54TMp (54tm)	I		(AE001876) 54TM- (III-	ſ
1216		mRNA, complete cds	le-17	4101574	(AF004876) 54TMp [Homo	0.006
		Mus musculus	_10-17	4101374	sapiens]	0.006
•		Pontin52 mRNA.				
1217	l l	complete cds	9e-18	<none></none>	<none></none>	<none></none>
					(AL033545) putative glycine-	ZUONES
ł	Į.	Rattus norvegicus Na-]		rich protein [Arabidopsis	ł
1218		K-2Cl cotransporter	4e-18	3892703	thalianal	0.30
	11	Homo sapiens			(AF023910) DNA	
- 1	ļı	PENIIB mRNA,	- 1		topoisomerase I [Physarum	
1219		complete cds	4e-18	2642493	polycephalum]	0.083
		1.sapiens IRLB gene			irlB protein - human (fragment)	
1220	X82333 (exon1-3)	4e-18		>gi 33969	2e-11

- -	Near	st Neighbor (BlastN v	s. Genbank)	Nearest Na	ighbor (BlassY us Name D.)	
SEC	2			- CSt Ne	ighbor (BlastX vs. Non-Redundant I	roteins)
ID	ACCESSI		1	E ACCESSION	DESCRIPTION	P VAL
	 	Human mRNA for				IF VAL
1221	ABooos	KIAA0385 gene,			(AF060181) zinc finger protein	+
1222			4e-18	3228540	[Homo sapiens]	
1222	X98485	P.vivax PV14 gene	le-18	<none></none>	<none></none>	6e-25
	1	H.sapiens flow-sort	ed		- CAONED	<non!< td=""></non!<>
	i	chromosome 6	ĺ			1
1223	279057	HindIII fragment,	1	Í	(AB012223) ORF2 [Canis	1
	2/9037	SC6pA21E8	1e-18	2981631	familiaris]	0.001
	j	Homo sapiens (clon			nucleolar 100K polymyositis-	0.001
	1	JH4B1) PM-scl	e j	1	scleroderma protein - human	ĺ
		PIVI-SCI			>gi 35555 (X66113) PM/Scl	ł
1224	L01457	autoantigen mRNA, complete cds.	1	1 .	100kD nucleolar protein [Homo	l
	201437	Dog nonerythroid	1e-18	346287	sapiens]	0.001
		beta-spectrin mRNA	1]	(AB017037) nonstructural	2.001
1225	L02897	3' end.	· 1	1	protein precursor [Himetobi P	l
		J. Cita.	4e-19	3493358	virus]	0.12
- 1		Homo sapiens mRN	ا	j		
		for APCL protein,	1	i '	1	
226	AB012162	complete cds	4e-19	2004245	(AB012162) APCL protein	i
			46-19	3894265	[Homo sapiens]	0.002
[Homo sapiens mRNA				
- 1		for KIAA0521	1		1,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	
227	AB011093	protein, partial cds	4e-19	3043566	(AB011093) KIAA0521 protein	
ľ		X.laevis AB21	1	3043366	[Homo sapiens]	9e-09
		mRNA for RPD3	1 1		HISTONE DE AGESTA	
228	X78454	homologue	4e-19	3023945	HISTONE DEACETYLASE (HD) thalianal	
- 1		**		5025545	(HD) thailana)	5e-34
		Human endogenous	1 1		1	
		retrovirus H DI	1		1	
- 1		leader			1	
ł		region/integrase-	1			
ĺ		derived ORF1,			1	
ı		ORF2, and putative	j	,	(Z14310) tripartite fusion	•
29	U88895	envelope protein			transcript PLA2L [Human	1
-		mRNA, complete cds Human tyrosine	2e-19	59977	endogenous retrovirus]	le-04
-	ľ	kinase TXK (txk)	1			10-04
30		gene, exon 13.	I		!!!! ALU SUBFAMILY J	
1		gene, extil 13.	1e-19	728831	WARNING ENTRY	3e-05
	1	i	- 1		(Z99167) putative peroxisomal	
-],	M.musculus rab3A	i		organisation and biogenesis	1
11	1/700//	tene	10.10		protein [Schizosaccharomyces	
1		, ciic	le-19	2408076	pombe]	2e-09
ı	1	Iomo sapiens	ſ	T		
ļ		nRNA, chromosome	1	1	1	l
1		specific transcript	1	İ	1	j
2 A		IAA0484	4e-20	Nove		j
			70-20	<none></none>	<none> <1</none>	NONE>

	Neare	st Neighbor (BlastN vs. (Genbank)	Negros Mai	the (D)	
SEQ			T	Nearest Neig	shbor (BlastX vs. Non-Redundant Pr	oteins)
ID	ACCESSIO	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALU
	 				(AB001535) similar to	I VALU
	i	Human gene for Zn-	1 1		C.elegans hypothetical protein	
	ĺ		1 1		CETOIH8.1,CEC05C12.3,CEF5	
1233	D14034	alpha2-glycoprotein, complete cds	1 1		4D1.5. similar to trp and trp-like	
	31,1034	H.sapiens HOK-2	2e-20	3928756	proteins [Homo sapiens]	le-07
1234	X82126	gene, exon 2			DNA-binding protein - mouse	16-07
		Luciferase reporter	2e-20	2137269	>gi 437444	le-19
		vector pXP2 *SA,				16-19
1235	AF093684	complete sequence	£ 2.	_	(AF041382) microtubule	
\Box		Tompiete sequence	5e-21	2773363	binding protein D-CLIP-190	5.5
ł		1	1		INOSINE-5'-	
- 1		Human IMP	- 1	• •	MONOPHOSPHATE	
- 1		dehydrogenase type 1			DEHYDROGENASE I (IMP	
236	J05272	mRNA complete cds.	5e-21	10.444	DEHYDROGENASE I)	
		protection of the second	Je-21	124417	(IMPDH-I) (IMPD I) I - human	2e-04
					(Z75712) Similarity to S. Pombe BEM1/BUD5 suppressor; cDNA EST EMBL:Z14470	
- 1		Human (lambda)	ŀ		comes from this gene; cDNA	
- 1		DNA for			EST yk482d4.3 comes from this	
37	Daras	immunoglobulin light	1		gene; cDNA EST yk482d4.5 comes from this gene	
3/	D86997	chain	5e-21	3878261	[Caenorhabditis elegans]	
					(Cachornabants elegans)	бе-46
1	ı		1		(AF024614) ADAM 10	
1	i	1	.]		[Caenorhabditis elegans] Zinc-	
	1		1	j	binding metalloprotease domain-	
- 1		H.sapiens	. 1	ŀ	cDNA EST CEMSA42F comes	
		chromosome 22 CpG	1	ľ	from this gene; cDNA EST	i
- 1	ļ _i	sland DNA genomic	J	{}	yk218f3.3 comes from this gene:	Į
1	la la	Asel fragment, clone	I		DNA EST yk443d9.3 comes	
1	13	02f3, forward read	- 1	ſſ	from this gene; cDNA EST	ı
8		02f3.f	2e-21		/k443d9.5 comes from this	į
			76-71	2739037 g	ene; cDNA	2.6

55	Ne	arest Neighbor (BlastN	vs. Genbank)	T	Nearest N	Neighbor (Black)	
SEC	`	SION DESCRIPTION	ON P VAL	.UE	ACCESSIO	Neighbor (BlastX vs. Non-Redundar	Duran
	—			-I		מווחפרטו שוווות (בפבפטסים:)	P VAL
1	ł	1	ı			B; cDNA EST yk450d8.5 cm	IIES
1	1		1	- 1		from this gene: cDNA EST	
1	1	ł	- 1	i		yk249a6.5 comes from this	ł
1	1		1	- 1		gene; cDNA EST vk219a2.5	1
1	1		1	ſ		comes from this gene; cDNA	1
l	ľ	1	[- 1		EST yk355e4.5 comes from the	vie
1	i		.	ı		gene; cDNA EST yk224f4.5	
ł	l			- 1		comes fr	1
	ł		j	- 1		>gi 3924881 gnl PID e1354569	.
	ľ	1 .	- 1			from this gene; cDNA EST	´
1		1	- 1	- 1 -	••	yk249a6.5 comes from this	1.
				- 1		gene; cDNA EST yk219a2.5	- 1
ł		Mus musculus	"	- 1		comes from this gene; cDNA	1
ł		Pontin52 mRNA,	- 1			EST yk355e4.5 comes from thi	_
1239	AF10069	4 complete cds		- 1		gene; cDNA EST yk224f4.5	*
		Human primary Al	6e-22		3924779	comes from	1 000
1240	U67824	transcript		- 1		!!!! ALU SUBFAMILY SB	0.35
		Homo sapiens clone	6e-22	_	728832	WARNING ENTRY	6-07
- 1		24686 mRNA	٠			fatty-acid synthase (EC	5e-07
241	AF070636	sequence	2 22	1		2.3.1.85) - Brevibacterium	1
		1	2e-22	-	98710	ammoniagenes	2.5
1		Human gene for Zn-	.	1	•		2.5
- 1		alpha2-glycoprotein	ſ	1			1 1
242	D14034	complete cds	2e-22	1	41070	(Y17832) pol protein [Human	
ı		Human lactase	20-22	╂	4185939	endogenous retrovirus K)	0.29
		phlorizin hydrolase	1	1 .			9.35
243	M61835	(LCT) gene, exon 2.	2e-22	1	72002.	!!!! ALU SUBFAMILY J	1
j			1	╁	728831	WARNING ENTRY	0.006
		Mus musculus		1		RABPHILIN-3A	
		Pontin52 mRNA,	1	l		>gi 477100 pir A48097	
44 /	AF100694	complete cds	6e-23		1350828	rabphilin-3A - bovine	ŀ
		Homo sapiens full		 	220028	>gi 285646 gnl PID d1003285	0.14
45 A	F074555	length insert cDNA	1			(A FORGLES)	
	F074985	YH73H06	8e-24	1 3	170548	(AF056116) unknown [Fugu	1
- [Human mRNA for			.,0340	rubripes]	0.24
6	D14970	protein D123,	1			1	
~	D14878	complete cds	7e-24	<1	NONE>	1	- 1
						<none> (U61955) contains multiple</none>	<none></none>
1	1	.,	' 1		j	region of strong significant	— — — — .
I	ŀ	Human HepG2 3'	ſ			region of strong similarity to	1
7 r	016917	region cDNA, clone	i			C2H2-type zinc fingers	ľ
	1091/	nmd3d07	6e-24	1.3	97345	(PS:PS00028) [Caenorhabditis elegans]	
						cicgans	2.4

├		st Neighbor (BlastN vs	i. Genbank)	Nearest Nei	ghbor (BlastX vs. Non-Redundant I	Protoine)
SE	-				· Consult is Non-Redundant	roteins)
II	ACCESSIO	DN DESCRIPTION	PVALUE	ACCESSION	DESCRIPTION	1
		Human DNA		ACCESSION	DESCRIPTION	P VAL
		sequence from		 		
	1	cosmid L98A6.	- 1	1	1	1
	İ	Huntington's Diseas	se	1		i
	_	Region, chromosom	ne	į.	(AF123462) neurexin III (Home	_
124	8 Z69654	4p16.3.	3e-24	4240566	(sapiens)	1
	1					4.5
	1	Homo sapiens mRN	A	1		j
1249	AB007914	for KIAA0445			(AF095568) amelogenin	l
127	AB00/914	protein, complete co	ls 2e-24	3885949	[Paleosuchus palpebrosus]	3.2
			. [immunodominant microneme	1
	1	Homo sapiens full	1	•	protein Etp100 - Eimeria tenella	ł
	1	length insert cDNA			>gi 2707733 (AF032905)	1
1250	AF088072	clone ZD93D10	2e-24	222001	microneme protein precursor	1
	1	Homo sapiens cAMI	7 - 20-24	323091	Etmic-1 [Eimeria tenella]	0.34
	l	specific				1
	ſ	phosphodiesterase 4/	4			,
	1	variant pde46	1. 1		1	İ
	I .	(PDE4A) gene, exon:	s			
		2 through 13 and	1 1			
		alternative splice] [1	
251	A E060480	exons 3a, 6a, 6b, and	1		!!!! ALU SUBFAMILY SP	
231	AF069489	9a	2e-24	728836	WARNING ENTRY	le-05
252	Y12853	Homo sapiens P2X7 gene, exon 4-8	0.05		!!!! ALU SUBFAMILY J	
	- 12005	Human 28S	9e-25	728831	WARNING ENTRY	le-05
		ribosomal RNA gene,	1 1			
253	M27830	complete cds.	8e-25	-NONE.]	
			00-25	<none></none>	<none></none>	<none></none>
		Homo sapiens	i .			
		mRNA, chromosome	1		1	
ا ہے		1 specific transcript	1			
254	AB007953	KIAA0484	8e-25	<none></none>	<none></none>	<none></none>
	.	H anniana C. C. Dania				ZIONE>
	Ì	H.sapiens CpG DNA,	1			
55		clone 195c8, forward read cpg195c8.ft1a.			(M81959) POU domain protein	ĺ
+		Mus musculus	8e-25	158154	[Drosophila melanogaster]	3.3
ł		Pontin52 mRNA,	1	ļ		
56		complete cds	7e-25	ALONIC		j
T		Mus musculus	76-23	<none></none>	<none> <</none>	NONE>
J		Pontin52 mRNA,	1	ŀ	1	
57		complete eds	7e-25	<none></none>	Along	
		Homo sapiens P2X7			<none></none>	:NONE>
	1.	ene, exon 1 and		j.		1
8		oined CDS	I	1	1	- (

-		st Neighbor (BlastN vs.	. Genbank)	Nearest Ne	ighbor (BlastX vs. Non-Redundant	Dentair = \
- 1	Q.				Single (Single V3: Non-Reddingant	Proteins)
L	DACCESSION	DN DESCRIPTION	P VALUE	ACCESSION	J. DESCRIPTION	1
		Mus musculus Tera		T ACCESSION	DESCRIPTION	P VALUE
		(Tera) mRNA,		 		
12	59 U64033		9e-26	<none></none>		
		Rattus norvegicus		CHOINES	<none></none>	<none></none>
i	1	Rabin3 mRNA.		1	(U19181) Rabin3 [Rattus	1
120	50 U19181	complete cds.	9e-26	624225	norvegicus]	1
-	1				SEL-TO PROTEIN Candida	le-13
	į	1			CDC4 gene (TR:E234056);	İ
1	ı		1		cDNA EST EMBL:D27699	1
1	1	1	ļ.		comes from this gene; cDNA	1
1	1				EST EMBL:D27698 comes	1
	1			٠.	from this gene; cDNA EST	
1	J	Caenorhabditis	1 1		EMBL:D32793 comes from this	
	į	elegans SEL-10 (sel-		•	gene; cDNA EST	
126	1 AF020788	10) mRNA, complete			EMBL:D33271 comes from this	
120	AF020788	cds	9e-26	3915881	gen	7e-32
	1	Cricetulus griseus	1 1			1.052
1	1	mRNA for	1 1			ł ·]
1	ı	Phosphatidylglycerop				/ I
	į.	hosphate synthase,	'i 1		(AB016930)	1 1
1262	AB016930		8e-26	4150400	Phosphatidylglycerophosphate	1 1
		Mus musculus	86-20	4159682	synthase [Cricetulus griseus]	0.045
1	ł	Pontin52 mRNA	1		(Z93385) predicted using	
1263	AF100694	complete cds	3e-26	3878629	Genefinder; Similarity to	
		H.sapiens SOM172	30 30	3070029	B.subtilis GTP-binding protein	2e-10
1264	X91195	mRNA	le-26	<none></none>	1,0712	
		Mus musculus	10.00	410HE>	<none></none>	<none></none>
		Pontin52 mRNA,	1		i	j
1265	AF100694	complete cds	le-26	1360637	(X95995) ENBPI [Vicia sativa]	a .
10//		Human MG21			(L08237) located at OATL1	3.1
1266	L08237	mRNA, partial cds.	1e-26	950411	[Homo sapiens]	9e-09
						96-09
		·			(AL032657) similar to EGF-like	- 1
					domain; cDNA EST yk299a12.3	- 1
		1	ľ		comes from this gene; cDNA	
					EST EMBL:D35398 comes	I
	-		1		from this gene; cDNA EST	- 1
[Mus musculus	i		yk331h6.5 comes from this	[
- 1		Pontin52 mRNA.	ł		gene; cDNA EST yk299a12.5	j
1267		complete cds	0- 22		comes from this gene; cDNA	[
_		Mus musculus	9e-27	3881080	EST yk467g8	0.001
- 1	1	Pontin52 mRNA.	j			
1268		complete cds	8e-27	173130	HYPOTHETICAL PROTEIN	j
		p.tete eas	0E- <u>-</u> /	1731324	>gi 166306	4.0

<u> </u>	Neares	t Neighbor (BlastN vs. C	Genbank)	Nearest Neig	thbor (BlastX vs. Non-Redundant Pr	oteins)
SEC	2				, secondarit I	Otellis)
D	ACCESSIO	N DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	
			T		DESCRIPTION	P VALUE
		H.sapiens DNA for		 		
1		endogenous retroviral	Í	f	(Y12713) Gag polyprotein [Mus	ļ
1269	X89211	like element	8e-27	2065209	musculus]	
1					11.0000100)	0.005
		Homo sapiens cosmid	1	İ		
[1	clone LUCA 15 from		1		ł
1	1	3p21.3, complete		ł	1	
1270	1172166	sequence [Homo			!!!! ALU SUBFAMILY J	
12/0	U73166	sapiens	3e-27	728831	WARNING ENTRY	4e-04
ł		Mouse mRNA for				
1271	D78255	PAP-1, complete cds	3- 07		(D78255) PAP-1 (Mus	•
	278233	Mus musculus	3e-27	1850098	musculus]	2e-10
ļ		Pontin52 mRNA.				
1272	AF100694	complete cds	le-27	2122570	spermatophorin Sp23 - yellow	
			10-27	2133579	mealworm molitor (Z83318) predicted using	0.39
	·	Homo sapiens gene			Genefinder; cDNA EST	
l .		for hippocalcin, exon			yk369e7.5 comes from this gene	
1273	AB015202	2, 3 and complete cds	le-27	3877698	[Caenorhabditis elegans]	0.37
i i		Mus musculus			[Cachemadanis elegans]	0.37
		Pontin52 mRNA,	1		(AF074902) laminin alpha chain	1
1274	AF100694	complete cds	le-27	3328188	[Caenorhabditis elegans]	0.19
		H.sapiens gene for	- 1			
1275	Z29336	Cu/Zn-superoxide			!!!! ALU SUBFAMILY J	ľ
12/3	229330	dismutase Mus musculus	le-27	728831	WARNING ENTRY	6e-05
		Pontin52 mRNA,	1			
1276	AF100694	complete cds	9e-28	2122670	spermatophorin Sp23 - yellow	ļ
		Mus musculus	96-28	2133579	mealworm molitor)	9.2
		Pontin52 mRNA.			gramatanharin S22	
1277	AF100694	complete cds	9e-28	2133579	spermatophorin Sp23 - yellow mealworm molitor]	225.
				2133317	PUTATIVE PRE-MRNA	0.054
ŀ	· .		1		SPLICING FACTOR ATP-	
ł		Homo sapiens mRNA	i		DEPENDENT RNA	
		for ATP-dependent	ı		HELICASE >gi 2275203	
1070		RNA helicase #46,	. 1		(AC002337) RNA helicase	
1278	AB001636	complete cds	4e-28	3913425	isolog [Arabidonsis thaliana]	3e-22
- 1	· [(AC005990) Contains repeated	
J	. 1	İ	- 1	•	region with similarity to	
- 1	1	į	- 1		gb U43627 extensin (atExt1)	
1	l _N	Aus musculus	1		gene from Arabidopsis thaliana.	
	1.	Pontin52 mRNA,	1	ļ	ESTs gb Z34165 and gb Z18788	
1279	1	omplete cds	3e-28		come from this gene.	
			20-20	4056454	[Arabidopsis thaliana]	0.066

	::: Near	est Neighbor (BlastN v	s. Genbank)	Nearest Na	ighbor (Blast Y us NI D	
SE	Q			realest Nei	ighbor (BlastX vs. Non-Redundant F	roteins)
11	D ACCESSI	ON DESCRIPTION	P VALUE	ACCESSION		P VALUE
-					(AC005990) Contains repeated	
- 1	ł		i		region with similarity to	
ĺ	ř			f	gb U43627 extensin (atExt1)	
- 1	ł	Mus musculus	j	1	gene from Arabidopsis thaliana.	ı
- I	1	Pontin52 mRNA,	1	1	ESTs gb Z34165 and gb Z18788	s
128	30 AF10069		1 2 22	1	come from this gene.	ı
	12 1000)	Mus musculus	3e-28	4056454	[Arabidopsis thaliana]	4e-05
- 1	j	Pontin52 mRNA,		J		
128	1 AF10069		1- 20		1	ľ
	1	Mus musculus	le-28	<none></none>	<none></none>	<none></none>
1	1	Pontin52 mRNA,	1	1		
128	2 AF100694	complete cds	10.79			
		Mus musculus	1e-28	<none></none>	<none></none>	<none></none>
i	1 .	Pontin52 mRNA,	, ,			
128	3 AF100694	complete cds	le-28	<none></none>		ĺ
		Mus musculus	1 - 10 20	CHOILES	<none></none>	<none></none>
1		Pontin52 mRNA,				
1284	AF100694		le-28	<none></none>	NONE	
	1	Mus musculus		4101122	<none></none>	<none></none>
1	.1	Pontin52 mRNA,			1	
1285	AF100694	estripiere eus	le-28	<none></none>	<none></none>	ANONTE
1	1	Mus musculus			CHOILES	<none></none>
1286	1510000	Pontin52 mRNA,	1 1			
1280	AF100694	complete cds	le-28	<none></none>	<none></none>	<none></none>
1	ł	Mus	i		PROBABLE INTRON	4.01.122
1	l	Mus musculus Pontin52 mRNA,	1 1	ι	MATURASE liverwort	1
1287	AF100694		1 1		(Marchantia polymorpha)	I I
-	74 100094	complete cds	le-28	140505	chloroplast >gi 11663	3.0
	l	Mus musculus	1 1		PROBABLE INTRON	
] ,		Pontin52 mRNA.	1		MATURASE liverwort	ļ
1288	AF100694	complete cds	1000	140555	(Marchantia polymorpha)	ŀ
		Mus musculus	le-28	140505	chloroplast >gi 1 1663	1.8
		Pontin52 mRNA,] [-			
1289	AF100694	complete cds	le-28	2133579	spermatophorin Sp23 - yellow	
				2133379	mealworm molitor] (AC005990) Contains repeated	0.50
I					region with similarity to	ł
- [1		gb U43627 extensin (atExt1)	1
ŀ				1	gene from Arabidopsis thaliana.	I
		Mus musculus	İ		ESTs gb Z34165 and gb Z18788	[
,,,,,		Pontin52 mRNA,	l l		come from this gene.	
1290	AF100694	complete cds	le-28	4056454	[Arabidopsis thaliana]	0.087
- 1	[Lpois thananaj	0.087
- 1		H.sapiens CpG DNA,	I	ł	HYPOTHETICAL 29.3 KD	1
1291		clone 77b3, forward	1		PROTEIN pseudotsugata	1
/1	Z63029	read cpg77b3.ftla.	1e-28			0.014

	14641	st Neighbor (Blast)	V vs. Genb	ank)	Nearest Ne	ighbor (BlastX vs. Non-Redundant F	
SEQ	· 1				1	I Silvoi (BlastA vs. Non-Redundant F	roteins)
ID	ACCESSI	ON DESCRIPTI	ON P	VALUE	ACCESSION		P VALU
					ļ	DEHYDRIN DHN3	
l	ľ	Mus musculus			1	>gi 100035 pir \$18139 dehydrii	1
1	Í	Pontin52 mRNA				DHN3 - garden pea >gi 20709	1
1292	AF10069		· 1	1. 00		(X63063) pea dehydrin DHN3	1
		· Jeompiete eus		le-28	118588	[Pisum sativum]	0.010
	ŧ					(AC005990) Contains repeated	
	ł					region with similarity to	l
	ſ		j			gb U43627 extensin (atExt1)	İ
		Mus musculus	1			gene from Arabidopsis thaliana.	ĺ
		Pontin52 mRNA	.			ESTs gb Z34165 and gb Z18788	ĺ
1293	AF100694	complete cds		e-28	1056454	come from this gene.	Ī
- 1			- -	J-20	4056454	[Arabidopsis thaliana]	0.007
		1	J			(AC005990) Contains repeated	
1			,		•	region with similarity to	
ł		1				gb U43627 extensin (atExt1)	
I		Mus musculus	}	f		gene from Arabidopsis thaliana.	
		Pontin52 mRNA,		I	,	ESTs gb Z34165 and gb Z18788	
1294	AF100694	complete cds	10	e-28	4056454	come from this gene.	
- 1		Mus musculus			7030434	[Arabidopsis thaliana] LAMININ ALPHA-I CHAIN	0.002
20.5		Pontin52 mRNA,				PRECIESOR	
295	AF100694	complete cds	le	-28	126363	PRECURSOR precursor -	
- 1						(AC005990) Contains repeated	3e-04
- 1			- 1	1		region with similarity to	
- 1			- 1	ſ		gb U43627 extensin (atExt1)	
- 1		h	ļ	- 1		gene from Arabidopsis thaliana.	
- 1		Mus musculus	1			ESTs gb Z34165 and gb Z18788	
296	AF100694	Pontin52 mRNA,		1		come from this gene.	
	11 100094	complete cds	le-	28	4056454	[Arabidopsis thaliana]	le-04
- 1			1			(AC005990) Contains repeated	10-04
- 1				}		region with similarity to	
i				- 1		gb U43627 extensin (atExt1)	ļ
ł	İ	Mus musculus	. .	i		gene from Arabidopsis thaliana.	
- 1		Pontin52 mRNA,	1	1		ESTs gb Z34165 and gb Z18788	į
97 A		complete cds	le-2	,	105615:	come from this gene.	J
T		F.0.0 CO3	16-2		4056454	[Arabidopsis thaliana]	3e-05
	l:	Mus musculus	1	- 1		(AC002131) Strong similarity to	
-	li li	Pontin52 mRNA,	1	- 1		extensin-like protein gb Z34465	ļ
98 A		complete cds	le-2	8	3157027	from Zea mays. [Arabidopsis	l
			1	~ -	3157926	thaliana]	2e-05
	İ			- 1	i.	(AC005990) Contains repeated	
	-		1	J	ľ	region with similarity to	1
				- 1]	gb U43627 extensin (atExt1)	1
1		lus musculus	1	- 1	Į,	gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788	.
	1_				11	じっきょう タウレス 5年 しんき きゅん ふんりつ 10つのでし	1
9 AI		ontin52 mRNA, omplete cds	1	J	E.	come from this gene.	ľ

-	Neare	st Neighbor (BlastN vs	s. Genbank)	Nearest Nei	ghbor (BlastX vs. Non-Redundant P	
SE		1		1	Wilder Vs. Non-Redundant P	roteins)
E	ACCESSIO	DESCRIPTION	P VALUE	ACCESSION		P VAL
		Mus musculus			kinetoplast-associated protein -	
ł	1	Pontin52 mRNA,	Į.	1	Trypanosoma cruzi >gil162142	
130	0 AF100694			1	(M25364) kinetoplast-associated	d
	12 1000)-	Complete cas	le-28	320919	protein	le-0
	ŀ		1		(AC005990) Contains repeated	
	Ĭ	1	ł]	region with similarity to	İ
	1		1]	gb U43627 extensin (atExt1)	l
	1	Mus musculus		Į .	gene from Arabidopsis thaliana.	
		Pontin52 mRNA,	1		ESTs gb Z34165 and gb Z18788	
1301	AF100694				come from this gene.	
	1	complete cas	le-28	4056454	[Arabidopsis thaliana]	9e-08
	1		- [(AC005990) Contains repeated	
	1		1 1		region with similarity to	
	1		1 1		gb U43627 extensin (atExt1)	
	1	Mus musculus			gene from Arabidopsis thaliana.	
	ĺ	Pontin52 mRNA,			ESTs gb Z34165 and gb Z18788	
1302	AF100694	complete cds	1 , 20		come from this gene.	
		Technolote eds	le-28	4056454	[Arabidopsis thaliana]	le-09
			1		(AC005990) Contains repeated	
	ł		1		region with similarity to	
			1		gb U43627 extensin (atExt1)	
		Mus musculus	1		gene from Arabidopsis thaliana.	
		Pontin52 mRNA,	1 1		ESTs gb Z34165 and gb Z18788	
303	AF100694	complete cds	le-28	1056454	come from this gene.	
ı			10.20	4056454	[Arabidopsis thaliana]	9e-10
J					(AC005990) Contains repeated	
- 1			1		region with similarity to	
- 1			ľ		gb U43627 extensin (atExt1)	
- 1		Mus musculus	ſ		gene from Arabidopsis thaliana.	
		Pontin52 mRNA,	i i		ESTs gb Z34165 and gb Z18788	
04		complete cds	le-28	4056454	come from this gene.	
j	•			4020404	[Arabidopsis thaliana] (AC005990) Contains repeated	4e-10
	i	i	I	•	region with similarity to	
ı	- 1	l	- 1		gb U43627 extensin (atExt1)	
I	ĺ	[- 1		gene from Arabidopsis thaliana.	
ı		Mus musculus	1		ESTs gb Z34165 and gb Z18788	
٦.	[1	Pontin52 mRNA,	1	i	come from this gene.	
05	AF100694	omplete cds	le-28	4056454	f A 1 / 1	
	1				(AC005990) Contains repeated	9e-11
- 1	ł		j	. 1	region with similarity to	
	[J	1	gb U43627 extensin (atExt1)	
]	1		l	- 13	gene from Arabidopsis thaliana.	
1		lus musculus	1	li li	ESTs gb Z34165 and gb Z18788	
	ID	ontin52 mRNA,	I	1,	Sole 100 min Rol 7 12 188	
6		omplete cds	ı	10	come from this gene.	L L

-	Neare	st Neighbor (BlastN vs. (Genbank)	Nearest Naio	hhor (Blank)	
SE				THE BEST THEIR	hbor (BlastX vs. Non-Redundant F	roteins)
Щ	ACCESSIO	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
-		Mus musculus				I VALUE
130	AF10000	Pontin52 mRNA.				
130	7 AF100694	complete cds	4e-29	<none></none>	<none></none>	<none></none>
		Homo sapiens cAMP				
130	8 AF079529		4e-29	<none></none>		
		T T T T T T T T T T T T T T T T T T T	40-23	KNONES	<pre><none> CYTOCHROME C OXIDASE</none></pre>	<none></none>
1	ł		ļ	j	POLYPEPTIDE I chain I -	1
1			ł		human mitochondrion (SGC1)	
	1 .		ĺ	f .	>gi 13006 (V00662) cytochrome	
İ	I	1	ĺ		oxidase I [Homo sapiens]	1
	ı	H.sapiens	٠.		>gi 506829 (J01415)	
1309	Young.	mitochondrial DNA,			cytochrome oxidase subunit 1	!
1305	X93334	complete genome	4e-29	116977	[Homo sapiens] sapiens]	3e-09
		Homo sapiens serine				
1	1	protease (Omi)			1	
1310	AF020760	mRNA, complete cds	4- 20	222224	(AF020760) serine protease	
		Xenopus laevis	4e-29	2738915	[Homo sapiens]	8e-12
		mitotic			(1105007) ' '	
1		phosphoprotein 43			(U95097) mitotic	ı
1311	U95097	mRNA, partial cds	4e-29	2072294	phosphoprotein 43 [Xenopus laevis]	
		Homo sapiens		2072274	RENAL TRANSCRIPTION	le-25
	<u> </u>	transcription factor	1		FACTOR KID-1 finger protein	
1312	L32162	mRNA, 5' end.	2e-29	2501706	[Mus musculus]	8e-15
İ	•				(AC005990) Contains repeated	- 00-13
			Į.		region with similarity to	I
					gb U43627 extensin (atExt1)	1
i i		M			gene from Arabidopsis thaliana.	1
		Mus musculus			ESTs gb Z34165 and gb Z18788	
1313	AF100694	Pontin52 mRNA, complete cds			come from this gene.	
10.5	711 100094	complete cas	1e-29	4056454	[Arabidopsis thaliana]	le-04
			- 1		FMRFAMIDE-RELATED	
ŀ		ľ	1		NEUROPEPTIDES	ľ
- 1		Mus musculus	1		PRECURSOR >gi 416208	ľ
	ľ	Pontin52 mRNA,	- 1		(U03137) neuropeptide	1
1314		complete cds	le-29		precursor FMRFamide-related	1.05
J				02043	peptide [Lymnaea stagnalis]	1e-05
		Homo sapiens g16	1	1		[
]		protein (g16) mRNA,	1	i.	(AF069517) RNA binding	
1315	U50839	complete cds	le-29		protein DEF-3 [Homo sapiens]	6e-10

19.4 · 1	Nearest !	Neighbor (BlastN vs. G	enbank)	Nearest Neigh	bor (BlastX vs. Non-Redundant Pr	oteins)
SEQ						
ΙD	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					intercellular adhesion molecule	
					3, ICAM-3=lymphocyte	
					function-associated antigen 1	
i I					counter-receptor homolog	
1316	X69711	H. sapiens mRNA for	5- 20	200256	[human, tonsil, Peptide Partial,	2- 00
1310	X09/11	ICAM-R Homo sapiens	5e-30	299356	[518 aa]	3e-08
		receptor-associated			(AF012108) Amplified in Breast	
1317	AF010227	coactivator 3	5e-30	2331250	Cancer [Homo sapiens]	8e-09
		Homo sapiens full	30_30		Canon (monto saprono)	35 02
		length insert cDNA			(AJ235273) CELL SURFACE	
1318	AF086395	clone ZD75C01	2e-30	3861241	ANTIGEN (sca5)	4.2
			٠.		PHOSPHOGLYCERATE	
i I					KINASE 2.7.2.3) - Pyrococcus	
		Human 28S			woesei >gi 1054832 (X73527)	
		ribosomal RNA gene,			phosphoglycerate kinase	
1319	M27830	complete cds.	2e-30	1730522	[Pyrococcus woesei] RAS-RELATED PROTEIN	3.8
		Mouse GTP-binding			RAS-RELATED PROTEIN RAB-17 Rab17 - mouse	
		protein (Rab17)			(fragment) >gi 297157	
1320		mRNA sequence.	2e-30	464564	(X70804) rab17 [Mus musculus]	9e-11
	1117707	Human DNA	20 30	101501	(Arrest) (as in (incomession)	70
		sequence from clone				,
		U247E12 on	į	,	}	
		chromosome Xq22-]	
		23, complete				
		sequence [Homo			(U93570) putative p150 [Homo	
1321	AL022168	sapiens]	1e-30	2072967	sapiens]	3e-11
1322	X85124	M.musculus pacsin gene	1e-30	2217964	(750708) p52 (Gallius gallius)	1e-34
1322	A03124	gene	16-20	221/304	(Z50798) p52 [Gallus gallus] structural polyprotein -	10-24
	i		ŀ		Venezuelan equine encephalitis	
					virus (strain TRD) >gi 323710	
		Homo sapiens	ļ	·	(J04332) poly-envelope protein	
	İ	phosphoprotein CtBP	ľ		[Venezuelan equine encephalitis	
1323	U37408	mRNA, complete cds	5e-31	74518	virus]	1.1
		Human lens				
İ	,	membrane protein	ł			
1,,,,		(mp19) gene, exon	I	70000	!!!! ALU SUBFAMILY J	7
1324	L04193	11.	2e-31	728831	WARNING ENTRY	7e-07
		Human 28S	ł		1	
1325		ribosomal RNA gene.	6e-32	<none></none>	<none></none>	<none></none>
	MITTIO	Hoosomal KINA gene.	06-34	CHUNES	CHONES	VIAOLIE >

	Nearest	Neighbor (BlastN vs. G	enbank)	Nearest Neigh	bor (BlastX vs. Non-Redundant Pi	roteins)
SEQ						
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Ī			1	1
		Human cAMP-				
		dependent protein				1
İ		kinase type I-alpha				i
1	ĺ	subunit (PRKARIA)				ļ
1326	M33336	mRNA, complete cds	2e-32	<none></none>	<none></none>	<none></none>
]		Human				
		glucocerebrosidase			1	ļ
1,,,,,	702040	pseudogene, complete			glucosylceramidase (EC	1
1327	J03060	cds Human lipid-	2e-32	2144479	3.2.1.45) precursor - human	le-05
		activated protein			· ·	i .
1 .		kinase PRK1 mRNA.			protein kinese (EC 2.7.1.37)	
1328	U33053	complete cds	7e-33	2137689	protein kinase (EC 2.7.1.37) -	1011
1555	233033	complete eds	10-33	213/009	inouse	le-14
		Human elongation			1	1
l i		factor EF-1-alpha				
1 1		gene, complete cds. >				
1		:: dbj E02629 E02629		1		1 '
		DNA of human]
ļ ļ		polypeptide chain				1
1220	•• • • • •	elongation factor-1				<u> </u>
1329	J04617	alpha Homo sapiens (clone	6e-33	<none></none>	<none></none>	<none></none>
		s22i71) mRNA			INTERMEDIATE FILAMENT	
1330	L40396	fragment	6e-33	124235	PROTEIN B protein B - common roundworm	1.00
1330		S.cerevisiae	00-55	124233	common roundworm	1.00
l I	,	chromosome VII			MSPI PROTEIN HOMOLOG	
		reading frame ORF	I		Yeast MSP1 protein (TAT-	
1331		YGR028w	6e-33	1709135	binding homolog 4)	8e-50
		Homo sapiens mRNA	j		(U42471) Wiscott-Aldrich	
,,,,,,		for KIAA0472			Syndrome protein homolog	
1332	AB007941	protein, partial cds	2e-33	1150834	[Mus musculus]	2.0
	l.	Rattus norvegicus	l			
		putative peroxisomal				
		2,4-dienoyl-CoA	J			
		reductase (DCR-			(AF044574) putative	
		AKL) mRNA,			peroxisomal 2,4-dienoyl-CoA	
1333		complete cds	2e-34	4105269	reductase [Rattus norvegicus]	6e-15
		Human mRNA for				
	13	KIAA0101 gene,	- 1		.	
1334	D14657	complete cds	7 e-3 5	<none></none>	<none></none>	<none></none>
1	<u> </u>	, , ,	T		trithorax homolog HTX - human	
1		H.sapiens p63 mRNA	ł		(fragment) homolog=MLL	į
1225		for transmembrane	, , , l		{alternative splicing, clone 14p-	
1335	X69910 [protein	7e-35	2136323	18B}	0.94

· · · · · · · · · · · · · · · · · · ·	Nearest l	Neighbor (BlastN vs. G	enbank)	Nearest Neigh	bor (BlastX vs. Non-Redundant Pr	oteins)
SEQ						
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens				
		tetraspan TM4SF				
		(TSPAN-5) gene,			(AF065389) tetraspan NET-4	
1336	AF053455	complete cds	7e-35	3152703	[Homo sapiens]	1e-25
		D.melanogaster crn				, ,
1337	X58374	mRNA	3e-35	117478	CROOKED NECK PROTEIN	6e-41
		Homo sapiens full			(AF031328) aminoglycoside 6'-	
1338	AF086492	length insert cDNA clone ZD95D11	9e-36	2909809	N-acetyltransferase It	1.9
1338	AI-080492	Cione ZD95D11	36 -30	2909009	14-acetyluansierase it	17
i l		H.sapiens telomeric			·	
		DNA sequence, clone		**		
		12PTEL 120, read				
1339	Z96223	12PTELOO120.seq	3e-36	2408068	(Z99165) hypothetical protein	0.61
l l	,	H.sapiens mRNA for				
		phenylalkylamine			emopamil-binding protein -	
1340	Z37986	binding protein.	1e-36	1362793	human >gi 780263	5e-11
		Human ribosomal			·	
		protein S27 mRNA.				l i
		complete cds. end				
ł l		similar to similar to			1	
i		metallopanstimulin 1				
i i		>::				
		gb AA316327 AA316				•
		327 EST188061 HCC			40S RIBOSOMAL PROTEIN	
		cell line (matastasis to			S27 growth factor-inducible zinc	
		liver in mouse) [[finger protein MPS-1 - human	
		Homo sapiens cDNA			>gi 431319 (L19739)	
1	:	5' end similar to			metallopanstimulin [Homo	
,,,,,	11570.45	similar to	2 . 22	1171014	sapiens] >gi 1373421 (U57847)	, ,
1341	U57847	metallopanstimulin l	3e-37	1171014	ribosomal protein S27 70 KD WD-REPEAT TUMOR-	1.4
		Rattus norvegicus	i.		SPECIFIC ANTIGEN	
		mRNA for 70 kDa			>gi 2505957 gnl PID e353992	
		tumor specific			(Y15054) 70 kD tumor-specific	
1342		antigen, partial	3e-37	3123027	antigen [Rattus norvegicus]	2e-15
						
		Rattus norvegicus				
		serine/threonine	j		(AF084205) serine/threonine	
		protein kinase TAO1			protein kinase TAO1 [Rattus	
1343		mRNA, complete cds	3e-37	3452473	norvegicus]	5e-4"
		R.norvegicus				
		(Sprague Dawley)				
1244		ARL5 mRNA for	12.27	-NONE-	NONE	<none></none>
1344	X78604	ARF-like protein 5	1e-37	<none></none>	<none></none>	<none></none>

-	Nearest l	Neighbor (BlastN vs. G	enbank)	Nearest Neighl	bor (BlastX vs. Non-Redundant Pr	oteins)
SEQ						
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
	· · · · · · · · · · · · · · · · · · ·	Homo sapiens				
		chromosome 22 CpG			,	j
		island DNA, genomic			l	1 1
		Mse l fragment, clone	·		İ	i I
		22CGIB49A3 .				
1345	AJ236644	complete read	1e-37	2239219	(Z97210) hypothetical protein	6e-05
		Human zinc finger			DNA-binding protein - mouse	
1346	U09367	protein ZNF136	4e-39	2137269	>gi 437444	7e-23
1 1		Human DNA				
1		sequence from	·		1	
1 1		cosmid L69F7B,		l	i	
		Huntington's Disease				
1 1		Region, chromosome			(AT 002004)	<u> </u>
1 1		4p16.3 contains			(AL023094) putative cyclase	
	50000	Huntington Disease	2 20	200/010	associated protein CAP	
1347	Z69649	(HD) gene.	3e-39	3096918	[Arabidopsis thaliana]	5.6
		Uomo conione			·	
		Homo sapiens tetraspan NET-4			(AF065389) tetraspan NET-4	
1240	A E045200	mRNA, complete cds	1e-39	3152703	[Homo sapiens]	6e-29
1348	AF065389	Homo sapiens clone	16-39	3132703	[Homo sapiens]	00-27
		23923 mRNA			(U60883) CapC [Bacillus	
1349	AF038172	sequence	le-40	1813464	firmus]	2.8
13.7	711 050172	H.sapiens Fanconi	10 10			
		anaemia group A				
		gene, exons 39, 40,			zinc finger protein - mouse	ł
1350	Z83095	41, 42 and 43	1e-40	2137870	(fragment)	3e-23
		Homo sapiens 17-				
		beta-hydroxysteroid				
[dehydrogenase IV			(AL008730) dJ487J7.1.1	
j i		(HSD17B4) gene,		•	(putative protein dJ487J7.1	
1351	AF057734	exon 16	1e-40	2842416	isoform 1) [Homo sapiens]	6e-61
 		Homo sapiens clone			1	
 		24544 beta-				
l I		dystrobrevin mRNA.			(Y15718) dystrobrevin B DTN-	
1352	AF070567	partial cds	4e-41	3133087	B2 [Homo sapiens]	7e-13
i I		Homo sapiens Arp2/3				
	·	protein complex				
		subunit p16-Arc	Į.			
		(ARC16) mRNA,			ARP2/3 COMPLEX 16 KD	
1252	V £005000	, ·	2e-41	2121747	SUBUNIT	3e-36
1353	AF006088	complete cds M.musculus mRNA	20-41	3121767	SOBOINT	30-30
		of enhancer-trap-			(AF016418) No definition line	
1354	X69942	locus I	6e-42	2291152	found [Caenorhabditis elegans]	6.4
1334	A07742	iocus i	06-45	2271132	fround [Cachornabulus clegans]	

SEQ ID ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION H. sapiens mRNA for beta-catenin 5e-42 1373019 (U28811) cysteine-fibroblast growth fill for KIAA0725 Homo sapiens mRNA for KIAA0725 (AB018268) KIAA0725 (AB018268) KIAA0725 (TSE) gene, exon 9 and complete cds. M84424 and complete cds. 2e-42 NONE> CNONE (U80776) ort; encochimeric protein with the complete conditions and complete cds. (U80776) ort; encochimeric protein with the complete conditions and complete cds. (U28811) cysteine-fibroblast growth fill fill fill fill fill fill fill fil	-rich actor receptor	P VALUE
ID ACCESSION DESCRIPTION P VALUE ACCESSION DESCRIPTION H. sapiens mRNA for beta-catenin 5e-42 1373019 (U28811) cysteine-fibroblast growth file Homo sapiens mRNA for KIAA0725 (AB018268) KIAA for KIAA0725 protein, partial cds 5e-42 3882171 [Homo sapiens] Human cathepsin E (CTSE) gene, exon 9 and complete cds. 2e-42 <none> <none (u80776)="" <none="" control="" control<="" encochimeric="" of="" ort;="" protein="" td="" the="" with=""><td>-rich actor receptor</td><td></td></none></none>	-rich actor receptor	
H.sapiens mRNA for beta-catenin 5e-42 1373019 (U28811) cysteine-fibroblast growth file	-rich actor receptor	
1355 X87838 beta-catenin 5e-42 1373019 fibroblast growth for KIAA0725 (AB018268) KIAA 1356 AB018268 protein, partial cds 5e-42 3882171 [Homo sapiens] Human cathepsin E (CTSE) gene, exon 9 1357 M84424 and complete cds. 2e-42 <none> <none con<="" content="" td="" =""><td>actor receptor</td><td>8e-05</td></none></none>	actor receptor	8e-05
1355 X87838 beta-catenin 5e-42 1373019 fibroblast growth for KIAA0725 (AB018268) KIAA 1356 AB018268 protein, partial cds 5e-42 3882171 [Homo sapiens] Human cathepsin E (CTSE) gene, exon 9 1357 M84424 and complete cds. 2e-42 <none> <none con<="" content="" td="" =""><td>actor receptor</td><td>8e-05</td></none></none>	actor receptor	8e-05
Homo sapiens mRNA for KIAA0725 (AB018268) KIAA 1356 AB018268 protein, partial cds 5e-42 3882171 [Homo sapiens] Human cathepsin E (CTSE) gene, exon 9 1357 M84424 and complete cds. 2e-42 <none <none="" cu80776)="" encochimeric="" ort;="" protein="" td="" w<="" =""><td></td><td></td></none>		
for KIAA0725 protein, partial cds Human cathepsin E (CTSE) gene, exon 9 and complete cds. 2e-42 NONE> (AB018268) KIAA [Homo sapiens] AB018268 (CTSE) gene, exon 9 and complete cds. (U80776) orf; encochimeric protein with the complete conditions and complete conditions are conditions.	\0725 protein	
1356 AB018268 protein, partial cds 5e-42 3882171 [Homo sapiens]	10725 protein	
Human cathepsin E (CTSE) gene, exon 9 1357 M84424 and complete cds. 2e-42 <none> <none (u80776)="" enco<="" ort;="" td=""><td></td><td></td></none></none>		
(CTSE) gene, exon 9 1357 M84424 and complete cds. 2e-42 <none> <none (u80776)="" enco<="" ort;="" td=""><td></td><td>2e-33</td></none></none>		2e-33
1357 M84424 and complete cds. 2e-42 <none> <none (u80776)="" enco<="" ort;="" td=""><td></td><td></td></none></none>		
(U80776) ort; enco		ANONTE
chimeric protein w		<none></none>
1 1 · · · · · · · · · · · · · · · · · ·	_	
Human EST clone domain in N-termin		1
NIB1543 mariner similarity to severa		
transposon Hsmarl human, Drosophila		
orf gene, complete and yeast proteins [
1358 U80776 cds 2e-42 2231380 sapiens]		3e-11
Human G protein		
Golf alpha gene, exon (AF067608) No de	finition line	
1359 U55184 12 and complete cds 2e-42 3165531 found [Caenorhabd	litis elegans]	le-16
Homo sapiens PAC		
clone DJ1152D16		
from Xq23, complete		i
sequence [Homo (AB007407) myelo		
1360 AC005190 sapiens] 6e-43 2978255 protein-2 [Mus mus	sculus	2.3
Homo sapiens mRNA		
for KIAA0741		į į
1361 AB018284 protein, complete cds 5e-43 <none> <none< td=""><td>€></td><td><none></none></td></none<></none>	€>	<none></none>
1301 Abortozo4 protein, complete eus 30 43 Cross		
Homo sapiens mRNA		
for KIAA0565 (AB011137) KIAA	.0565 protein	
1362 AB011137 protein, complete cds 5e-43 3043654 [Homo sapiens]		1e-07
Human set gene,		
1363 M93651 complete cds. 2e-43 <none> <none< td=""><td>≧></td><td><none></none></td></none<></none>	≧>	<none></none>
(U84404) E6-assoc	-	
H.sapiens mRNA for E6-AP/ubiquitin-pr		
RNA polymerase II [Homo sapiens] >g		
elongation factor-like (AF016708) E6-AF		7.2
1364 Z47087 protein. 2e-43 1872514 protein ligase [Hom Drosophila	io sapiens)	7.2
melanogaster pelota PELOTA PROTEII	N >011973224	
(pelo) mRNA. (U27197) pelota [D		
1365 U27197 complete cds 2e-43 1352736 melanogaster]	· * F	1e-46

PCT/US00/18374

75, 75	Nearest N	Neighbor (BlastN vs. G	enbank)	Nearest Neigh	bor (BlastX vs. Non-Redundant Pr	oteins)
SEQ						
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					RRP5 PROTEIN HOMOLOG	
		Human mRNA for			(KIAA0185) hypothetical	
		KIAA0185 gene.			protein YM9959.11C of	
1366	D80007	partial cds	·6e-44	2498864	S.cerevisiae. [Homo sapiens]	6e-09
		Homo sapiens			1	
		secretory carrier			(AF005039) secretory carrier	[
		membrane protein			membrane protein [Homo	1
1367	AF005039	(SCAMP3) mRNA, complete cds	6e-44	2232243	sapiens]	2e-09
1307	AI-003039	R.norvegicus trg	00-44	2232273	(X68101) trg gene product	2007
1368	X68101	mRNA	2e-44	550420	[Rattus norvegicus]	1e-37
		Homo sapiens				
		cyclooxygenase				l . l
		(COX-2) gene,			(U93565) putative p150 [Homo	
1369	AF044206	promoter and exon I	2e-45	2072953	sapiens)	5e-06
ĺ		Homo sapiens			1	
		faciogenital dysplasia				
1270	7.49700	(FGD1) gene, 5' end	0 - 46	AMONTES	NONES	<none></none>
1370	L48708	of intron 17	8e-46	<none></none>	<none></none>	KNONES
					POLYPEPTIDE VIIA-LIVER	
					PRECURSOR	
					>gi 2144370 pir OSHU7L	
					cytochrome-c oxidase (EC	
		Human COX VIIa-L			1.9.3.1) chain VIIa precursor.	
		mRNA for liver-			hepatic - human >gi 30147	
		specific cytochrome c			(X15822) precursor (AA -23 to	
1371	X15822	oxidase (EC 1.9.3.1.)	3e-46	117121	60) [Homo sapiens]	5e-13
		N	1			
		Mus musculus	ł		(U47323) stromal cell protein	
1372	U47323	stromal cell protein mRNA, complete cds	3e-46	1493833	[Mus musculus]	le-48
13/2	U41343	nikava, complete cus	30-40	1773033	HYPOTHETICAL 113.1 KD	10 10
			Ī		PROTEIN T28D9.7 IN	
					CHROMOSOME II >gi 861264	
			J		(U28738) coded for by C.	
			ı		elegans cDNA yk8h5.3; coded	
	İ				for by C. elegans cDNA	
		Homo sapiens	1		yk8h5.5; similar to C. elegans	
		reticulon gene family	1		deg-1 and mec-4 in exon 2	7.
1373	AF059524	protein	7e-47	1731169	[Caenorhabditis elegans]	7.8
		Homo sapiens mRNA for puromycin				
		sensitive				
		aminopeptidase,			(U39123) T cell receptor beta	
1374	1	partial	3e-47	1777519	chain [Homo sapiens]	9.7
13/4	V2135393	Partial	36-47	1111319	Jenam (Fromo Sapiens)	

	Nearest I	Neighbor (BlastN vs. G	enbank)	Nearest Neigh	bor (BlastX vs. Non-Redundant Pr	oteins)
SEQ					1	T
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
						1
		Homo sapiens histone			(U83821) NADH	
]		binding protein			dehydrogenase subunit 3	
1375	M97856	mRNA, complete cds.	3e-47	2645327	[Oryzomys palustris]	5.7
		Human				
1		retinoblastoma-		•	CMP-SIALIC ACID	
		related Rb2/p130			TRANSPORTER CMP-sialic]
		gene, 5' flanking			acid transporter [Cricetulus	
1376	U53220	region and partial cds	3e-47	2499225	griseus]	5.3
		H.sapiens mRNA for			E	3.5
		hepatocyte nuclear			!!!! ALU SUBFAMILY SB	
1377	X87870	factor 4a	1e-47	728832	WARNING ENTRY	7.3
		Mus musculus		•		
	,	proteasome regulator				
1378	AF060195	PA28 beta subunit gene, complete cds	3e-48	478681	limb deformity protein - chicken	0.25
13/8	A1 000193	gene, complete cus	36-46	4/0001	TESTIS SPECIFIC PROTEIN	0.23
					A (ZINC FINGER PROTEIN	
					TSGA) >gi 281040 pir S28499	
		Homo sapiens mRNA			probable zinc finger protein - rat	
l l		for KIAA0742			>gi 57504 (X59993) zinc finger	
1379		protein, partial eds Human endogenous	le-48	3122969	protein	1e-30
1 1		retrovirus clone				
		c5.11, HERV-H	1			
	j	multiply spliced	1			
, [ŀ	subgenomic leader,	ļ		1	
		protease and integrase			1	
		region mRNA, partial			retroviral proteinase-like protein	
1380	U35032	cds	4e-49	88558	- human	6e-05
			. 7	-		
		Homo sapiens				
		mRNA, chromosome I specific transcript	ł			
1381		KIAA0487	le-49	<none></none>	<none></none>	<none></none>
1201	73007930	INTO TO 1	10-47	ZHONE>	ALPHA SCRUIN >gi 633238	ZHONE>
	ł		ľ		(Z38132) scruin [Limulus	
	ŀ	Homo sapiens mRNA			polyphemus]	
- 1	Ì	for KIAA0214	`. [>gi 1093326 prf 2103269A	
1382		protein, complete cds	1e-49	2497944	scrulin [Limulus sp.]	9.7
		Human transcription				
		factor (SC1) gene,				
1383	U25826	complete cds.	4e-50	<none></none>	<none></none>	<none></none>

	Nearest	Neighbor (BlastN vs. C	ienbank)	Nearest Neigh	bor (BlastX vs. Non-Redundant Pr	oteins)
SEO		T	1		Diastr 13. I Ton-Reddinguit 11	T T
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus ATP-	1			Î
		dependent RNA			* -	
1	İ	helicase mRNA,	ļ		(U46690) ATP-dependent RNA	1
1384	U46690	partial cds.	4e-50	1335873	helicase [Mus musculus]	3e-24
		Mus musculus				
		claudin-2 mRNA,	İ		(AF072128) claudin-2 [Mus	
1385	AF072128	complete cds	2e-50	3335184	musculus]	4e-24
		Homo sapiens				
		snRNA activating			·	
		protein complex			1	
		19kDa subunit			(AF093593) snRNA activating	
1		(SNAP19) mRNA,		• •	protein complex 19kDa subunit	
1386	AF093593	complete cds	1e-50	3668416	[Homo sapiens]	0.003
						0.003
		Homo sapiens				
1		monocarboxylate				
	'	transporter				
		homologue MCT6			(X92485) pva1 [Plasmodium	
1387	U79745	mRNA, complete cds	le-50	1177607	vivax	2e-07
		Rattus norvegicus				
		hepatocyte nuclear			(L10409) fork head related	
1388	L09647	factor 3a	1e-50	404764	protein [Mus musculus]	2e-21
	-	Mouse E46 mRNA				
1389	X61506	for E46 protein	4e-51	114909	BRAIN PROTEIN E46	1e-20
! !					LINE-I REVERSE	
		Human debrisoquine	ı		TRANSCRIPTASE	i
i j		4-hydroxylase			HOMOLOG protein	
1390	M33387	(CYP2D8P) and	1e-51	126296	[Nycticebus coucang]	5e-15
1 1		Homo sapiens zinc				
1 1		finger protein (ZPR1)				
1391	AF019767	mRNA, complete cds	4c-52	961507	(D63788) anchor protein, LCM	5.9
- 1	•	.				,
		H.sapiens mRNA for	J.		i	
<u> </u>		phenylalkylamine				
1392	Z37986	binding protein.	2e-52	<none></none>	<none></none>	<none></none>
	1		1		(Z49128) weak similarity with	
1	l				SINR protein (Swiss Prot	
		ļ	i		accession number P06533);	
[1	į	ļ	,	cDNA EST EMBL:T00631	
l	-		i		comes from this gene; cDNA	
J	1	Human MHC class I	Į		EST yk293d10.5 comes from	
		molecule (MICB)	[this gene (Caenorhabditis	
1393	U65416	gene, complete cds	2e-52	3878637	elegans]	8.7

PCT/US00/18374

	Nearest	Neighbor (BlastN vs. G	enbank)	Negrest Mainh	ibor (BlastX vs. Non-Redundant P	
SEO		Treignoor (Diasar Vs. O	Cildair,	TACTICS! IACIBL	iooi (Biasta vs. Non-Redundant Pi	roteins)
ID ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					beta-globin DNA-binding	
1394	Z 57647	H.sapiens CpG DNA, clone 189a6, forward read cpg189a6.ft1a.	2e-52	111187	protein B1, transcription factor PU.1 - mouse >gi 200586 (M32370) PU.1 protein [Mus musculus] >gi 200972 (M38252) transcription factor Pu.1 [Mus musculus]	5.8
1395		Human activated p21cdc42Hs kinase (ack) mRNA.			(AF037260) non-receptor protein tyrosine kinase Ack	
1393	L13738	complete cds.	2e-52	2921447	[Mus musculus]	7e-23
1396	AF042379	Homo sapiens spindle pole body protein spc97 homolog GCP2 mRNA, complete cds	7e-53	2801701	(AF042379) spindle pole body protein spc97 homolog GCP2	
		Homo sapiens RNA polymerase I 40kD subunit mRNA,		2001/01	DNA-DIRECTED RNA POLYMERASE I 40 KD POLYPEPTIDE (RPA40) (RPA39) >gi 2266929 (AF008442) RNA polymerase I subunit hRPA39 [Homo	lc-16
1397		complete cds	6e-53	3914807	sapiens]	4e-19
1398		Homo sapiens cell cycle protein (PA2G4) gene, exons 6 through 13, and complete cds	2e-53	<none></none>	<none></none>	<none></none>
		{VNTR locus DXZ4, hypervariable tandem repeat cluster} [human, Genomic, 2991 nt] > :: gb L07935 HUMVNT RA Homo sapiens microsatellite VNTR			(U38810) CAGR1 [Homo sapiens] >gi 3098420 (AF040945) homeotic regulator homolog MAB21 [Mus	
1399		DNA sequence.	2e-53	1209669	musculus]	4.6
1400	į.	Human mRNA for KIAA0218 gene, complete cds	le-53	3426041	(AC005168) unknown protein [Arabidopsis thaliana]	9.1

PCT/US00/18374

T	Nearest	Neighbor (BlastN vs. G	ienbank)	Negrect Neig	hbor (BlastX vs. Non-Redundant F	
SEQ				14cmest 14clB	Mooi (Diasoc vs. Non-Redundant F	Toteins)
ID	ACCESSION	DESCRIPTION	DVALUE		DESCRIPTION	
—	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
-		Homo sapiens				
	i	chromosome 22 CpG		ľ	1	
1		island DNA, genomic				J
I		Msel fragment, clone		1	(AL034355) putative	ł
	1	22CGIB49E6 .			cytochrome oxidase subunit I	
1401	AJ236682	complete read	7e-54	3928721	[Streptomyces coelicolor]	0.30
						
ł		Homo sapiens				ĺ
	Ī	chromosome 22 CpG			}	1
1	ĺ	island DNA, genomic]
		Mse1 fragment, clone 22CGIB49E6.			(AL034355) putative	
1402	AJ236682	complete read	6e-54	2020721	cytochrome oxidase subunit I	
1	1.5250002	Human histone	06-24	3928721	[Streptomyces coelicolor]	0.28
j	i	(H2A.Z) mRNA,			histone H2A.F, embryonic -	
1403	M37583	complete cds.	6e-54	70711	chicken	2e-16
		Homo sapiens mRNA				20-10
[for putative ATPase.			(AJ009947) putative ATPase	1
1404	AJ009947	partial	6e-54	3550295	[Homo sapiens]	3e-18
ł		B.taurus mRNA for				
1405	V09450	novel cytoplasmic				
1403	Y08459	protein Homo sapiens BC-2	2e-54	<none></none>	<none></none>	<none></none>
		protein mRNA,	ı		(AE042284) BC 2	
1406	AF042384	complete cds	2e-54	2828147	(AF042384) BC-2 protein [Homo sapiens]	2.11
				2020147	[Homo sapiens]	2e-14
			· i			
		Homo sapiens spindle	I		·	1 1
1		pole body protein	I]
		spc97 homolog GCP2	ì		(AF042379) spindle pole body	
1407		mRNA, complete cds	8e-55	2801701	protein spc97 homolog GCP2	2e-17
]		Oryctolagus cuniculus translation	.		<u> </u>	
ļ		initiation factor	1	•		
	1	eIF2C mRNA.	ļ		(AE005355) ********	
1408		complete cds	7e-55	3253159	(AF005355) translation initiation factor eIF2C	3e-53
				5255157	initiation factor en ac	36-33
- 1		Homo sapiens RNA				
		polymerase I subunit			·	i i
	1	nRPA39 mRNA,	ļ		(AF047441) RNA polymerase I	<u> </u>
1409		complete cds	3e-55	3335138	40kD subunit [Homo sapiens]	3e-20
- 1		Homo sapiens RNA	İ			
	1.	oolymerase I 40kD abunit mRNA,	ł		(i
1410		complete cds	3e-55	2225120	(AF047441) RNA polymerase I	2 22
	0 1, 771 10	ompiete eus	26-22	3335138	40kD subunit [Homo sapiens]	3e-20

	Nearest l	Neighbor (BlastN vs. G	enbank)	Nearest Neigh	bor (BlastX vs. Non-Redundant Pr	roteins)
SEQ						
ID	ACCESSION		P VALUE	ACCESSION	DESCRIPTION	P VALUE
ļ		Human mRNA for				ļ
		Rap1B protein > ::				ļ
		emb A08693 A08693				1
1	*****	H.sapiens rap1b			transforming protein rap lb - rat	
1411	X08004	cDNA	2e-55	539995	(strain Copenhagen)	2e-18
		II AID			(AFOIO403) ALB (III	
1412	AF010403	Homo sapiens ALR	2- 55	2358285	(AF010403) ALR [Homo	
1412	AF010403	mRNA, complete cds	2e-55	2338283	sapiens]	le-49
1 :						
		Human tropomodulin			(S52010) orf1 5' of EpoR [mice,	l .
1413	M77016	mRNA, complete cds.	8e-56	. 262249	Peptide, 85 aa] [Mus sp.]	0.027
					- opined as any (inter spr)	1 0.02.
		Homo sapiens mRNA	· [1
		for KIAA0826				
1414	AB020633	protein, partial cds	2e-56	<none></none>	<none></none>	<none></none>
		H.sapiens genomic				
		DNA (chromosome			(U84501) cuticle collagen	
1415	X87489	3; clone NL1243D)	2e-56	1814029	[Caenorhabditis briggsae]	0.038
i f		Homo sapiens				
		KIAA0433 mRNA,			(AB007893) KIAA0433 [Homo	1
1416		partial cds	2e-56	2887437	sapiens]	9e-21
		H.sapiens HZF2	l l	•	(AF054180) hematopoietic cell	
1417		mRNA for zinc finger		22.42000	derived zinc finger protein	
1417		protein H.sapiens mRNA for	1e-56	3342002	[Homo sapiens] INTERFERON	2e-21
		interferon regulatory	ł		REGULATORY FACTOR 3	
1418		factor 3	9e-57	2497442	factor 3 [Homo sapiens]	2e-21
		Homo sapiens nuclear		2431442	Tactor 5 (Florito sapiens)	20-21
		VCP-like protein	i		(U68140) nuclear VCP-like	
1419		NVLp.1	8e-57	2406565	protein NVLp.2 [Homo sapiens]	5e-20
		Human mRNA for			(D79994) similar to ankyrin of	
		KIAA0172 gene,	•		Chromatium vinosum. [Homo	
1420		partial cds	3e-57	1136404	sapiens]	9e-38
	1	Human mRNA for				
Į.		KIAA0344 gene,	1		(AB002342) KIAA0344 [Homo	
1421	AB002342	complete cds	1e-57	2224629	sapiens]	4e-20
į	1	1	- 1			
Į			1			
l	1	Human transaldolase	1			
		mRNA containing	j		(4162150) 5000 00 11010 00 104	
1422		transposable element,	10.57	1652110	(U63159) transaldolase [Mus	2, 20
1422	L19437	complete cds	le-57	1553119	musculus] PROBABLE ATP-	2e-20
- 1			į		DEPENDENT RNA	
	ŀ		1		HELICASE P54 (ONCOGENE	
- 1	1,	Human mRNA for	ļ	•	RCK) (DEAD BOX PROTEIN	
1423		RCK, complete cds	9e-58	129376	6)	le-10
1723	U11334	CCR, complete cus	26-28	1293/0	101	16-10

(7)2-3	Nearest	Neighbor (BlastN vs. 0	Genbank)	Nearest Neigh	hbor (BlastX vs. Non-Redundant Pr	entaine)
SEQ		T		Treatest Preigi	The Chases vs. 1401-Reguldant Fi	T T
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
<u> </u>						
	i e	H.sapiens BDPI				
1	i	mRNA for protein-			(X79568) protein-tyrosine-	ļ
1424	X79568	tyrosine-phosphatase	9e-58	1871531	phosphatase	le-22
			Ĭ			
i	[H.sapiens BDP1			•	[
1,406	1470.540	mRNA for protein-	1]	(X79568) protein-tyrosine-	
1425	X79568	tyrosine-phosphatase	9e-58	1871531	phosphatase	9e-23
İ		Homo sapiens HKE1.5 mRNA for			1	
1			ļ	1		
1426	AB012295	GDS-related protein,	7 50			
1420	AB012293	complete cds	7e-58	2648021	(Z97184) RGL2 [Homo sapiens]	9e-19
ı	l	Homo sapiens full			glutamine (Q)-rich factor 1,	
1	l	length insert cDNA			QRF-1 - mouse factor 1, QRF-1	
1427	AF086040	clone YX52E07	le-58	542222	[mice, B-cell leukemia, BCL1,	
	14 000040	Homo sapiens ca xi	. 16-36	543222	Peptide Partial, 84 aa]	3e-36
		mRNA for carbonic				
		anhydrase-related	1			
1		protein XI, complete			· ·	
1428	AB018195	cds	4e-59	<none></none>	<none></none>	<none></none>
		Mus musculus IRE1			- CHOILE	CHORES
		(Ire1) mRNA,			(AF071777) IRE1 [Mus	
1429	AF071777	complete cds	4e-59	3766209	musculus]	7e-28
			,			
l I		Homo sapiens mRNA			1	I
		for SH3 binding				i
1420		protein, complete cds,			1	ď
1430		clone:RES4-23A	3e-59	<none></none>	<none></none>	<none></none>
		Homo sapiens clone				
1431		23923 mRNA	2 60		(Z98551) MAL3P6.11	
1431		sequence Human DNA	3e-59	3758855	[Plasmodium falciparum]	1.3
1 1		sequence from phage	· · · · · · · · · · · · · · · · · · ·			
!!		pTEL from a contig			ľ	- 1
ŀ		from the tip of the	i	•		
İ		short arm of	1			
	Į,	chromosome 16,	1		ļ·	i
		spanning 2Mb of	ł		RIBONUCLEOPROTEIN	
		6p13.3 Contains	1		RB97D ribonucleoprotein	j
1432	Z84812	ESTs	le-59	400927	[Drosophila melanogaster]	2.5
		luman laminin-	[
- 1	1	pinding protein gene.	. [İ		
- 1		partial cds, and E2			l l	J
- 1		mall nucleolar RNA	ł	ļ		ł
]		ene, complete			·	
1433	U36484 s	equence	1e-59	226005	protein 40kD [Mus musculus]	7e-05

	Nearest	Neighbor (BlastN vs. C	Genbank)	Nearest Neig	hbor (BlastX vs. Non-Redundant P	roteins)
SEQ						T
ΙD	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
	<u> </u>				DUAL SPECIFICITY	1
		1			MITOGEN-ACTIVATED	<u> </u>
1	1		ļ		PROTEIN KINASE KINASE 2	
	l	Homosapiens ERK			(MAP KINASE KINASE 2)	1
1	1	activator kinase			(MAPKK 2) kinase type 2	
1434	L11285	(MEK2) mRNA.	le-59	2499630	[Gallus gallus]	3e-21
1	ĺ	Homo sapiens full				
1		length insert cDNA		·	(AC005239) F23149_1 [Homo	1
1435	AF086555	clone ZE14E04	4e-60	3287674	sapiens]	2e-04
1	1	Human (clone				
1		pHAIV2-12) alpha-2			(X05610) alpha (2) chain	1 .
1436	M24766	collagen type IV	4e-60	29551	[Homo sapiens]	6e-15
1	1	H.sapiens mki67a	٠.		ANTIGEN KI-67	
1	Ī	mRNA (long type)			>gi 539555 pir A48666 cell	[
		for antigen of			proliferation antigen Ki-67, long	
1437	X65550	monoclonal antibody			form - human Ki-67 [Homo	
143/	A03330	Ki-67	4e-60	1170654	sapiens]	3e-15
1		Human calmodulin			(X05949) Calmodulin (AA 2 -	1
1438	M27319	mRNA, complete cds.	4e-60	1246461	59) (449 is 1st base in codon)	
1450	1412/319	mikiva, complete cus.	46-00	1345451	[Drosophila melanogaster]	7e-20
		Homo sapiens mRNA				i
		for transducin (beta)	ĺ		(X06172) put. 134 kD protein	
1439	Y12781	like I protein	3e-60	62133	(AA 1 - 1187); put. replicase	7.4
		Human mRNA for	30.00	02133	(AA 1 - 1187); put. repricase	7.4
		KIAA0385 gene.			,	
1440	AB002383	complete cds	1e-60 .	1001548	(D64000) hypothetical protein	4.4
		Homo sapiens clone			(20 (00) nypemeneur protein	7.7
		24732 unknown	[(AF070614) unknown [Homo	
1441	AF070614	mRNA, partial cds	2e-61	3283879	sapiens	3e-17
I					MICROTUBULE-	
		Human mRNA for	1		ASSOCIATED PROTEIN 4	
		KIAA0328 gene,			microtubule-associated protein-	_
1442		partial cds	6e-62	547891	U [Bos taurus]	5.6
j	4	Homo sapiens full				
, ,]		length insert cDNA				
1443	AF086471	clone ZD88A01	5e-62	<none></none>	<none></none>	<none></none>
	ł		ł		DINADBOANDENAL BROBE	
ļ	ļ		- 1		DIHYDROXYPHENYLPROPI	
- 1	1	. 1			ONATE 1,2-DIOXYGENASE	·
i	1	1	i		>gi 1657544 (U73857) similar	1
1	ĺ	1	1		to mcpl gene (catechol 2.3-	
- 1	ĺ		1		dioxygenase) of A. eutrophus 3-	1
- 1			1		(2,3-	1
- 1	,	Human mRNA for	ľ		dihydroxyphenylpropionate)1, 2-	l
- 1	1	KIAA0313 gene,	ļ		dioxygenase 2.3-	į
1444		complete cds	2e-62	2506257	dihydroxyphenylpropionate 1,2-	, l
		ompicie cus	20-02	2506357	dioxygenase	3.4

	Nearest	Neighbor (BlastN vs. C	Jenhank)	Nac N	bhos (BlassY Y	
SEQ		Table (Diasit 43. C	Zenounk)	inearest ineig	hbor (BlastX vs. Non-Redundant Pr	oteins)
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
	 					
İ	İ	Xenopus laevis				
1445	A F0 (0707	notchless (nle)			(AF069737) notchless [Xenopus	
1443	AF069737	mRNA, complete cds	2e-62	3687833	[aevis]	1e-55
J	i	Homo sapiens nuclear	ļ		nuclear receptor co-repressor N-	
	i	receptor co-repressor		ŀ	CoR - mouse musculus]	
1	ĺ	N-CoR mRNA,			>gi 1583865 prf 2121436A	
1446	AF044209	complete cds	5.63	2127602	thyroid hormone receptor co-	
1.770	711 044209	complete cus	5e-63	2137603	repressor [Mus musculus]	2e-47
		Human aryl			1	
1		hydrocarbon receptor			1	
ļ		nuclear translocator			(AF001207)	
	ļ	(ARNT) mRNA.			(AF001307) aryl hydrocarbon	
1447	M69238	complete cds.	2e-63	2702319	receptor nuclear translocator;	
			20-05	2702319	Arnt [Homo sapiens]	5e-19
		ļ !			KINASE ALPHA	Ī
1					REGULATORY CHAIN.	Ĭ
		ļ	J		LIVER ISOFORM	
1 1					(PHOSPHORYLASE KINASE	ł
		ļ	i		ALPHA L SUBUNIT)	
1 1					>gi 663010 (X80497)	
1 1			!		phosphorylase kinase	ľ
		H.sapiens PHKLA			phosphorylase kinase alpha	
1448	X80497	mRNA	2e-63	1170685	subunit [Homo sapiens]	5e-22
		Homo sapiens			(AF031141) ubiquitin	30
[]	_	ubiquitin conjugating	!		conjugating enzyme [Homo	1
1449	AF031141	епzуте	2e-63	2623260	sapiens	1e-23
	ſ		1		PROBABLE ATP-	1
l	j				DEPENDENT RNA	1
j	ļ	i			HELICASE P47	1
1	1		- 1	•	>gi 2135840 pir 137201 nuclear	ļ
ŀ	1,	U anniana P a Tr			RNA helicase (DEAD family)	- 1
- 1		H.sapiens BAT1	i		BATI - human >gi 587146	1
1450	_	mRNA for nuclear			(Z37166) nuclear RNA helicase	
4730	Z37166	RNA helicase	6e-64	2500529	(DEAD family) [Homo sapiens]	9e-24
j		nelix zipper protein	İ	1		
j		max) mRNA,	ł		j	ł
ı		complete cds. > ::			i	ŀ
- 1		36 141138 141138	- 1		1	J
- 1		Sequence 1 from	1		j	
- 1		patent US 5624818 >	1			1
1		gb I77062 I77062	Ì			
Į.		sequence 1 from	- 1	į	No. 12 diamental and a second	i
1451	L L	atent US 5693487	5e-64		Myc-binding factor Max, short	
	10.2.0		36-04	88175	form - human	8e-22

PCT/US00/18374

5	Nearest	Neighbor (BlastN vs. C	enbank)	Negract Maial	hhor (PlaceV va. Nr. D	
SEQ		Elloot (Diasut vs. C		i venest iveigi	hbor (BlastX vs. Non-Redundant P	roteins)
ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
<u> </u>					PROCOLLAGEN-LYSINE.2-	T
1	ł	Homo sapiens lysyl			OXOGLUTARATE 5-	1
j	l	hydroxylase (partial			DIOXYGENASE	1
1	l	clone 2.2 Kb LH)	ļ		PRECURSOR (LYSYL	1
1,450	1,000,00	RNA, complete	}		HYDROXYLASE) lysyl	ĺ
1452	M98252	mature peptide.	2e-64	400205	hydroxylase [Homo sapiens]	7e-22
1	ł	<u>[</u>			OVIDÚCT-SPECIFIC	
ł	Î	Human oviductal			GLYCOPROTEIN	1
1	ł	glycoprotein mRNA,			PRECURSOR (OVIDUCTAL	
1453	U09550	complete cds.	0- 65	2402676	GLYCOPROTEIN)	1 _ 1
1.133	009330	complete cus.	8e-65	2493676	(OVIDUCTIN) resiniteratoxin-binding protein	2e-11
1					RBP-26, cytosolic - rat	
1			• •	*	>gi 311660 (X67877) cytosolic	
				•	resiniferatoxin binding protein	[.]
		R.norvegicus mRNA			RBP-26 [Rattus norvegicus]	j l
		for cytosolic			>gi 1093373 prf 2103310A	, ·
1 1		resiniferatoxin-	1		resiniferatoxin-binding protein	
1454	X67877	binding protein	7e-65	423664	[Rattus norvegicus]	2e-40
					[Addies not regions]	20-40
1 1		Homo sapiens mRNA			1	1
		for KIAA0711	Ì		glutamine/glutamic acid-rich	
1455	AB018254	protein, complete cds	6e-65	92298	protein	0.98
i i		Human 40-kDa				
1 1		keratin intermediate	j			
امدرا	100.00	filament precursor			keratin 19, type I, cytoskeletal -	
1456	J03607	gene.	3e-65	1070608	human sapiens]	4e-07
]]		Human gamma-	· [
		glutamyl carboxylase			i	
1457		gene, complete cds	2e-65	NONE		
1.57	003070	gene, complete cus	26-63	<none></none>	<none></none>	<none></none>
			i		DEHYDROGENASE (NAD),	
1	ĺ		1	•	MITOCHONDRIAL SUBUNIT	1
	ł		j		ALPHA PRECURSOR	ł
			- 1		(ISOCITRIC	
	·		1		DEHYDROGENASE) (NAD+-	
	_ I	Human NAD(H)-	j		SPECIFIC ICDH)	
1		specific isocitrate	j	!	dehydrogenase alpha chain	I
- 1		lehydrogenase alpha	ı		precursor - human >gi 706839	ł
]		ubunit precursor	ł		subunit precursor [Homo	
1458	U07681 r	nRNA, complete cds.	2e-65	1708399	sapiens]	4e-26
i		luman zinc tinger	T			
- 1		protein (LD5-1) gene.	į.			
1450		xons 4, 5 and 6, and			(U57796) zinc finger protein	
1459	U88080 c	omplete cds	2e-65	1373394	[Homo sapiens] >gi 2306773	2e-39

1.76	Nearest	Neighbor (BlastN vs. C	enhank)	Negrace Neighbor (Place V. vs. Non-Dadus Lace Davis)				
		Treignor (Blashy Vs. C	Jenoank)	Nearest Neig	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEQ		D 5000 0000	1	ł				
10	ACCESSION	DESCRIPTION	PVALUE	ACCESSION	DESCRIPTION	P VALUE		
	 				tensin - chicken (fragment)			
1		Gallus domesticus	l		>gi 63805 (Z18529) tensin			
1,460		tensin mRNA			[Gallus gallus] >gi 212755	ĺ		
1460	M96625	sequence.	3e-66	2134419	(L06662) tensin [Gallus gallus]	1e-51		
1	l) /	l i					
1		Mus musculus myelin				Ì		
1	1	gene expression			(U13262) myelin gene			
1461	U13262	factor (MEF-2)	. ~~		expression factor [Mus	1		
1401	013202	mRNA, partial cds. Mus musculus Tera	1e-70	536926	musculus]	9e-42		
		(Tera) mRNA,			i			
1462	U64033	complete cds	52.72	1675505	(TIC 1000) TO CO.			
1.402	004033	M.musculus mRNA	5e-72	1575505	(U64033) Tera [Mus musculus]	9c-34		
1463	X78989	for testin	6e-74	1251010	TESTIN 2 (TES2)			
1,00	17 0707	Mus musculus Tera	0e-74	1351218	[CONTAINS: TESTIN I	8e-31		
J		(Tera) mRNA,						
1464	U64033	complete cds	2e-74	1575505	(I)(4022) T (I) (
	001033	complete cus	26-74	1575505	(U64033) Tera [Mus musculus]	5e-37		
1		Canis familiaris UDP			1			
1		N-acetylglucosamine			(AF057365) UDP N-			
li		transporter mRNA.	1		acetylglucosamine transporter			
1465	AF057365	complete cds	9e-79	3298605	[Canis familiaris]	0-10		
		Rattus norvegicus		3270003	[Cams tammaris]	9e-10		
		mRNA for coronin-	l l		(AJ006064) coronin-like protein			
1466	AJ006064	like protein	le-82	3757680	[Rattus norvegicus]	3e-62		
		Macaca fascicularis			[Tiding hor regions]	30-02		
		UDP-	Į					
		glucuronosyltransfera			KARYOGAMY PROTEIN			
	i	se mRNA, complete			KAR4 yeast (Saccharomyces			
1467		cds	4e-89	140396	cerevisiae)	1e-08		
		Mouse Hox2.3			HOMEOBOX PROTEIN HOX-			
1468	X06762	mRNA	3e-92	123255	B7 (HOX-2C)	9e-23		
į	7		. 1					
1		Cricetulus griseus	i		·			
1		mRNA for	ĺ					
		Phosphatidylglycerop	i		(AB016930)	j		
		nosphate synthase,	1		Phosphatidylglycerophosphate	İ		
1469	AB016930	complete cds	5e-94	4159682	synthase [Cricetulus griseus]	7e-34		
- 1					SER/THR-RICH PROTEIN			
- 1	.	, ,,	į	ı	TIO IN DGCR REGION	1		
1470		M.musculus T10	[>gi 480900 pir S37488 gene	1		
14/0	X74504 r	nRNA	7e-97	1711658	T10 protein - mouse	3e-59		

-	Neares	t Neighbor (BlastN vs.	Genback)	Non N	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEC		A THEISHOOF (Blastit Vs.	Genoank)	Nearest Neig	hbor (BlastX vs. Non-Redundant P	roteins)		
ID	~	N DESCRIPTION	 	.]		1		
<u> </u>	ACCESSIO	N DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE		
	- 		 -		OBIQUITIN-CONJUGATING			
1	1		1		CURIOUTING PROTEIN			
i	ı				(UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN	1		
1	1		İ		CARRIER PROTEIN)			
		1	Į	1 .	(E2(17)KB 3)	ł		
1	ł	1	1		>gi 1085588 pir \$53358	ľ		
			1	İ	ubiquitin conjugating enzyme	ł		
J	1		1 -	j	(E217kB) - rat >gi 595666	1		
ł	I	Rattus norvegicus	İ	}	(U13175) ubiquitin conjugating			
1		clone ubc 10a	1	ľ	enzyme [Rattus norvegicus]			
1	1	ubiquitin conjugating	ł	'	norvegicus] >gi 1145691			
1471	U13175	enzyme (E217kB)		ł	(U39318) UbcH5C [Homo]		
13/1	013173	mRNA, complete cds h-lamp-2=lysosome-	3e-98	1351345	sapiens]	5e-05		
}		associated membrane						
1	l	protein-2 protein-2b	1		ì	İ		
i	1	(LAMP2) mRNA,	İ		į .	İ		
1	ľ	alternatively spliced	Ì			ľ		
ł		form h-lamp-2b,			1	i		
1472	S79873	complete cds.	e-119	<none></none>	<none></none>	<none></none>		
	[D . DV . 5			·			
1473	D13623	Rat mRNA for p34			ribosome-binding protein p34 -	1		
14/3	D13023	protein, complete cds	e-112	480379	rat sp.]	2e-05		
1		Mus musculus mRNA			}	1		
		for 49 kDa zinc finger		•	(AB012367) (0 1-D			
1474	AB013357	protein, complete cds	e-136	4153886	(AB013357) 49 kDa zinc finger	5e-08		
				122200	protein	36-08		
		Cricetulus griseus	ı			1		
	j	mRNA for	ſ		.	- 1		
		Phosphatidylglycerop	Į.		(AB016930)	l		
1475		hosphate synthase, complete cds	1		Phosphatidylglycerophosphate			
14/3	AB010930	complete cas	e-117	4159682	synthase [Cricetulus griseus]	4c-32		
	ſ	Rattus norvegicus	ļ		TRANSLATION INITIATION]		
		initiation factor eIF-	1	j	FACTOR EIF-2B GAMMA			
		2B gamma subunit	i		SUBUNIT (EIF-2B GDP-GTP			
1		(eIF-2B gamma)	İ		EXCHANGE FACTOR)	1		
1476	U38253	mRNA, complete cds	e-103		subunit [Rattus norvegicus]	3e-42		

	Neares	t Neighbor (BlastN vs.	Genbank)	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)				
SE		Total (Diage vo.	T	ivearest iveig	Nearest Neighbor (BlastA Vs. Non-Redundant Proteins)			
ID		N DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE		
-					(H2 20)			
					(H3.3Q) histone H3.3 - fruit fly- (Drosophila melanogaster) histone H3.3B - chicken >gi 2119023 pir S61218 histone H3.3 - fruit fly (Drosophila hydei) 1-136) [Oryctolagus cuniculus] >gi 8046 (X53822) Histone H3.3Q gene product [Drosophila melanogaster] >gi 51198 gallus] >gi 161190 (M17876) histone H3 [Spisula solidissima] >gi 211853 (M11393) histone 3.3 [Gallus gallus] >gi 306848 (M11354)			
1477		R.norvegicus mRNA for histone H3.3 Rattus norvegicus rsec8 mRNA, partial	e-117 e-108	122075 2143962	H3.3 histone [Homo sapiens] melanogaster] >gi 963031 (X81205) histone H3.3 H3.3A variant [Drosophila melanogaster] musculus] rsec8 - rat (fragment) >gi 1019441 (U32498) rsec8 [Rattus norvegicus]	le-45		
1479	U41736	Mus musculus ancient ubiquitous 46 kDa protein AUP1 precursor (Aup1) mRNA, complete cds	e-146	1517822	(U41736) ancient ubiquitous 46 kDa protein AUP46 precursor [Mus musculus]	7e-48 5e-49		
1480	AF041338	Bos taurus vacuolar proton pump subunit SFD alpha isoform (SFD) mRNA, complete cds	e-119	2895578	(AF041338) vacuolar proton pump subunit SFD alpha isoform [Bos taurus]	3e-49		
1481		Mus musculus NSDI protein mRNA, complete cds	e-121	3329465	(AF064553) NSD1 protein [Mus musculus]	2e-50		
1482	AB000517	Rattus sp. mRNA for CDP-diacylglycerol synthase, complete cds	e-146	1517822	(U41736) ancient ubiquitous 46 kDa protein AUP46 precursor [Mus musculus]	2e-51		
1483		Mouse mRNA for Dhm1 protein, complete cds	e-118		mouse Dhm1 protein - mouse musculus]	6e-54		

	Neares	t Neighbor (BlastN vs.	Genbank)	Nearest Mais	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEC			1	Acarest Neig	mbor (BlastX vs. Non-Redundant P	roteins)		
B	-		P VALUE	ACCESSION	DESCRIPTION	P VALUE		
1.10		M.domesticus MD6			CDC4 repeat unit-containing	1		
1484	X54352	mRNA	e-139	1085499	protein - mouse	1e-55		
			·		PROTEIN N-TERMINAL ASPARAGINE AMIDOHYDROLASE (PROTEIN NH2-TERMINAL ASPARAGINE DEAMIDASE) (NTN-AMIDASE) (PNAD) (PROTEIN NH2-TERMINAL			
1485	U57692	Mus musculus N- terminal asparagine amidohydrolase (Ntan1) mRNA, complete cds	e-118	2498797	ASPARAGINE AMIDOHYDROLASE) (PNAA) >gi 1373365 (U57691) N-terminal asparagine amidohydrolase [Mus musculus] amidohydrolase [Mus musculus]	5e-57		
1486	X80169	M.musculus mRNA for 200 kD protein	e-119	1717793	PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR) >gi 1083553 pir A55117 tsg24	9e-58		
1487		Mus musculus N- terminal asparagine amidohydrolase (Ntanl) mRNA, complete cds	e-120	2498797	PROTEIN N-TERMINAL ASPARAGINE AMIDOHYDROLASE (PROTEIN NH2-TERMINAL ASPARAGINE DEAMIDASE) (NTN-AMIDASE) (PNAD) (PROTEIN NH2-TERMINAL ASPARAGINE AMIDOHYDROLASE) (PNAA) > gi 1373365 (U57691) N-terminal asparagine amidohydrolase [Mus musculus] amidohydrolase [Mus musculus]	8e-58		
1488	U08215	Mus musculus Hsp70- related NST-1 (hsr.1) nRNA, complete cds.	e-109	473407	(U08215) NST-1 [Mus musculus]	7ė-58		
1489		Mouse mRNA for Ray, complete cds	e-110	1944389	(D85926) Ray [Mus musculus]	2e-58		
1490	e n	Rattus norvegicus lihydroxypolyprenylb nzoate nethyltransferase nRNA, complete cds	e-123	·	(L20427) dihydroxypolyprenylbenzoate methyltransferase dihydroxypolyprenylbenzoate methyltransferase [Rattus			
491	N	1.musculus mRNA			norvegicus) (X56044) protein Htf9C [Mus	4e-59		
771	X56044 f	or protein Htf9C	e-121		musculus]	le-60		

	Nearest	Neighbor (BlastN vs. G	enbank)	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
CEO	- ivearest	Telghoor (Blastit Vs. O	I I	Nearest Neignbor (BlastX vs. Non-Redundant Proteins)			
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
					PROTO-ONCOGENE		
1.					TYROSINE-PROTEIN		
1					KINASE FYN (P59-FYN)		
1		p59tyn(T)=OKT3-			>gi 420217 pir A44991 protein-		
1		induced calcium		Í	tyrosine kinase (EC 2.7.1.112)	l	
1492	S74774	influx regulator	e-163	729896	fyn - mouse	8e-63	
1		Mus musculus BUB2-					
		like protein 1				İ	
		(HBLPI) mRNA,			(U88873) BUB2-like protein I]	
1493	U88873	complete cds	e-123	4099611	[Mus musculus]	le-63	
		Cricetulus griseus HT					
1		protein mRNA,	į		(U48852) HT protein		
1494	U48852	complete cds.	e-117	1216486	[Cricetulus griseus]	7e-64	
		Rattus norvegicus					
1.405	1 F000 6 6 F	rexo70 mRNA,			(AF032667) rexo70 [Rattus		
1495	AF032667	complete cds	e-142	2827160	norvegicus]	5e-66	
1					PHOSPHATIDYLSERINE		
1 1					DECARBOXYLASE		
1 1		Chinese hamster			PROENZYME		
! !					>gi 109423 pir A38732		
1 1		phosphatidyIserine decarboxylase			phosphatidylserine		
1496	M62722	-	- 114	110010	decarboxylase (EC 4.1.1.65) -	2 (2	
1470	1/102/22	mRNA, 3' end.	e-114	118910	Chinese hamster (fragment)	2e-67	
1 1		Mus musculus fatty		•	(AF072758) fatty acid transport		
		acid transport protein		•	protein 3; FATP3 [Mus		
1497		3 mRNA, partial cds	e-130	3335567	musculus]	le-67	
		J Hadrid Quarter Cus		333301	Illusculus	16-07	
] [Rattus norvegicus	İ				
l		mRNA for atypical	, [(AB005549) atypical PKC		
		PKC specific binding	1		specific binding protein [Rattus		
1498		protein, complete cds	e-113	3868778	norvegicus]	2e-69	
		Mus musculus					
]	·	homeobox protein	ı				
		Meis3 mRNA,			HOMEOBOX PROTEIN		
1499		complete cds	e-143	3024124	MEIS3	6e-72	
	· ·	Mus musculus SKD3			SKD3 PROTEIN SKD3 [Mus		
1500		mRNA, complete cds.	e-142	2493735	musculus]	1e-72	
		Mus musculus					
		muskelin mRNA,	ĺ		(U72194) muskelin [Mus		
1501	U72194	complete cds	e-148	3493462	musculus]	2e-74	
					PROTEIN TSG24 (MEIOTIC		
			- 1		CHECK POINT		
1		M.musculus mRNA	İ		REGULATOR)		
1502	X80169	or 200 kD protein	e-155	1717793	>gi 1083553 pir A55117 tsg24	3e-77_	

	Nearest l	Neighbor (BlastN vs. C	ienbank)	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE	
		Mus musculus					
1503	U72194	muskelin mRNA, complete cds	e-154	3493462	(U72194) muskelin [Mus musculus]	2e-78	
1504		Cricetulus griseus mRNA for Zn finger factor	e-146	3150148	(Y12836) Zn finger factor [Cricetulus griseus]	3e-83	

Table 5

SEQ ID	Start	Stop	Score	Direction	Description
29	295	421	5872	For	mkk like kinases
30	31	182	3943	For	Basic region plus leucine zipper transcription factors
31	298	397	5625	For	mkk like kinases
186	175	395	7660	For	SH2 Domain
187	358	432	4320	For	Ank repeat
196	37	322	6049	For	mkk like kinases
234	23	121	4607	For	SH3 Domain
308	110	172	4150	For	Zinc finger, C2H2 type
410	42	191	4036	For	Basic region plus leucine zipper transcription factors
431	71	428	5538	Rev	ATPases Associated with Various Cellular Activities
552	116	288	3930	Rev	Basic region plus leucine zipper transcription factors
639	157	561	5797	For	ATPases Associated with Various Cellular Activities
746	209	427	5379	For	Fibronectin type III domain
768	116	288	3930	For	Basic region plus leucine zipper transcription factors
807	339	392	3620	For	Zinc finger, C2H2 type
820	341	406	2930	Rev	EF-hand
822	108	262	4179	For	Basic region plus leucine zipper transcription factors
836	158	353	4430	For	Basic region plus leucine zipper transcription factors
1157	41	444	5279	Rev	protein kinase
1192	186	416	5469	For	Fibronectin type III domain
1268	238	315	3540	For	Ank repeat
1269	79	240	11640	For	LIM domain containing proteins
1288	73	234	3953	For	Basic region plus leucine zipper transcription factors

SEQ ID	Start	Stop	Score	Direction	Description
1309	248	404	8226	for	LIM domain containing proteins
1324	294	356	4690	for	Zinc finger, C2H2 type
1325	1	234	8981	for	C2 domain (prot. kinase C like)
1336	66	164	6390	for	WD domain, G-beta repeats
1360	222	377	8686	for	LIM domain containing proteins
1365	69	257	5221	for	Basic region plus leucine zipper transcription factors
1380	42	140	7130	for	WD domain, G-beta repeats
1386	243	398	8736	for	LIM domain containing proteins
1410	222	350	10553	for	Trypsin
1417	8	354	6073	for	Protein Tyrosine Phosphatase
1454	49	209	3996	for	Basic region plus leucine zipper transcription factors
1464	4	180	4978	for	RNA recognition motif. (aka RRM, RBD, or RNP domain)
1478	54	437	5176	for	protein kinase
1496	241	520	3929	for	Helicases conserved C-terminal domain
1496	40	612	5187	for	protein kinase
1503	154	216	4870	for	Zinc finger, C2H2 type
1514	2	252	4662	for	RNA recognition motif. (aka RRM, RBD, or RNP domain)
1527	156	212	3520	for	Zinc finger, C2H2 type
1538	9	635	11087	for	wnt family of developmental signaling proteins
1540	289	471	4107	for	Basic region plus leucine zipper transcription factors
1549	200	391	4118	for	Basic region plus leucine zipper transcription factors
1556	163	354	3958	for	Basic region plus leucine zipper transcription factors
1557	207	398	4038	for	Basic region plus leucine zipper transcription factors
1563	107	298	3978	for	Basic region plus leucine zipper transcription factors

SEQ ID	Start	Stop	Score	Direction	Description
1622	180	365	4022	for	Basic region plus leucine zipper transcription factors
1630	100	291	3998	for	Basic region plus leucine zipper transcription factors
1674	196	258	4880	for	Zinc finger, C2H2 type
1676	9.	86	6610	for	Homeobox Domain
1677	316	369	5780	rev	Thioredoxins
1688	109	410	17414	for	Ras family
1704	184	372	3977	for	Basic region plus leucine zipper transcription factors
1707	92	439	24100	rev	Phosphatidylinositol-specific phospholipase C, Y domain
1711	263	361	6400	for	WD domain, G-beta repeats
1744	238	433	10572	rev	Serine carboxypeptidases
1755	281	367	2580	for	EF-hand
1762	236	334	5880	for	WD domain, G-beta repeats
1779	64	126	4790	for	Zinc finger, C2H2 type
1801	295	351	4030	for	Zinc finger, C2H2 type
1804	301	378	3460	for	Ank repeat
1808	36	161	4170	for	Basic region plus leucine zipper transcription factors
1811	184	315	8390	for	N-terminal homology in Ets domain
1814	127	294	10770	for	Bromodomain (conserved sequence found in human, Drosophila and yeast proteins.)
1818	9	146	4741	for	Double-stranded RNA binding motif
1819	278	355	3460	for	Ank repeat
1820	123	299	12150	for	Homeobox Domain
1821	127	303	12180	for	Homeobox Domain
1830	184	267	4270	for	Ank repeat
1832	18	173	8987	for	SH3 Domain
1835	51	206	8987	for	SH3 Domain
1839	224	307	4270	for	Ank repeat
1846	12	398	36700	for	G-protein alpha subunit

SEQ ID	Start	Stop	Score	Direction	Description
1909	160	258	6370	for	WD domain, G-beta repeats
1911	• 35	151	9335	for	Zinc finger, C3HC4 type (RING finger)
1980	60	197	7917	for	Zinc finger, C3HC4 type (RING finger)
2065	253	306	5410	for	Zinc finger, CCHC class
2135	233	401	10596	for	ATPases Associated with Various
2133	2	401	10370	101	Cellular Activities
2216	90	179	5380	for	WW/rsp5/WWP domain containing
2210	70		2300	101	proteins
2218	127	225	5500	for	WD domain, G-beta repeats
2281	20	387	6044	for	Protein Tyrosine Phosphatase
2282	183	353	5136	for	C2 domain (prot. kinase C like)
2286	12	382	5228	for	protein kinase
2310	20	371	5962	for	Protein Tyrosine Phosphatase
2363	48	211	4132	for	Basic region plus leucine zipper
2303			, , , , ,		transcription factors
2424	43	194	3996	for	Basic region plus leucine zipper
			,		transcription factors
2428	25	350	4675	for	Dual specificity phosphatase, catalytic
					domain
2562	18	101	4560	for	Ank repeat
2577	0	311	10295	for	4 transmembrane segments integral
					membrane proteins
2591	60	165	4560	for	SH2 Domain
2684	9	461	5759	for	ATPases Associated with Various
					Cellular Activities
2826	116	400	16107	for	DEAD and DEAH box helicases
2859	100	320	5550	rev	ATPases Associated with Various
		_			Cellular Activities
2871	198	392	9384	for	DEAD and DEAH box helicases
2944	18	281	10480	for	Calpain large subunit, domain III
2969	5	387	5976	rev	protein kinase
3015	131	214	3600	for	Ank repeat
3047	191	292	5295	for	WD domain, G-beta repeats
3081	190	252	4360	for	Zinc finger, C2H2 type
3108	275	367	5791	for	WD domain, G-beta repeats
3147	190	369	4022	for	Basic region plus leucine zipper
					transcription factors
3152	129	320	3947	for	Basic region plus leucine zipper
					transcription factors
3158	167	334	4180	for	Basic region plus leucine zipper
					transcription factors
3175	14	164	5951	for	mkk like kinases

GEO ID	Ctont	Cham	Score	Direction	Description
SEQ ID	Start	Stop			
3175	8	112	5968	for	protein kinase
3178	45	386	19398	for	ATPases Associated with Various
					Cellular Activities
3183	14	215	9133	for	4 transmembrane segments integral
:					membrane proteins
3190	229	390	6089	for	mkk like kinases
3190	118	390	8063	for	protein kinase
3193	293	355	3570	for	Zinc finger, C2H2 type
3195	0	215	10146	for	4 transmembrane segments integral
1					membrane proteins
3197	281	343	4490	for	Zinc finger, C2H2 type
3208	34	256	4190	for	Basic region plus leucine zipper
,				:	transcription factors
3258	138	394	9877	for	Ras family
3266	8	139	9328	for	ATPases Associated with Various
					Cellular Activities
3267	97	180	3820	for	Ank repeat
3274	11	187	15442	for	Fork head domain, eukaryotic
					transcription factors
3281	15	182	9681	for	mkk like kinases
3285	16	102	4680	for	EF-hand
3292	208	300	5585	for	WD domain, G-beta repeats
3297	7	153	6100	for	Helicases conserved C-terminal domain
3306	161	223	4900	for	Zinc finger, C2H2 type
3307	43	321	8740	for	SH2 Domain
3339	94	342	14970	for	SH2 Domain
3345	65	271	12512	for	PDZ domain
3351	124	270	6068	for	Phorbol esters/diacylglycerol binding

Example 4 DIFFERENTIAL EXPRESSION OF POLYNUCLEOTIDES OF THE INVENTION: DESCRIPTION OF LIBRARIES AND DETECTION OF DIFFERENTIAL EXPRESSION

The relative expression levels of the polynucleotides of the invention was assessed in several libraries prepared from various sources, including cell lines and patient tissue samples. Table 6 provides a summary of these libraries, including the shortened library name (used hereafter), the mRNA source used to prepare the cDNA library, the abbreviated name of the library that is used in the tables below (in quotes), and the approximate number of clones in the library.

<u>Table 6</u> Description of cDNA Libraries

Library	Description	Number of
(lib #)	•	Clones in
` ′		this
		Clustering
1	Km12 L4	
	Human Colon Cell Line, High Metastatic Potential	307133
	(derived from Km12C)	
	"High Colon"	
2	Km12C	
	Human Colon Cell Line, Low Metastatic Potential	284755
	"Low Colon"	
3	MDA-MB-231	
	Human Breast Cancer Cell Line, High Metastatic Potential;	326937
	micro-metastases in lung	
	"High Breast"	
4	MCF7	
	Human Breast Cancer Cell, Non Metastatic	318979
	"Low Breast"	
8	MV-522	
	Human Lung Cancer Cell Line, High Metastatic Potential	223620
	"High Lung"	
9	UCP-3	
	Human Lung Cancer Cell Line, Low Metastatic Potential	312503
	"Low Lung"	

Library	Description	Number of
(lib #)		Clones in
		this
		Clustering
12	Human microvascular endothelial cells (HMEC) – Untreated	44000
	PCR (OligodT) cDNA library	41938
13	Human microvascular endothelial cells (HMEC) -	
	Basic fibroblast growth factor (bFGF) treated	42100
<u> </u>	PCR (OligodT) cDNA library	
14	Human microvascular endothelial cells (HMEC) -	
	Vascular endothelial growth factor (VEGF) treated	42825
	PCR (OligodT) cDNA library	
15	Normal Colon – UC#2 Patient	
	PCR (OligodT) cDNA library	34285
	"Normal Colon Tumor Tissue"	
16 .	Colon Tumor – UC#2 Patient	
	PCR (OligodT) cDNA library	35625
	"Normal Colon Tumor Tissue"	
17	Liver Metastasis from Colon Tumor of UC#2 Patient	
	PCR (OligodT) cDNA library	36984
	"High Colon Metastasis Tissue"	
18	Normal Colon – UC#3 Patient	
	PCR (OligodT) cDNA library	36216
	"Normal Colon Tumor Tissue"	
19	Colon Tumor – UC#3 Patient	
	PCR (OligodT) cDNA library	41388
	"High Colon Tumor Tissue"	
20	Liver Metastasis from Colon Tumor of UC#3 Patient	
	PCR (OligodT) cDNA library	30956
	"High Colon Metastasis Tissue"	
21	G RRpz	
	Human Prostate Cell Line	164801
22	WOca	
	Human Prostate Cancer Cell Line	162088

The KM12L4 and KM12C cell lines are described in Example 1 above. The MDA-MB-231 cell line was originally isolated from pleural effusions (Cailleau, J. Natl. Cancer. Inst. (1974) 53:661), is of high metastatic potential, and forms poorly differentiated adenocarcinoma grade II in nude mice consistent with breast carcinoma.

. The MCF7 cell line was derived from a pleural effusion of a breast adenocarcinoma and is non-metastatic. The MV-522 cell line is derived from a human lung carcinoma and is of high metastatic potential. The UCP-3 cell line is a low metastatic human lung carcinoma cell line; the MV-522 is a high metastatic variant of UCP-3. These cell lines are well-recognized in the art as models for the study of human breast and lung cancer (see, e.g., Chandrasekaran et al., Cancer Res. (1979) 39:870 (MDA-MB-231 and MCF-7); Gastpar et al., J Med Chem (1998) 41:4965 (MDA-MB-231 and MCF-7); Ranson et al., Br J Cancer (1998) 77:1586 (MDA-MB-231 and MCF-7); Kuang et al., Nucleic Acids Res (1998) 26:1116 (MDA-MB-231 and MCF-7); Varki et al., Int J Cancer (1987) 40:46 (UCP-3); Varki et al., Tumour Biol. (1990) 11:327; (MV-522 and UCP-3); Varki et al., Anticancer Res. (1990) 10:637; (MV-522); Kelner et al., Anticancer Res (1995) 15:867 (MV-522); and Zhang et al., Anticancer Drugs (1997) 8:696 (MV522)). The samples of libraries 15-20 are derived from two different patients (UC#2, and UC#3). The bFGF-treated HMEC were prepared by incubation with bFGF at 10ng/ml for 2 hrs; the VEGF-treated HMEC were prepared by incubation with 20ng/ml VEGF for 2 hrs. Following incubation with the respective growth factor, the cells were washed and lysis buffer added for RNA preparation. The GRRpz cell line refers to low passage (3 passages or fewer) human prostate cells, and the WOca cell line refers to low passage (3 passages or fewer) human prostate cancer cells.

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Each of the libraries is composed of a collection of cDNA clones that in turn are representative of the mRNAs expressed in the indicated mRNA source. In order to facilitate the analysis of the millions of sequences in each library, the sequences were assigned to clusters. The concept of "cluster of clones" is derived from a sorting/grouping of cDNA clones based on their hybridization pattern to a panel of roughly 300 7bp oligonucleotide probes (see Drmanac et al., Genomics (1996) 37(1):29). Random cDNA clones from a tissue library are hybridized at moderate stringency to 300 7bp oligonucleotides. Each oligonucleotide has some measure of specific hybridization to that specific clone. The combination of 300 of these measures of hybridization for 300 probes equals the "hybridization signature" for a specific clone. Clones with similar sequence will have similar hybridization signatures. By developing a sorting/grouping algorithm to analyze these signatures, groups of clones in a library can be identified and brought together computationally. These groups of clones are termed "clusters". Depending on the stringency of the selection in the algorithm (similar to the stringency of hybridization in a classic library cDNA screening protocol), the "purity" of each cluster can be controlled. For example, artifacts of clustering may

occur in computational clustering just as artifacts can occur in "wet-lab" screening of a cDNA library with 400 bp cDNA fragments, at even the highest stringency. The stringency used in the implementation of cluster herein provides groups of clones that are in general from the same cDNA or closely related cDNAs. Closely related clones can be a result of different length clones of the same cDNA, closely related clones from highly related gene families, or splice variants of the same cDNA.

Differential expression for a selected cluster was assessed by first determining the number of cDNA clones corresponding to the selected cluster in the first library (Clones in 1st), and the determining the number of cDNA clones corresponding to the selected cluster in the second library (Clones in 2nd). Differential expression of the selected cluster in the first library relative to the second library is expressed as a "ratio" of percent expression between the two libraries. In general, the "ratio" is calculated by: 1) calculating the percent expression of the selected cluster in the first library by dividing the number of clones corresponding to a selected cluster in the first library by the total number of clones analyzed from the first library; 2) calculating the percent expression of the selected cluster in the second library by dividing the number of clones corresponding to a selected cluster in a second library by the total number of clones analyzed from the second library; 3) dividing the calculated percent expression from the first library by the calculated percent expression from the second library. If the "number of clones" corresponding to a selected cluster in a library is zero, the value is set at 1 to aid in calculation. The formula used in calculating the ratio takes into account the "depth" of each of the libraries being compared, i.e., the total number of clones analyzed in each library.

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In general, a polynucleotide is said to be significantly differentially expressed between two samples when the ratio value is greater than at least about 2, preferably greater than at least about 3, more preferably greater than at least about 5, where the ratio value is calculated using the method described above. The significance of differential expression is determined using a z score test (Zar, <u>Biostatistical Analysis</u>. Prentice Hall, Inc., USA, "Differences between Proportions," pp 296-298 (1974)).

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EXAMPLE 5 POLYNUCLEOTIDES DIFFERENTIALLY EXPRESSED IN HIGH METASTATIC POTENTIAL BREAST CANCER CELLS VERSUS LOW METASTATIC BREAST CANCER CELLS

A number of polynucleotide sequences have been identified that are differentially expressed between cells derived from high metastatic potential breast cancer tissue and low metastatic breast cancer cells. Expression of these sequences in breast cancer can be valuable in determining diagnostic, prognostic and/or treatment information. For example, sequences that are highly expressed in the high metastatic potential cells can be indicative of increased expression of genes or regulatory sequences involved in the metastatic process. A patient sample displaying an increased level of one or more of these polynucleotides may thus warrant more aggressive treatment. In another example, sequences that display higher expression in the low metastatic potential cells can be associated with genes or regulatory sequences that inhibit metastasis, and thus the expression of these polynucleotides in a sample may warrant a more positive prognosis than the gross pathology would suggest.

The differential expression of these polynucleotides can be used as a diagnostic marker, a prognostic marker, for risk assessment, patient treatment and the like. These polynucleotide sequences can also be used in combination with other known molecular and/or biochemical markers.

The following tables summarize polynucleotides that are differentially expressed between high metastatic potential breast cancer cells and low metastatic potential breast cancer cells.

Table 7

Differentially expressed polynucleotides: Higher expression in high metastatic potential breast cancer (lib3) relative to low metastatic breast cancer cells (lib4)

SEQ ID NOs:	Lib3 clones	Lib4 clones	lib3/lib4
472	64	0	62
1851	6	0	6
1856	8	0	8
1867	6	0	6
1872	6	0	6
1875	12	3	4
1923	89	22	4

SEQ ID NOs:	Lib3 clones	Lib4 clones	lib3/lib4
2118	7	0	7
2119	7	0	7
2135	37	13	3
2190	19	0	19
2193	16	5	3
2232	12	2	6
2239	6	0	6
2338	21	2	10
2378	16	4	4
2394	6	0	6
2395	6	0	6
2490	13	3	4
2505	16	2	8
2540	8	1	8
2542	11	1	11
2607	11	2	5
2640	22	5	4
2674	8	0	8
2679	19	0	19
2684	14	4	3
2707	8	0	8
2724	9	0	. 9
2757	6	0	6
2776	10	0	10
2804	13	2	6
2818	6	0	6
2906	14	0	14
2959	26	. 8	3
2964	17	4	4
2968	6	0	6
2977	22	3	7
2980	13	1	13
3010	6	0	6
3043	10	1	10
3071	33	12	3
3072	9	1	9
3095	19	3	6
3097	11	2	5
3173	12	2	6
3203	8	1	8
3210	27	8	3

SEQ ID NOs:	Lib3 clones	Lib4 clones	lib3/lib4
3212	13	1	13
3284	8	0	8
3288	6	0	6
3331	14	3	5
3335.	13	1	13

Table 8
Differentially expressed polynucleotides: Higher expression in low metastatic breast cancer cells (lib4) relative to high metastatic potential breast cancer (lib3)

SEQ ID NOs:	Lib 3 Clones	Lib 4 Clones	lib4/lib3
402	0	6	6
614	3	21	7
624	0	6	6
626	0	8	8
712	0	9	9
744	0	7	7
1325	2	29	15
1452	2	13	7
1880	0	9	9
1915	0	7	7
1951	0	6	6
1955	8	32	4
2015	0	7	7
2046	0	7	7
2076	1	22	23
2087	0	6	6
2124	0	9	9
2145	0	8	8
2162	0	6	6
2163	0	12	12
2164	5	19	4
2172	2	15	8
2192	5.	16	3
2244	20	43	2
2266	3	18	6
2313	24	56	2
2346	1	13	13

SEQ ID NOs:	Lib 3 Clones	Lib 4 Clones	lib4/lib3
2355	0	10	10
2371	. 0	6	6
2393	1	17	17
2404	1	21	22
2443	0	6	6
2460	0	11	11
2523	0	6	6
2575	. 1	10	10
2578	0	6	6
2584	1	17	17
2590	0	6	6
2609	1	9	9
2632	5	24	5
2714	5	24	5
2728	0	6	6
2752	1	14	14
2794	4	15	4
2826	0	7	7
2987	5	15	3
3005	1	14	14
3009	20	58	3
3047	4	17	4
3057	2	17	9
3075	2	11	6
3076	0	6	6
3102	0	6	6
3128	15	52	4
3132	15	52	4
3142	0	6	6
3187	22	49	2
3253	23	96	4
3282	19	46	2
3285	20	40	2
3346	0	9	9

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EXAMPLE 6

POLYNUCLEOTIDES DIFFERENTIALLY EXPRESSED IN HIGH METASTATIC POTENTIAL LUNG
CANCER CELLS VERSUS LOW METASTATIC LUNG CANCER CELLS

A number of polynucleotide sequences have been identified that are differentially expressed between cells derived from high metastatic potential lung cancer cells and low metastatic lung cancer cells. Expression of these sequences in lung cancer tissue can be valuable in determining diagnostic, prognostic and/or treatment information. For example, sequences that are highly expressed in the high metastatic potential cells can be indicative of increased expression of genes or regulatory sequences involved in the metastatic process. A patient sample displaying an increased level of one or more of these polynucleotides may thus warrant more aggressive treatment. In another example, sequences that display higher expression in the low metastatic potential cells can be associated with genes or regulatory sequences that inhibit metastasis, and thus the expression of these polynucleotides in a sample may warrant a more positive prognosis than the gross pathology would suggest.

The differential expression of these polynucleotides can be used as a diagnostic marker, a prognostic marker, for risk assessment, patient treatment and the like. These polynucleotide sequences can also be used in combination with other known molecular and/or biochemical markers.

The following tables summarize polynucleotides that are differentially expressed between high metastatic potential lung cancer cells and low metastatic potential lung cancer cells:

Table 9

Differentially expressed polynucleotides: Higher expression in high metastatic potential lung cancer cells (lib8) relative to low metastatic lung cancer cells (lib9)

SEQ ID NO:	Lib8 clones	Lib9 clones	lib8/lib9
14	10	0	10
137	5	0	5
151	5	0	7
152	9	0	13
171	6	0	8
200	10	0	14
254	5	0	7
262	5	0	7
271	5	0	7
.348	6	1	8
412	5	0	7
507	5	0	7
520	6	0	8
530	5	0	7
588	5	0	7
623	7	0	10
637	7	0	10
660	5	0	7
678	8	0	11
680	5	0	7
700	9	2	6
714	28	13	3
774	11	0	15
812	5	0	7
834	8	2	6
901	11	2	8
1168	5	0	7
1333	6	0	8
1352	5	0	7
1524	11	1	15
1706	5	0	7
1752	17	9	3
1768	20	4	7
1769	5	0	7
1780	6	0	8

SEQ ID NO:	Lib8 clones	Lib9 clones	lib8/lib9
1781	40	3	19
1799	6	1	8
1803	6	1	8
1811	16	9	2
1884	6	0	8
1919	8	1	11
1939	6	^ 0	8
1975	43	9	7
2024	12	1	17
2045	8	1	11
2060	20	13	2
2071	16	4	6
2128	5	0	7
2177	10	2	7
2181	44	13	5
2184	11	1	. 15
° 2185	10	4	3
2283	7	0	10
2311	10	4	3
2314	10	0	14
2393	14	6	3
2398	6	1	8
2460	10	4 .	3
2514	. 6	0	8
2597	5	0	7
2657	8	2	6
2669	6	1	8
2670	6	1	8
3047	21	3	10
3050	16	5	4
3092	7	1	10
3140	181	119	2
3157	5	0 .	7
3187	16	5	. 4
3210	5	0	7
3220	28	4	10
3236	7	1	10
3249	16	0	22
3264	8	2	6
3305	7	0	10
3309	20	0	28

SEQ ID NO:	Lib8 clones	Lib9 clones	lib8/lib9
3318	24	4	8
3330	5	0	7
3331	5	0	7

Table 10

Differentially expressed polynucleotides: Higher expression in low metastatic lung cancer cells (lib 9) relative to high metastatic potential lung cancer cells (lib 8)

SEQ ID NO:	Lib 8 clones	Lib 9 clones	lib 9/lib 8
24	3	20	5
53	0	18	13
64	0	8	6
70	0	11	8
. 105	10	66	5
129	0	16	11
214	1	14	10
233	4	35	6
237	0	13	9
264	0	29	21
329	- 2	17	6
368	1	37	26
370	0	11	8
418	0	8	6
450	0	9	6
461	0	9	6
484	0	26	19
494	0	41	29
517	1	12	9
522	1	11	8
581	1	17	12
614	3	23	5
706	0	11	8
726	5	23	3
806	0	14	10
824	. 0	9	6
836	1	14	10
874	0	12	9
900	5	21	3
1017	2	14	5

SEQ ID NO:	Lib 8 clones	Lib 9 clones	lib 9/lib 8
1144	0	8	6
1154	0	12	9
1166	2	45	16
1170	1	13	9
1302	2	13	5
1326	1	13	9
1327	1	13	9
1367	0	12	9
1377	0	12	9
1437	2	18	6
1442	1	14	10
1466	0	13	9
1476	0	13	9
1495	0	8	. 6
1496	1	13	9
1664	38	253	. 5
1682	1	17	12
1687	0	9	6
1758	0	8	6
1817	4	18	3 .
1837	3	16	4
1845	3	23	5
1856	2	17	6
1910	1	18	13
2146	2	16	9
2156	0	9	6
2463	0	12	9
2724	10	38	3
2749	403	2000	4
2801	6	25	3
2993	3	18	4
3080	0	10	7
3107	3	23	5
3292	0	20	14
3324	110	548	4

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EXAMPLE 7

POLYNUCLEOTIDES DIFFERENTIALLY EXPRESSED IN HIGH METASTATIC POTENTIAL COLON CANCER CELLS VERSUS LOW METASTATIC COLON CANCER CELLS

A number of polynucleotide sequences have been identified that are differentially expressed between cells derived from high metastatic potential colon cancer cells and low metastatic colon cancer cells. Expression of these sequences in colon cancer tissue can provide diagnostic, prognostic and/or treatment information. For example, sequences that are highly expressed in the high metastatic potential cells can be indicative of increased expression of genes or regulatory sequences involved in the metastatic process. A patient sample displaying an increased level of one or more of these polynucleotides may thus warrant more aggressive treatment. In another example, sequences that display higher expression in the low metastatic potential cells can be associated with genes or regulatory sequences that inhibit metastasis, and thus the expression of these polynucleotides in a sample may warrant a more positive prognosis than the gross pathology would suggest.

The differential expression of these polynucleotides can be used as a diagnostic marker, a prognostic marker, for risk assessment, patient treatment and the like. These polynucleotide sequences can also be used in combination with other known molecular and/or biochemical markers.

The following table summarizes identified polynucleotides with differential expression between high metastatic potential colon cancer cells and low metastatic potential colon cancer cells:

Table 11

25 Differentially expressed polynucleotides: Higher expression in low metastatic colon cancer cells (lib 2) relative to high metastatic potential colon cancer cells (lib 1)

SEQ ID NOs:	Lib 1 clones	Lib 2 clones	lib 2/lib 1
429	0	9	10
1494	0	.8	9
1923	34	114	4
1986	3	12	4
2018	0	9	10
2036	2	10	5
2049	8	25	3
2135	24	87	4

SEQ ID NOs:	Lib 1 clones	Lib 2 clones	lib 2/lib 1
2146	2	16	9
2208	6	27	5
2215	2	11	6
2239	1	10	11
2307	2	12	6
2313	28	62	2
2357	5	14	3
2360	3	21	8
2362	0	6	6
2378	3	12	4
2569	3	20	7
2571	0	6	. 6
2588	54	172	3
2592	15	41	3
2611	0	6	6
2636	0	9	10
2641	7	20	3
2650	0	9	10
2662	0	9	10
2674	4	13	4
2682	0	6	6
2702	9	25	3
2704	8	23	3
2715 ·	2	12 (6
2804	9	22	3
2821	13	-29	2
2840	1	8	9
2846	2	15	8
2866	0	6	6
2906	0	6	6
2915	• 44	109	3
2933	0	6	6
2935	5	16	3
2957	1	11	12
2959	3	27	10
2977	16	30	2
2980	12	27	2
3000	2	13	7
3009	12	29	3
3115	0 .	7	8
3156	502	2170	5

SEQ ID NOs:	Lib 1 clones	Lib 2 clones	lib 2/lib 1
3210	2	21	11
3211	0	9	10
3213	0	7	8
3235	2	12	6
3251	2	12	. 6
3296	3	12	4
3335	1	8	9

EXAMPLE 8

POLYNUCLEOTIDES DIFFERENTIALLY EXPRESSED IN HIGH METASTATIC POTENTIAL

COLON CANCER PATIENT TISSUE VERSUS NORMAL PATIENT TISSUE

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A number of polynucleotide sequences have been identified that are differentially expressed between cells derived from high metastatic potential colon cancer tissue and normal tissue. Expression of these sequences in colon cancer tissue can provide diagnostic, prognostic and/or treatment information. For example, sequences that are highly expressed in the high metastatic potential cells can be indicative of increased expression of genes or regulatory sequences involved in the advanced disease state which involves processes such as angiogenesis, dedifferentiation, cell replication, and metastasis. A patient sample displaying an increased level of one or more of these polynucleotides may thus warrant more aggressive treatment.

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The differential expression of these polynucleotides can be used as a diagnostic marker, a prognostic marker, for risk assessment, patient treatment and the like. These polynucleotide sequences can also be used in combination with other known molecular and/or biochemical markers.

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The following tables summarize polynucleotides that are differentially expressed between high metastatic potential colon cancer tissue and normal colon tissue:

Table 12
Differentially expressed polynucleotides isolated from samples from two patients (patient 2 and patient 3 and): Lower expression in high metastatic potential colon tissue (patient 2:lib 17; patient 3:lib 20) vs. normal colon tissue (patient 2:lib 15; patient 3:lib 18)

SEQ ID NO:	lib 15 clones	lib 17 clones	lib 15/lib 17
69	19	7	3
123	6	0	6
140	24	8	3
197	6	0	6
198	113	0	121
254	28	9	3
412	28	9	3
512	11	1	12
641	. 17	7	3
642	7	0	8
954	12	3	4
1011	209	16	14
1024	8	0	9
1040	12	3	4
1055	26	7	4
1106	31	15	2
1125	17	0	18
1129	17	0	18
1138	109	0	117
1244	14	1	15
1253	73	0	78
1283	34	7	5
1285	34	7	5
1339	13	4	3
1474	73	0	78
1505	18	3	6
1553	68	6	12
1554	2542	14	195
1605	2542	14	195
1628	6	0	6
1643	142	4	38
1753	12	0	10
1764	13	0	14

SEQ ID NO:	lib 15 clones	lib 17 clones	lib 15/lib 17
SEQ ID NO:	Lib18 Clones	Lib20 Clones	lib18/lib20
105	28	11	2
198	21	0	18
254	9	0	8
412	9	0	8
1011	11	1	9
1138	14	0	12
1253	23	0	20
1643	18	0	15
1764	12	0	10
3156	140	43	13

Table 13

Differentially expressed polynucleotides isolated from samples from two patients (patient 2 and patient 3): Lower expression in normal colon tissue (patient 2:lib 15; patient 3:lib 18)vs. high metastatic potential colon tissue (patient 2:lib 17; patient 3:lib 20).

SEQ ID NO:	Lib 15 Clones	Lib 17 Clones	lib 17/lib 15
321	3	23	7
363	1	9	8
836	21	99	4
859	6	20	3
885	13	28	2
916	13	28	2
981	2	11	. 5
1226	8	70	8
1308	0	8	7
1317	29	84	3
1429	27	127	4
1442	0	9	8
1534	1	12	11
1540	12	43	3
1552	0	7	7
1556	1	9	8
1557	1	9	8
1569	2189	5122	2
1571	6	18	3
1576	3	25	8



SEQ ID NO:	Lib 15 Clones	Lib 17 Clones	lib 17/lib 15
1581	4	22	5
1601	25	157	6
1613	9	48	5
1616	15	61	4
1620	2	17	8
1622	4	99	23
1626	6	35	5
1647	4	22	5
1664	4	28	7
1683	2	18	8
1704	3	15	5
1800	0	7	7
2749	23	60	2
2784	4	14	3
2805	1	9	8
2976	3	14	4
3128	18	57	3
3129	26	124	4
3146	64	210	3
3150	940	2267	2
3151	2	15	7
SEQ ID NO:	lib 18 clones	lib 20 clones	lib 20/lib 18
865	0	5	6
1569	1	7	8
1580	1	7	8
1590	1	7	8
2790	0	. 5	6

EXAMPLE 9

POLYNUCLEOTIDES DIFFERENTIALLY EXPRESSED IN HIGH COLON TUMOR POTENTIAL PATIENT TISSUE VERSUS METASTASIZED COLON CANCER PATIENT TISSUE

A number of polynucleotide sequences have been identified that are differentially expressed between cells derived from colon cancer tissue and cells derived from colon cancer tissue metastases to liver. Expression of these sequences in colon cancer tissue can provide diagnostic, prognostic and/or treatment information associated with the transformation of precancerous tissue to malignant tissue. This information

can be useful in the prevention of achieving the advanced malignant state in these tissues, and can be important in risk assessment for a patient.

The following table summarizes identified polynucleotides with differential expression between high tumor potential colon cancer tissue and cells derived from high metastatic potential colon cancer cells:

Table 14

Differentially expressed polynucleotides:

Greater expression in metastatic colon tumor tissue (lib 20) vs.

colon tumor tissue (lib 19)

SEQ ID NO:	lib 19 clones	lib 20 clones	lib 20/lib 19
937	0	6	8
976	0	5	7
1520	1	8	11
1546	1	11	15
1550	1	11	. 15
1574	1	8	11
1580	0	7	9
1590	0	7	9
1599	8	21	4
1607	158	632	5
1622	1	7	9

<u>Table 15</u>
Greater expression in colon tumor tissue (lib 19) than metastatic colon tissue (lib 20)

SEQ ID NO:	lib 19 clones	lib 20 clones.	lib 19/lib 20
105	64	11	4
1011	53	1	40
1226	18	4	3
1571	8	0	6
1726	15	3	4
1811	17	2	6
2749	47	6	6
3146	19	2	7
3324	20	1	15

EXAMPLE 10

POLYNUCLEOTIDES DIFFERENTIALLY EXPRESSED IN HIGH TUMOR POTENTIAL COLON CANCER PATIENT TISSUE VERSUS NORMAL PATIENT TISSUE

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A number of polynucleotide sequences have been identified that are differentially expressed between cells derived from high tumor potential colon cancer tissue and normal tissue. Expression of these sequences in colon cancer tissue can provide diagnostic, prognostic and/or treatment information associated with the prevention of the malignant state in these tissues, and can be important in risk assessment for a patient. For example, sequences that are highly expressed in the potential colon cancer cells are associated with or can be indicative of increased expression of genes or regulatory sequences involved in early tumor progression. A patient sample displaying an increased level of one or more of these polynucleotides may thus warrant closer attention or more frequent screening procedures to catch the malignant state as early as possible.

The following tables summarize polynucleotides that are differentially expressed between high metastatic potential colon cancer cells and normal colon cells:

Table 16

Differentially expressed polynucleotides detected in samples from patient (patient 2)

Higher expression in normal colon tissue (patient 2, lib 15)

vs. tumor potential colon tissue (patient 2:lib16)

SEQ ID NO:	lib 15 clones	lib 16 clones	lib 16/lib 15
69	19	7	3
105	116	54	2
140	24	4	6
197	6	0	6
198	113	3	40
254	28	6	5
412	28	6	5
642	7	0	7
830	10	2	5
938	31	13	3
1011	209	37	6
1095	12	3	4
1125	17	0	18

SEQ ID NO:	lib 15 clones	lib 16 clones	lib 16/lib 15
1129	17	0	18
1138	109	1	115
1253	73	1	77
1283	34	13	3
1285	34	13	3
1339	13	3	5
1453	11	3	4
1474	73	1	77
1505	18	6	3
1554	2542	448	6
1605	2542	448	6
1614	36	14	3
1630	24	9	3
1643	142	2	75
1646	39	14	3
1649	24	8	3
1677	19	6	3
1753	13	0	14
1764	13	0	14
1766	177	65	3
1772	24	8	3

Table 17

Differentially expressed polypeptides detected in samples from patient. Lower expression in normal colon tissue (lib 18) than colon tumor tissue (lib 19)

SEQ ID NO:	lib 18 clones	lib 19 clones	lib 19/lib 18
3146	3	19	6
3150	21	228	10
3324	3	20	6

Table 18

Differentially expressed polypeptides detected in samples from patient. Higher expression in normal colon tissue (lib 18) than colon tumor tissue (lib 19)

SEQ ID NO:	lib 18 clones	lib 19 clones	lib 18/lib 19
198	21	2	12
465	6	0	7
489	6	0	7
745	6	0	7
859	11	2	6
976	7	0	8
1011	209	37	6
1045	8	1	9
1138	14	0	16
1253	23	0	26
1392	16	4	5
1474	23	0	26
1589	6	0	7
1591	22	11	2
1607	386	158	3
1643	18	0	21
1753	12	0	14
1764	12	0	14
SEQ ID NO:	lib 18 clones	lib 19 clones	lib 19/lib 18
105	28	64	2
1011	11	53	4
1226	2	18	8
1251	6	19	3
1559	1	9	8
1571	0	8	7
1608	1	9	8
1766	2	13	6
1782	1	9	8
1811	1	17	15

Table 19
Differentially expressed polynucleotides:
Higher expression in colon tumor tissue
(patient 2, lib 16) vs. normal colon tissue (patient 2, lib 15)

SEQ ID NO:	lib 15 clones	lib 16 clones	lib 16/lib 15
7	1	9	9
164	6	19	3
734	4	15	4
836	21	53	2
928	2	11	5
965	2	11	5
987	2	11	5
1026	7	19	3
1044	4	16	4
. 1119	4	16	4
1226	8	46	5
1227	0	9	9
1251	7	95	. 13
1316	0	6	6
1429	27	81	3
1442	0	9	9
1540	12	28	2
1553	68	590	8
1560	4	24	6
1577	1	10	9
1588	5	20	4
1610	3 .	13	4
1620	2	23	11
1626	6	23	4
1673	2	15	7
2416	0	7	7
2749	23	54	2
2976	3	14	4
3129	26	64	2
3132	18	54	3

EXAMPLE 11

POLYNUCLEOTIDES DIFFERENTIALLY EXPRESSED IN GROWTH FACTOR-STIMULATED HUMAN MICROVASCULAR ENDOTHELIAL CELLS (HMEC) RELATIVE TO UNTREATED HMEC

A number of polynucleotide sequences have been identified that are differentially expressed between human microvascular endothelial cells (HMEC) that have been treated with growth factors relative to untreated HMEC.

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Sequences that are differentially expressed between growth factor-treated HMEC and untreated HMEC can represent sequences encoding gene products involved in angiogenesis, metastasis (cell migration), and other developmental and oncogenic processes. For example, sequences that are more highly expressed in HMEC treated with growth factors (such as bFGF or VEGF) relative to untreated HMEC can serve as markers of cancer cells of higher metastatic potential. Detection of expression of these sequences in colon cancer tissue can provide diagnostic, prognostic and/or treatment information associated with the prevention of achieving the malignant state in these tissues, and can be important in risk assessment for a patient. A patient sample displaying an increased level of one or more of these polynucleotides may thus warrant closer attention or more frequent screening procedures to catch the malignant state as early as possible.

The following table summarizes identified polynucleotides with differential expression between growth factor-treated and untreated HMEC.

Table 20

Differentially expressed polynucleotides:
Higher expression in untreated HMEC (lib 12) vs. bFGF treated HMEC (lib 13)

SEQ ID NO:	lib 12 clones	lib 13 clones	lib 12/lib 13
849	6	0	6
1059	6	0	6
1206	12	2	6
3208	12	0	12

Lower expression in untreated HMEC (lib 12) vs. bFGF treated HMEC (lib 13)

ſ	2748	3	12	4
Ī	3325	0	6	6

<u>Table 21</u>
Differentially expressed polynucleotides:

Higher expression in untreated HMEC (lib 12) VEGF treated HMEC (lib14)

SEQ ID NO:	lib 12 clones	lib 14 clones	lib 12/lib 14
1150	9	0	9

Lower expression in untreated HMEC (lib 12) vs. VEGF treated HMEC (lib14)

3324	22	50	2

EXAMPLE 12

POLYNUCIEOTIDES DIFFERENTIALLY EXPRESSED IN NORMAL PROSTATE CELLS

RELATIVE TO PROSTATE CANCER CELLS

A number of polynucleotide sequences have been identified that are differentially expressed between cells derived from normal prostate cells and prostate cancer cells. Expression of these sequences prostate tissue suspected of being cancerous can provide diagnostic, prognostic and/or treatment information. These polynucleotide sequences can also be used in combination with other known molecular and/or biochemical markers. The following table summarizes identified polynucleotides with differential expression between high metastatic potential colon cancer cells and low metastatic potential colon cancer cells:

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Table 22
Differentially expressed polynucleotides: normal prostate cell line (lib 21)
vs. prostate cancer cell line (lib 22)

Higher in lib 21

SEQ ID NO:	lib 21 clones	lib 22 clones	lib 21/lib 22
53	17	2	8
1754	22	8	3
1801	7	0	7
1845	22	6	4
446	8	0	8
1410	6	0	6
2060	18	6	3
2143	12	3	4
2632	13	1	13
2899	16	2	8
3338	12	2	6

Higher in lib 22

86	2	13	7
93	0	9	9
687	0	9	9
1269	1	15	15
1581	25	74	3
1647	25	74	3
1649	12	27	2
1710	5	16	3
1717	5	16	3
1772	12	27	2
1960	0	6	6
2987	0	6	6
3128	13	42	3
3132	13	42	3
3150	263	962	4
3222	0	6	6
3268	0	6	6

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EXAMPLE 13

POLYNUCLEOTIDES DIFFERENTIALLY EXPRESSED ACROSS MULTIPLE LIBRARIES

A number of polynucleotide sequences have been identified that are differentially expressed between cancerous cells and normal cells across two or more tissue types tested (*i.e.*, breast, colon, lung, and prostate). Expression of these sequences in a tissue of any origin can provide diagnostic, prognostic and/or treatment information associated with the prevention of achieving the malignant state in these tissues, and can be important in risk assessment for a patient. These polynucleotides can also serve as non-tissue specific markers of, for example, risk of metastasis of a tumor. The following polynucleotides were differentially expressed but without tissue type-specificity in at least two of the breast, colon, lung, and prostate libraries tested: 53, 105, 355, 412, 614, 836, 1442, 1581, 1647, 1649, 1664, 1772, 1782, 1811, 1845, 1856, 1875, 1923, 2060, 2071, 2135, 2146, 2239, 2313, 2378, 2393, 2416, 2460, 2490, 2632, 2674, 2704, 2724, 2749, 2784, 2804, 2959, 2976, 2977, 2980, 2987, 3009, 3047, 3128, 3129, 3132, 3146, 3150, 3156, 3210, 3324, 3331, and 3335.

Those skilled in the art will recognize, or be able to ascertain, using not more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such specific embodiments and equivalents are intended to be encompassed by the following claims.

All publications and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference. The citation of any publication is for its disclosure prior to the filing date and should not be construed as an admission that the present invention is not entitled to antedate such publication by virtue of prior invention.

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it is readily apparent to those of ordinary skill in the art in light of the teachings of this invention that certain changes and modifications may be made thereto without departing from the spirit or scope of the appended claims.

Deposit Information:

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The following materials were deposited with the American Type Culture Collection (ATCC); CMCC = Chiron Master Culture Collection:

cDNA Libraries Deposited with ATCC

ES137			ATCC	CMCC
ES138	Tube Number		Accession No.	Accession No.
ES139	ES137			
ES140	ES138			
ES141	ES139	May 30, 2000		
ES142	ES140	May 30, 2000		
ES144	ES141	May 30, 2000		
ES144	ES142	May 30, 2000		
ES145 May 30, 2000 ES146 May 30, 2000 ES147 May 30, 2000 ES148 May 30, 2000 ES149 May 30, 2000 ES150 May 30, 2000 ES151 May 30, 2000 ES151 May 30, 2000 ES152 May 30, 2000 ES153 May 30, 2000 ES154 May 30, 2000 ES155 May 30, 2000 ES155 May 30, 2000 ES156 May 30, 2000 ES157 May 30, 2000 ES158 May 30, 2000 ES159 May 30, 2000 ES160 May 30, 2000 ES161 May 30, 2000 ES161 May 30, 2000 ES161 May 30, 2000 ES161 May 30, 2000 ES162 May 30, 2000 ES163 May 30, 2000 ES164 May 30, 2000 ES165 May 30, 2000 ES165 May 30, 2000 ES166 May 30, 2000 ES161 May 30, 2000 ES165 May 30, 2000 ES164 May 30, 2000 ES165 May 30, 2000 ES165 May 30, 2000 ES165 May 30, 2000	ES143	May 30, 2000		
ES146	ES144	May 30, 2000		
ES147	ES145	May 30, 2000		
ES148	ES146	May 30, 2000		
ES149 May 30, 2000 ES150 May 30, 2000 ES151 May 30, 2000 ES152 May 30, 2000 ES153 May 30, 2000 ES154 May 30, 2000 ES155 May 30, 2000 ES156 May 30, 2000 ES157 May 30, 2000 ES158 May 30, 2000 ES159 May 30, 2000 ES160 May 30, 2000 ES161 May 30, 2000 ES161 May 30, 2000 ES162 May 30, 2000 ES163 May 30, 2000 ES164 May 30, 2000 ES165 May 30, 2000 ES165 May 30, 2000 ES166 May 30, 2000 ES166 May 30, 2000 ES166 May 30, 2000 ES166 May 30, 2000 ES166 May 30, 2000	ES147	May 30, 2000		
ES150 May 30, 2000 ES151 May 30, 2000 ES152 May 30, 2000 ES153 May 30, 2000 ES154 May 30, 2000 ES155 May 30, 2000 ES156 May 30, 2000 ES157 May 30, 2000 ES158 May 30, 2000 ES159 May 30, 2000 ES160 May 30, 2000 ES161 May 30, 2000 ES161 May 30, 2000 ES161 May 30, 2000 ES162 May 30, 2000 ES163 May 30, 2000 ES164 May 30, 2000 ES165 May 30, 2000 ES165 May 30, 2000 ES166 May 30, 2000 ES166 May 30, 2000	ES148	May 30, 2000		
ES151	ES149	May 30, 2000		
ES152 May 30, 2000 ES153 May 30, 2000 ES154 May 30, 2000 ES155 May 30, 2000 ES156 May 30, 2000 ES157 May 30, 2000 ES158 May 30, 2000 ES159 May 30, 2000 ES160 May 30, 2000 ES161 May 30, 2000 ES161 May 30, 2000 ES162 May 30, 2000 ES163 May 30, 2000 ES164 May 30, 2000 ES165 May 30, 2000 ES166 May 30, 2000 ES166 May 30, 2000	ES150	May 30, 2000		
ES153	ES151	May 30, 2000		
ES154	ES152	May 30, 2000		
ES155 May 30, 2000 ES156 May 30, 2000 ES157 May 30, 2000 ES158 May 30, 2000 ES159 May 30, 2000 ES160 May 30, 2000 ES161 May 30, 2000 ES162 May 30, 2000 ES163 May 30, 2000 ES164 May 30, 2000 ES165 May 30, 2000 ES166 May 30, 2000 ES166 May 30, 2000	ES153	May 30, 2000		
ES156 May 30, 2000 ES157 May 30, 2000 ES158 May 30, 2000 ES159 May 30, 2000 ES160 May 30, 2000 ES161 May 30, 2000 ES162 May 30, 2000 ES163 May 30, 2000 ES164 May 30, 2000 ES165 May 30, 2000 ES166 May 30, 2000 ES166 May 30, 2000	ES154	May 30, 2000		·
ES157 May 30, 2000 ES158 May 30, 2000 ES159 May 30, 2000 ES160 May 30, 2000 ES161 May 30, 2000 ES162 May 30, 2000 ES163 May 30, 2000 ES164 May 30, 2000 ES165 May 30, 2000 ES166 May 30, 2000	ES155	May 30, 2000		
ES158 May 30, 2000 ES159 May 30, 2000 ES160 May 30, 2000 ES161 May 30, 2000 ES162 May 30, 2000 ES163 May 30, 2000 ES164 May 30, 2000 ES165 May 30, 2000 ES166 May 30, 2000	ES156	May 30, 2000		
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ES161 May 30, 2000 ES162 May 30, 2000 ES163 May 30, 2000 ES164 May 30, 2000 ES165 May 30, 2000 ES166 May 30, 2000	ES159	May 30, 2000		
ES162 May 30, 2000 ES163 May 30, 2000 ES164 May 30, 2000 ES165 May 30, 2000 ES166 May 30, 2000	ES160	May 30, 2000		
ES163 May 30, 2000 ES164 May 30, 2000 ES165 May 30, 2000 ES166 May 30, 2000	ES161	May 30, 2000		
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ES165 May 30, 2000 ES166 May 30, 2000	ES163	May 30, 2000		
ES166 May 30, 2000	ES164			
	ES165			
ES167 May 30, 2000	ES166	May 30, 2000		
	ES167	May 30, 2000	,	

Table 23 lists the clones for each deposit, designated as "tube" number.

This deposit is provided merely as convenience to those of skill in the art, and is not an admission that a deposit is required under 35 U.S.C. §112. The sequence of the polynucleotides contained within the deposited material, as well as the amino acid sequence of the polypeptides encoded thereby, are incorporated herein by reference and are controlling in the event of any conflict with the written description of sequences

herein. A license may be required to make, use, or sell the deposited material, and no such license is granted hereby.

Retrieval of Individual Clones from Deposit of Pooled Clones

Where the ATCC deposit is composed of a pool of cDNA clones, the deposit was prepared by first transfecting each of the clones into separate bacterial cells. The clones were then deposited as a pool of equal mixtures in the composite deposit. Particular clones can be obtained from the composite deposit using methods well known in the art. For example, a bacterial cell containing a particular clone can be identified by isolating single colonies, and identifying colonies containing the specific clone through standard colony hybridization techniques, using an oligonucleotide probe or probes designed to specifically hybridize to a sequence of the clone insert (e.g., a probe based upon unmasked sequence of the encoded polynucleotide having the indicated SEQ ID NO). The probe should be designed to have a T_m of approximately 80°C (assuming 2°C for each A or T and 4°C for each G or C). Positive colonies can then be picked, grown in culture, and the recombinant clone isolated. Alternatively, probes designed in this manner can be used to PCR to isolate a nucleic acid molecule from the pooled clones according to methods well known in the art, e.g., by purifying the cDNA from the deposited culture pool, and using the probes in PCR reactions to produce an amplified product having the corresponding desired polynucleotide sequence.

Table 23

Glone Name	畫 Tube書
M00001351A:B02	ES 137
M00001356A:H11	ES 137
M00001363D:D09	ES 137
M00001395D:H02	ES 137
M00001439C:H06	ES 137
M00001476B:G10	ES 137
M00001582A:E02	ES 137
M00003750D:E06	ES 137
M00003761C:F02	ES 137
M00003770A:E05	ES 137
M00003786A:A11	ES 137
M00003800A:F09	ES 137
M00003816D:E11	ES 137
M00003902A:C03	ES 137
M00003991C:F06	ES 137

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Clone Name	Tube
M00003995B:E03	ES 137
M00004046C:A08	ES 137
M00004105D:D05	ES 137
M00004139B:B10	ES 137
M00004140D:C03	ES 137
M00004144A:H05	ES 137
M00004152A:C12	ES 137
M00004155D:A10	ES 137
M00004168A:G11	ES 137
M00004197B:H10	ES 137
M00004222C:E03	ES 137
M00004234A:E07	ES 137
M00004239B:F11	ES 137
M00004241B:H07	ES 137
M00004264B:A05	ES 137

Clone Name	Tube
M00004278A:F09	ES 137
M00004282D:C11	ES 137
M00004308C:C06	ES 137
M00004340C:C07	ES 137
M00004354D:E05	ES 137
M00004361A:H02	ES 137
M00004372B:F07	ES 137
M00004372B:107	ES 137
M0000437671:B10	ES 137
M00004393B:E07	ES 137
M00023282A:C02	ES 137
M00023300D:C11	ES 137
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M00023333D:C12	ES 137
M00023352B:F03	ES 137
M00023352D:H03	ES 137
M00023376B:G04	ES 137
M00023377B:F01	ES 137
M00023398B:D12	ES 137
M00023399C:E10	ES 137
M00026803A:F08	ES 137
M00026843B:D10	ES 137
M00026850D:F09	ES 137
M00026851B:F01	ES 137
M00026856D:F02	ES 137
M00026857D:G12	ES 137
M00026859D:D01	ES 137
M00026860B:C05	ES 137
M00026865B:A06	ES 137
M00026868C:E11	ES 137
M00026878A:F05	ES 137
M00026882D:G09	ES 137
M00026885A:H09	ES 137
M00026901A:G07	ES 137
M00026914A:H10	ES 137
M00026915B:C06	ES 137
M00026918B:D01	ES 137
M00026922C:B02	ES 137
M00026922C:G03	ES 137
M00026926A:E10	ES 137
M00026927D:F02	ES 137
M00026928D:A03	ES 137
M00026935C:B04	ES 137
M00026941D:A04	ES 137
M00026944B:E03	ES 137
M00026946A:F12	ES 137
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Clone Name	Tübe
M00026980A:D09	ES 137
M00027016A:B06	ES 137
M00027018A:C09	ES 137
M00027021A:G02	ES 137
M00027022D:G11	ES 137
M00027030C:H06	ES 137
M00027035D:C06	ES 137
M00027049B:F05	ES 137
M00027078A:B02	ES 137
M00027080A:B01	ES 137
M00027085C:E11	ES 137
M00027094A:B03	ES 137
M00027103B:A09	ES 137
M00027108C:B03	ES 137
M00027121D:C05	ES 137
M00027135A:B11	ES 137
M00027136C:C09	ES 137
M00027141C:H03	ES 137
M00027159D:F03	ES 137
M00027162B:F05	ES 137
M00027178B:G09	ES 137
M00027179D:E06	ES 138
M00027181D:A05	ES 138
M00027195C:E04	ES 138
M00027198B:B08	ES 138
M00027200A:F02	ES 138
M00027207B:F07	ES 138
M00027212D:E03	ES 138
M00027228D:A01	ES 138
M00027232D:B08	ES 138
M00027233B:C01	ES 138
M00027236A:E04	ES 138
M00027237C:B08	ES 138
M00027248A:C02	ES 138
M00027256B:H09	ES 138
M00027258A:A07	ES 138
M00027263A:F10	ES 138
M00027292D:F10	ES 138
M00027297A:C04	ES 138
M00027299B:B12	ES 138
M00027301A:G05	ES 138
M00027301B:B08	ES 138
M00027314C:D09	ES 138
M00027319D:B11	ES 138
M00027324D:C05	ES 138

Clone Name	Tube
M00027347C:G07	ES 138
M00027355A:B07	ES 138
M00027359B:G05	ES 138
M00027366A:F11	ES 138
M00027379C:B07	ES 138
M00027392B:H02	ES 138
M00027396D:G08	ES 138
M00027398C:F07	ES 138
M00027438C:G07	ES 138
M00027462A:D07	ES 138
M00027462B:H07	ES 138
M00027468A:C09	ES 138
M00027475B:E10	ES 138
M00027476A:C09	ES 138
M00027486A:F06	ES 138
M00027520A:C05	ES 138
M00027525B:D06	ES 138
M00027526D:F03	ES 138
M00027528C:B10	ES 138
M00027537C:B01	ES 138
M00027546C:B10	ES 138
M00027591B:C04	ES 138
M00027596A:A10	ES 138
M00027596C:E06	ES 138
M00027602B:C01	ES 138
M00027615A:F10	ES 138
M00027617B:C12	ES 138
M00027620D:F11	ES 138
M00027625A:H01	ES 138
M00027634A:D11	ES 138
M00027641C:A03	ES 138
M00027647C:D03	ES 138
M00027652B:F11	ES 138
M00027668C:H12	ES 138
M00027729D:H06	ES 138
M00027733A:A02	ES 138
M00027741B:F09	ES 138
M00027743A:C03	ES 138
M00027801C:C11	ES 138
M00027813C:F01	ES 138
M00027818C:C07	ES 138
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M00027837C:D09	ES 138
M00028120D:F12	ES 138
M00028066C:D07	ES 138
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Clone Name	Feliuber
M00032578A:G06	ES 139
M00032584A:H08	ES 139
M00032592A:H11	ES 139
M00032597C:B01	ES 139
M00032638C:G08	ES 139
M00032638D:A06	ES 139
M00032668D:G12	ES 139
M00032678C:D06	ES 139
M00032688D:D11	ES 139
M00032712B:G02	ES 139
M00032724A:C05	ES 139
M00032725C:F06	ES 139
M00032726C:C01	ES 139
M00032731B:C10	ES 139
M00032731C:C07	ES 139
M00032737B:E09	ES 139
M00032737B:209	ES 139
M00032744B:F10	ES 139
M00032766B:D12	ES 139
M00032766C:A04	ES 139
M00032790B:A07	ES 139
M00032793A:F06	ES 139
M00032797B:G02	ES 139
M00032797B:G02	ES 139
M00032811B:D02	ES 139
M00032817B:B02	ES 139
M00032830D:G03	ES 139
M00032831C:G07	ES 139
M00032853D:G12	ES 139
M00032864B:B09	ES 139
M00032871D:E11	ES 139
M00032876C:D06	ES 139
M00032977A:G04	ES 139
M00032907A:804	ES 139
M00032907A:B00	ES 139
M00032917B:D08	ES 139
M00032918B:E06	ES 139
M00032918B:E00	ES 139
M00032918C:B10	ES 139
M00032921B:1108	ES 139
M00032939A:C10	ES 139
M00032939B:C07	ES 139
M00032940A:C02 M00032942D:C12	ES 139
M00032944B:B02	ES 139
M00032944B.B02 M00032984C:G05	ES 139
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Clone Name	Tube
M00032990B:A11	ES 139
M00032994A:A08	ES 139
M00032995C:C05	ES 139
M00033007C:E01	ES 139
M00033019B:E10	ES 139
M00033033C:H01	ES 139
M00033034C:A06	ES 139
M00033034C:F02	ES 139
M00033037D:C11	ES 139
M00033074A:C08	ES 139
M00033130B:F06	ES 139
M00033140D:F06	ES 139
M00033173D:C01	ES 139
M00033176B:E12	ES 139
M00033186C:D11	ES 139
M00033189D:F08	ES 139
M00033202D:G06	ES 139
M00033204B:A07	ES 139
M00033205A:F03	ES 139
M00033217B:H07	ES 139
M00033218A:C04	ES 139
M00033223B:H07	ES 139
M00033226A:A11	ES 139
M00033231D:B09	ES 139
M00033231D:G10	ES 139
M00033243B:A05	ES 139
M00033246C:E08	ES 139
M00033248A:B02	ES 139
M00033261C:D12	ES 139
M00033262D:A11	ES 139
M00033263B:G04	ES 139
M00033276B:G08	ES 139
M00033185C:D01	ES 139
M00033288B:D12	ES 140
M00033300D:H12	ES 140
M00033306D:G08	ES 140
M00033306D:H09	ES 140
M00033308B:G05	ES 140
M00033343C:H08	ES 140
M00033345D:A09	ES 140
M00033346C:A05	ES 140
M00033347C:F02	ES 140
M00033349D:F05	ES 140
M00033358A:H12	ES 140
M00033362C:C05	ES 140

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Clone Name	Tube
M00033375A:G04	ES 140
M00033376A:C12	ES 140
M00033377D:A05	ES 140
M00033410B:C09	ES 140
M00033424B:A04	ES 140
M00033424D:H12	ES 140
M00033425A:C10	ES 140
M00033427D:F01	ES 140
M00033432B:H10	ES 140
M00033437C:A07	ES 140
<u> </u>	ES 140
M00033437C:C03	<u> </u>
M00033442A:D06	ES 140
M00033446C:G08	ES 140
M00033446D:B02	ES 140
	ES 140
M00033451A:H01	ES 140
M00033454A:D09	ES 140
M00033457D:A05	ES 140
M00033560D:G07	ES 140
M00033561C:A02	ES 140
M00033566C:E08	ES 140
M00033570B:C08	ES 140
M00033570B:E06	ES 140
M00033570C:C10	ES 140
M00033578D:G02	ES 140
	ES 140
M00033581D:D08	ES 140
M00033583B:E06	ES 140
M00033583D:B05	ES 140
M00033584D:G11	ES 140
	ES 140
M00033588C:G04	ES 140
M00033594C:B03	ES 140
M00033595A:C11	ES 140
M00033393A:C11	ES 140
M00038259A:G08 M00038259B:A02	ES 140
M00038259B:G08	ES 140
M00038259B:G08 M00038259C:H09	ES 140
1	ES 140
M00038272A:G01	ES 140
M00038272D:F11	i
M00038279C:A11	ES 140
M00038284B:H04	ES 140
M00038303A:C03	ES 140
M00038303C:D02	ES 140
M00038303D:E07	ES 140

Clone Name	Tube
M00038315C:G11	ES 140
M00038325D:F12	ES 140
M00038326B:D04	ES 140
M00038327A:C11	ES 140
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M00038616D:B12	ES 140
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M00038619B:A03	ES 140
M00038620B:E09	ES 140
M00038631C:B10	ES 140
M00038631D:B02	ES 140
M00038632C:B09	ES 140
M00038633A:D07	ES 140
M00038633B:G02	ES 140
M00038635A:G09	ES 140
M00038635B:C08	ES 140
M00038638D:H03	ES 140
M00038639B:C03	ES 140
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M00038999D:C11	ES 140
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M00039013A:C09	ES 141
M00039013D:F02	ES 141
M00039014A:H10	ES 141
M00039014B:C04	ES 141

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M00039061B:F08	ES 141
M00039063B:D08	ES 141
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M00039072C:E02	ES 141
M00039079A:A05	ES 141
M00039080C:H06	ES 141
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M00039082B:A05	ES 141
M00039084C:G07	ES 141
M00039084C:H03	ES 141
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M00039096A:E07	ES 141
M00039097D:D06	ES 141
M00039099A:H08	ES 141
M00039104D:C09	ES 141
M00039105C:B08	ES 141
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M00039112B:C05	ES 141
M00039118B:C05	ES 141
M00039118D:A06	ES 141
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M00039167B:H09	ES 141
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M00039179A:G09 M00039180A:A07	ES 141
M00039180A:A07 M00039196B:H06	ES 141
M00039196D:A07	ES 141
M00039190D:A07 M00039200A:C10	ES 141
M00039200A.C10 M00039211A:C12	ES 141
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M00039213B:F05	ES 142
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M00039221A:H03	ES 142
M00039224A:E12	ES 142
M00039228A:B05	ES 142
M00039230A:A10	ES 142
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M00039230D:G12	ES 142
M00039233A:A03	
M00039238A:B12	ES 142
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M00039241A:E11	ES 142
M00039249A:C12	ES 142
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M00039257D:C03	ES 142
M00039258B:E06	ES 142
M00039258D:B08	ES 142
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M00039279C:B08	ES 142
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M00039299B:G12	ES 142
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M00039304D:B09	ES 142
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M00039318B:B09	ES 142
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M00039403A:G12	ES 142
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M00039407B:G02	ES 142
M00039411C:E07	ES 142

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M00039415D:E01	ES 142
M00039417A:D03	ES 142
M00039417A:E12	ES 142
M00039417B:F01	ES 143
M00039417C:A01	ES 143
M00039417C:G01	ES 143
M00039418B:D08	ES 143
M00039420D:D03	ES 143
M00039422D:F04	ES 143
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M00039795B:H10	ES 143
M00039795D:E10	ES 143
M00039795D:G06	ES 143
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M00039810A:H10	ES 143
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M00039816B:D04	ES 144
M00039816C:D05	ES 144
M00039820A:F11	ES 144
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M00039859A:F06	ES 144
M00039859C:G10	ES 144
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M00039869B:F06	ES 144 ES 144
M00039875D:A10	ES 144
M00039876D:H09	ES 144
M00039877C:C03	ES 144
M00039879C:F05	ES 144
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M00039887C:E07	ES 144
M00039887D:C04	ES 144
M00039888B:D03	ES 144
M00039890A:H05	ES 144
M00039894C:H07	ES 144
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M00039936C:C05	ES 144
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M00039990C:D10	ES 144
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M00040005B:C11	ES 144
M00040005D:B07	ES 144
M00040007D:A06	ES 144
M00040009D:B07	ES 144

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M00040014D:D10	ES 144
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M00040017A:C06	ES 144
M00040017D:G03	ES 144
M00040019A:E01	ES 144
M00040021A:F09	ES 144
M00040022C:D06	ES 144
M00040026B:F06	ES 144
M00040029A:B03	ES 144
M00040029A:G04	ES 144
M00040031A:E06	ES 144
M00040032A:B03	ES 144
M00040032A:D09	ES 144
M00040037A:E11	ES 145
M00040038D:G04	ES 145
M00040039D:D06	ES 145
M00040040A:A06	ES 145
M00040041C:C09	ES 145
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M00040088C:E10	ES 145
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M00040089B:E04	ES 145
M00040089C:E06	ES 145
M00040090B:G09	ES 145
M00040092B:F05	ES 145

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M00040097A:C12	ES 145
M00040098C:B01	ES 145
M00040098D:E04	ES 145
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M00040115B:H12	ES 145
M00040118D:G10	ES 145
M00040121B:C05	ES 145
M00040122D:A02	ES 145
M00040123A:A09	ES 145
M00040124D:H01	ES 145
M00040129D:E10	ES 145
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M00040304B:F06	ES 145
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M00004832D:H02	ES 145
M00004839C:H02	ES 145
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M00005449B:D01	ES 145

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M00007124D:H10	ES 146
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M00007149A:G02	ES 146
M00007157C:F11	ES 146
M00007165B:G11	ES 146
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M00007943D:C09	ES 146
M00007972B:H12	ES 146
M00007976A:C10	ES 146
M00007992C:F06	ES 146
M00007994A:G02	ES 146
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M00022264B:G10	ES 146
M00022363C:G12	ES 146
M00022365D:A03	ES 146
M00022373A:B05	ES 146
M00022373C:B07	ES 146

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M00022440B:E01	ES 146
M00022444D:G01	ES 146
M00022467C:B12	ES 146
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M00022492C:A02	ES 146
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M00022830D:D01	ES 147
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M00022968B:E02	ES 147
M00022976C:F04	ES 147
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M00022986D:H09	ES 147
M00022997A:F06	ES 147
M00023001C:C08	ES 147
M00023003C:D07	ES 147
M00023007A:H04	ES 147
M00023007C:E10	ES 147
M00023020C:G08	ES 147
M00023024D:F12	ES 147
M00023032A:B05	ES 147
M00023039D:B05	ES 147
M00023042D:D02	ES 147
M00023044B:D02	ES 147
M00023094A:B11	ES 147
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M00039181D:E05	ES 147
M00039184A:D03	ES 147
M00039184B:B09	ES 147
M00039361B:E01	ES 147
M00039363A:C09	ES 147
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M00039371B:H06	ES 147
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M00039374B:B07	ES 147
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M00039376D:H07	ES 147
M00039377D:E12	ES 147
M00039378D:H07	ES 147
M00039379A:B03	ES 147
M00039380C:C09	ES 147
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M00039496B:D08	ES 147
M00039496B:H09	ES 147

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M00039497C:C06	ES 147
M00039499C:A04	ES 147
M00039500C:C04	ES 147
M00039505C:E03	ES 147
M00039508A:C12	ES 147
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M00039510C:G02	ES 147
M00039512C:D06	ES 147
M00039515A:A06	ES 147
M00039515D:C11	ES 147
M00039517B:G12	ES 147
M00039521A:A02	ES 147
M00039521A:A02	ES 147
M00039528B:B12	ES 147
M00039529C:D07	ES 147
M00039530B:E02	ES 147
	ES 147
M00039533A:C12	
M00039533B:G08	
M00039533D:F04	
M00039535D:D10	ES 147
M00039536C:C10	ES 147
M00039536C:H11	ES 147
M00039561A:B07	ES 147
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M00039562B:G02	ES 147
M00039564B:C01	ES 147
M00039570A:D10	ES 147
M00039570B:D10	ES 147
M00039584C:C01	ES 147
M00039584C:C11	ES 147
M00039587C:F12	ES 147
M00039590D:D02	ES 147
M00039591C:D06	ES 147
M00039595C:E05	ES 147
M00039597D:F04	ES 147
M00039600A:A11	ES 148
M00039604B:E05	ES 148
M00039604D:G03	ES 148
M00039606B:D08	ES 148
M00039607D:E08	ES 148
M00039608D:H01	ES 148
M00039609D:F07	ES 148
M00039624A:H09	ES 148
M00039624B:F12	ES 148
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13	ES 148
1	ES 148
M00039629D:B04	ES 148
M00039630A:C08	ES 148
M00039630C:H04	ES 148
M00039641A:A05	ES 148
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M00039643C:B04	ES 148
M00039645C:E01	ES 148
M00039647A:H11	ES 148
M00039736D:G08	ES 148
M00039740B:F10	ES 148
M00039752B:G08	ES 148
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M00039756B:H06	ES 148
M00039760B:B08	ES 148
M00040131B:D11	ES 148
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M00040131D:G08	ES 148
M00040133B:B03	ES 148
M00040136C:F08	ES 148
M00040138B:H03	ES 148
	ES 148
	ES 148
M00040145D:D03	ES 148
	ES 148
M00040160B:A10	ES 148
	ES 148
	ES 148
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	ES 148
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M00040230A:H02	ES 148

Clone Name: 42	4 Tibe:
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M00040253C:A05	ES 148
M00040254B:C10	ES 148
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M00040260C:D04	ES 148
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M00040262B:B06	ES 148
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M00039746D:D11	ES 148
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M00039748C:F11	ES 148
M00039749D:D05	ES 148
M00039761D:E10	ES 148
M00039762B:F07	ES 148
	ES 148
M00039766A:G07	ES 148
M00039766D:H01	ES 149
M00039767B:A04	ES 149
M00039767C:E12	ES 149
M00039770A:G11	ES 149

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Clone Name	Tube
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M00039943B:F10	ES 149
M00039945C:F09	ES 149
M00039946B:F08	ES 149
M00039947A:D06	ES 149
M00039947C:G03	ES 149
M00039948A:E03	ES 149
M00039948D:D11	ES 149
M00039951A:B07	ES 149
M00039951B:B12	ES 149
M00039951B:C03	ES 149
M00039955C:C04	ES 149
M00039957C:C09	ES 149
M00039957D:A12	ES 149
M00039958A:A08	ES 149
M00039958C:B09	ES 149
M00040201C:G11	ES 149
M00040202A:F05	ES 149
M00040203A:H06	ES 149
M00040203B:A05	ES 149
M00040203D:H11	ES 149
M00040206A:A07 M00040207B:D08	ES 149 ES 149
M00040207B.D08	ES 149
M00040208A:C03	ES 149
M00040208D:A07	ES 149
M00040203D:807	ES 149
M00040218C:C02	ES 149
M00040219B:D02	ES 149
M00040219D:E08	ES 149
M00040291D:C05	ES 149
M00040293D:G04	ES 149
M00040294D:D12	ES 149
M00040296D:E09	ES 149
M00040298B:G02	ES 149
M00040299B:F10	ES 149
M00040313C:D05	ES 149
M00040313D:E04	ES 149
M00040314D:H05	ES 149
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M00040317D:F02	ES 149
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M00040318C:H11	ES 149
M00040320D:F02	ES 149

Clone Name	æ\Tube*∷
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M00040323C:G11	ES 149
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M00040327B:G06	ES 149
M00040332D:B05	ES 149
M00040333D:G05	ES 149
M00040333D:B02	ES 149
	ES 149
M00040342B:D12	ES 149
M00040342D:D12	ES 149
M00040345D:A05	ES 149
M00040347D:F09	ES 149
M00040347D:B09	ES 149
M00040349D:B09	ES 149
	ES 149
M00040351D:A11	ES 149
M00040364A:E05	ES 149
M00040366A:B01	
M00040368A:A12	1
M00040368A:F01	ES 149
M00040368D:E09	ES 149
M00040371C:H05	ES 149
M00040375C:B06	ES 149
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M00040377C:G07	ES 149
M00040383A:H02	ES 149
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M00040386A:A02	ES 149
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M00040390A:H02	ES 149
M00040390B:F02	ES 149
M00040391A:D10	ES 149
M00040392B:H01	ES 149
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M00040394A:D04	ES 149
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	ES 149
M00042565C:A08	ES 149
M00042566C:C05	ES 149
M00042567B:H10	ES 149
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ACIóne Name	-Tube
M00042693D:E04	ES 149
M00042693D:E04 M00042696B:E05	ES 149
	ES 149
M00042697D:C07	ES 150
M00042698D:D10	
M00042698D:E01	ES 150
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M00042711B:A11	ES 150
M00042717A:C07	ES 150
M00042737C:H04	ES 150
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M00042742D:D05	ES 150
M00042887C:D07	ES 150
M00042895A:D10	ES 150
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M00042431D:C10	ES 150
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M00042439B:B03	ES 150
M00042439B:D03	ES 150
M00042440B:E09	ES 150
M00042463A:F09	ES 150
M00042470C:E05	ES 150
M00042511A:H04	ES 150
M00042515C:F08	ES 150
M00042751C:C12	ES 150
M00042752A:E11	ES 150
M00042756B:F11	ES 150
M00042756D:A10	ES 150
M00042759B:G11	ES 150
M00042760A:C12	ES 150 ES 150 ES 150 ES 150
M00042765C:D04	ES 150
M00042767B:G10	ES 150

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Clone Name	a Tübe 👯
M00042769C:E09	ES 150
M00042770B:B12	ES 150
M00042770C:C04	ES 150
M00042771C:F06	ES 150
M00042774C:C05	ES 150
M00042774C:C03	ES 150
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M00042792A:H01	ES 150
M00042797D:D10	ES 150
M00042799D:F08	ES 150
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M00042802C:C04	ES 150
M00042806C:F07	ES 150
M00042807D:D05	ES 150
M00042823C:C02	ES 150
M00042830B:E02	ES 150
M00042839B:B11	ES 150
M00042841D:H07	ES 150
M00042849D:F11	ES 150
M00042852B:A03	ES 150
M00042852C:A01	ES 150
M00042856B:H02	ES 150
M00042352C:H03	ES 150
M00042352D:C01	ES 150
M00042352D:G09	ES 150
M00042448A:C09	ES 150
M00042448C:H12	ES 150
M00042453B:G09	ES 150
M00042518D:A06	ES 150
M00042518D:D04	ES 150
M00042316B:B04	ES 150
M00043290B:005	ES 150
M00043304B:D03	ES 150
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M00043305B:G02	ES 150
	ES 150
M00043306D:B07	ES 150
M00043310C:G06	ES 150
M00043311C:E03	
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M00043320B:A07	ES 150
M00043324D:H11	ES 150
M00043328D:H02	ES 150
M00043332C:G04	ES 150

Clone Name	Tube
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M00043338B:A03	ES 150
M00043338B:C11	ES 150
M00043339A:F11	ES 150
M00043340B:H08	ES 150
M00043344D:E04	ES 150
M00043345C:A06	ES 150
M00043346A:G01	ES 150
M00043350D:B11	ES 151
M00043351D:A11	ES 151
M00043352D:B05	ES 151
M00043352D:C03	ES 151
M00043359B:D10	ES 151
M00043359C:G01	ES 151
M00043361B:A01	ES 151
M00043366A:A02	ES 151
M00043366C:H05	ES 151
M00043367B:A08	ES 151
M00043368C:F09	ES 151
M00043370B:C08	ES 151
M00043372C:G05	ES 151
M00043377A:C03	ES 151
M00043378A:H10	ES 151
M00043379D:H02	ES 151
M00043383C:F12	ES 151 ES 151
M00043383D:A02 M00043384B:B02	ES 151
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M00043389C:E03	ES 151
M00043389D:D07	ES 151
M00043391A:C10	ES 151
M00043391A:G08	ES 151
M00043392D:C11	ES 151
M00043393A:B08	ES 151
M00043401D:G08	ES 151
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M00043405A:D11	ES 151
M00043405C:G12	ES 151
M00043405C:G02	ES 151
M00043406B:G12	ES 151
M00043407C:E05	ES 151
M00043408B:D11	ES 151
M00043409B:B03	ES 151
M00043410C:A09	ES 151
M00043411B:D08	ES 151

Clone Name	Tube 🥞
M00043411D:H06	ES 151
M00042584B:C10	ES 151
M00042623D:D07	ES 151
M00042625C:B04	ES 151
M00042626B:D08	ES 151
M00042627C:D01	ES 151
M00042630A:C05	ES 151
M00042955C:D05	ES 151
M00042956C:B06	ES 151
M00042960D:H08	ES 151
M00042962D:C05	ES 151
M00042964D:A03	ES 151
M00042966B:F07	ES 151
M00042966C:E06	ES 151
M00042970C:A04	ES 151
M00042970C:H10	ES 151
M00042976A:H04	ES 151
M00042979B:E02	ES 151
M00042981B:D11	ES 151
M00042983C:A11	ES 151
M00042983C:G06	ES 151
M00042986C:G12	ES 151
M00042988A:F06	ES 151
M00042997B:D06	ES 151
M00042998A:E03	ES 151
M00042998A:G04	ES 151
M00043001B:H10	ES 151
M00043001D:D03	ES 151
M00043002A:E05	ES 151
M00043003C:D08	ES 151
M00043011A:H12	ES 151
M00043015A:H10	ES 151
M00043022A:E12	ES 151
M00043026C:D07	ES 151
M00043028A:G05	ES 151
M00043029C:A06	ES 151
M00043032C:A10	ES 151
M00043034D:C01	ES 151
M00043036C:E05	ES 151
M00043036D:C09	ES 151
M00043040B:B07	ES 151
M00043044B:A12	ES 151
M00043044D:A09	ES 151
M00043045D:G12	ES 151
M00043046D:B11	ES 151

Noma Nama	Tube:
Glone Name	ALC: CALCAL KARON
M00043060D:G12	ES 151 ES 151
M00043066B:H11	ES 151 ES 151
M00043067D:D10	
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M00043125C:A11	
M00042611A:A06	ES 151
M00042611D:B12	ES 151
M00042612D:F06	ES 151
M00042614B:B05	ES 151
M00043073A:C12	ES 151
M00043078D:D04	ES 151
M00043081D:F05	ES 151
M00043087B:G07	ES 151
M00043093C:G11	ES 151
M00043095A:F09	ES 152
M00043096A:G04	ES 152
M00043108A:F06	ES 152
M00043109C:G01	ES 152
M00043131B:A09	ES 152
M00043133B:C11	ES 152
M00043138D:B11	ES 152
M00043143B:A10	ES 152 ES 152
M00043148C:A09	
M00043154A:B07	ES 152
M00043162A:B08	ES 152 ES 152
M00043162D:C12	ES 152 ES 152
M00043164C:E12	
M00043165B:G01	ES 152 ES 152
M00043173D:G03	ES 152
M00043184A:H08	ES 152
M00043187A:C04	ES 152
M00043191A:A07	ES 152
M00043192C:B12	ES 152
M00043200A:H09	ES 152
M00043200B:C08	
M00043202B:F01	ES 152 ES 152
M00043203A:B09	
M00043210C:E05	
M00043211A:F01	ES 152
M00043213B:B12	
M00043215A:D02	ES 152
M00043220B:C04	ES 152
M00042591D:H03	ES 152
M00042592A:H10	ES 152
M00042593A:C02	ES 152

Clone/Name	* Tube
M00042593C:G06	ES 152
M00042595A:A11	ES 152
M00042595A:B01	ES 152
M00042596B:F06	ES 152
M00042596C:D07	ES 152
M00042597B:E12	ES 152
M00043416C:A02	ES 152
M00043417C:D05	ES 152
M00043418A:H10	ES 152
M00043419D:A10	ES 152
M00043428D:G08	ES 152
M00043420D:G00 M00043430B:C02	ES 152
M00043430D:C02	ES 152
M00043431B:B08	ES 152
M00043433B:G07	ES 152
M00043437D:D04	ES 152
M00043437D:D04 M00043440C:B07	ES 152
M00043446C:E12	ES 152
M00043446C:E12	
M00043447A:C07	
M00043449A:E12	
M00043453B:B09	~
M00043458A:B12	ES 152 ES 152
M00043458A:B12	
M00043461D:C02	
M00043461D:E06	
M00043465C:A03	ES 152
M00043465C:C09	ES 152
	ES 152
M00043476A:F07	ES 152
M00043483B:G10	ES 152
M00043491C:F04	ES 152
M00043492A:E01 M00043513D:G08	ES 152
	ES 152
M00043516B:H09 M00043518B:D06	ES 152 ES 152
L	1
M00043526B:D10	ES 152
M00043527C:E09	ES 152
M00043528C:A02	ES 152
M00043616B:F02	ES 152
M00043616C:A05	ES 152
M00043632D:F09	ES 152
M00043634A:C10	ES 152
M00043635C:C11	ES 152
	ES 152
M00043637C:H01	ES 152

Glone Names	Tube
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M00043649B:E07	ES 152
M00001338C:B02	ES 153
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M00001340D:F07	ES 153
M00001344D:E08	ES 153
M00001346B:G11	ES 153
M00001348B:B03	ES 153
M00001349C:B04	ES 153
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M00001353A:H07	ES 153
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M00001353D:E05	ES 153
M00001356D:E06	ES 153
M00001358A:E08	ES 153
M00001359A:H10	ES 153
M00001361A:C12	ES 153
M00001361B:A12	ES 153
M00001362A:F09	ES 153
M00001364A:C09	ES 153
M00001364C:H10	ES 153
M00001368A:A08	ES 153
M00001368A:B07	ES 153
M00001368A:C02	ES 153
M00001369A:G06 M00001374A:B02	ES 153
M00001374A:B02	ES 153
M00001374C:B10	ES 153 ES 153
M00001373B.D04 M00001378C:E10	ES 153
M00001378C.E10	ES 153
M00001379A:P09	ES 153
M00001382D:H08	ES 153
M00001382D:1108	ES 153
M00001385A:E07	ES 153
M00001386B:F11	ES 153
M00001380B:111	ES 153
M00001387B:A11	ES 153
M00001387B:E10	ES 153
M00001389D:D06	ES 153
M00001389D:E00	ES 153
M00001391D:D03	ES 153

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Clone Name	J. Tübe
M00001393B:C03	ES 153
M00001393C:E08	ES 153
M00001393C:F04	ES 153
M00001393D:E02	ES 153
M00001396B:B01	ES 153
M00001396B:B12	ES 153
M00001396D:H02	ES 153
M00001397C:H08	ES 153
M00001399B:B01	ES 153
M00001399C:A01	ES 153
M00001403C:B03	ES 153
M00001403D:C12	ES 153
M00001406B:H09	ES 153
M00001406D:F06	ES 153
M00001410A:G10	ES 153
M00001416B:A05	ES 153
M00001410B:A03	ES 153
M00001421B:D06	ES 153
M00001422B:B00	ES 153
M00001424D:D02	ES 153
M00001424D:D02	ES 153
M00001428B:C10	ES 153
M00001428B:C10	ES 153
M00001429B:G03	ES 153
M00001430B:E02	ES 153
M00001433B:E02	ES 153
M00001442A:108	ES 153
M00001442E:G12	ES 153
	ES 153
M00001445B:F06	ES 153
M00001449B:H10	ES 153
M00001449B:H10	ES 153
M00001451C.E10	ES 153
M00001461D:B10	ES 153
M00001461D:C10	ES 153
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M00001467C:D04	ES 153
	ES 153
	ES 153
	ES 153
	ES 153
	ES 153
	ES 153
M00001512D:F08	ES 153

Clone Name	Tube
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M00001528C:C03	ES 153
M00001532A:G08	ES 153
M00001533C:G11	ES 153
M00001533D:A01	ES 153
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M00001546B:C11	ES 154
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M00001568C:A03	ES 154 ES 154
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M00003763A:B02	ES 154
M00003763B:B10	ES 154
M00003764A:H09	ES 154
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M00004171B:B03	ES 156
M00004172C:A08	ES 156
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Glone Name	Tube
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M00032580D:A09	ES 158
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€ Clone Name	Tübe
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M00032613A:E11	ES 158
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M00039349D:B11	ES 160
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M00039433B:D06	ES 160
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M00005379A:D10	ES 161
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M00005423C:A10	ES 161
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M00005505B:E01	ES 161
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M00006885A:F07	ES 162
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M00006989B:G05	ES 162
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M00022475D:C07	ES 164

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M00022525B:D09	ES 164
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M00054781D:A11	ES 167
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M00042586A:B01	ES 167
M00042588C:E02	ES 167
M00042621C:C04	ES 167
M00042951D:G12	ES 167
M00042960B:C06	ES 167
M00042967D:C01	ES 167
M00042970C:B01	ES 167
M00042972C:F04	ES 167
M00042976D:C01	ES 167
M00042982D:A10	ES 167
M00042986D:E03	ES 167
M00042996B:H08	ES 167
M00043013B:E03	ES 167
M00043015D:D05	ES 167
M00043016B:F09	ES 167
M00043017C:D08	ES 167
M00043063C:H05	ES 167
M00043070A:C03	ES 167
M00043113C:G09	ES 167

《 基Clone Name - 分	Withber
M00042617B:E01	ES 167
M00043074C:D07	ES 167
M00043076D:A02	ES 167
M00043077B:F11	ES 167
M00043077C:D12	ES 167
M00043077C:G10	ES 167
M00043099A:H04	ES 167
M00043101D:G11	ES 167
M00043134A:F05	ES 167
M00043152C:B10	ES 167
M00043213A:D05	ES 167
M00043219C:C02	ES 167
M00043221D:C12	ES 167
M00043222C:B06	ES 167
M00043455B:C08	ES 167
M00043465C:H11	ES 167
M00043470A:C10	ES 167
M00043485C:C03	ES 167
	ES 167
	ES 167
	ES 167
	ES 167
M00043640A:B01	ES 167

CLAIMS

We claim:

- 1. A library of polynucleotides, the library comprising the sequence information of at least one of SEQ ID NO:1-3351.
- 2. The library of claim 1, wherein the library is provided on a nucleic acid array.
- 3. The library of claim 1, wherein the library is provided in a computer-readable format.
- 4. The library of claim 1, wherein the library comprises a polynucleotide corresponding to a gene differentially expressed in a cancer cell of high metastatic potential relative to a control cell, wherein the control cell is a normal cell or a cell of low metastatic potential, wherein the expression is greater in the metastatic tissue, and wherein the sequence is selected from the group consisting of SEQ ID NOs:14, 137, 151, 152, 171, 200, 254, 262, 271, 348, 412, 472, 507, 520, 530, 588, 623, 637, 660, 678, 680, 700, 714, 774, 812, 834, 901, 937, 976, 1168, 1333, 1352, 1520, 1524, 1546, 1550, 1574, 1580, 1590, 1599, 1607, 1622, 1706, 1752, 1768, 1769, 1780, 1781, 1799, 1803, 1811, 1851, 1856, 1867, 1872, 1875, 1884, 1919, 1923, 1939, 1975, 2024, 2045, 2060, 2071, 2118, 2119, 2128, 2135, 2177, 2181, 2184, 2185, 2190, 2193, 2232, 2239, 2283, 2311, 2314, 2338, 2378, 2393, 2394, 2395, 2398, 2460, 2490, 2505, 2514, 2540, 2542, 2597, 2607, 2640, 2657, 2669, 2670, 2674, 2679, 2684, 2707, 2724, 2757, 2776, 2804, 2818, 2906, 2959, 2964, 2968, 2976, 2980, 2987, 3010, 3043, 3047, 3050, 3071, 3072, 3092, 3095, 3097, 3140, 3157, 3173, 3187, 3203, 3210, 3212, 3220, 3236, 3249, 3264, 3284, 3288, 3305, 3309, 3318, 3330, 3331, and 3335.
- 5. The library of claim 1, wherein the library comprises a polynucleotide corresponding to a gene differentially expressed in normal colon tissue relative to colon cancer tissue, wherein the expression is greater in the cancer tissue, and wherein the sequence is selected from the group consisting of SEQ ID NOs:7, 164, 734, 836, 928, 965, 987, 1026, 1044, 1119, 1226, 1227, 1251, 1316, 1429, 1442, 1540, 1553, 1560, 1577, 1588, 1610, 1620, 1626, 1673, 2416, 2749, 2976, 3129 and 3132.

6. The library of claim 1, wherein the library comprises a polynucleotide corresponding to a gene differentially expressed in normal colon tissue relative to colon cancer tissue, wherein the expression is greater in normal tissue than cancer tissue, and wherein the sequence is selected from the group consisting of SEQ ID NOs:105, 198, 465, 489, 745, 859, 976, 1011, 1045, 1138, 1226, 1251, 1253, 1392, 1474, 1559, 1571, 1589, 1591, 1607, 1608, 1643, 1753, 1764, 1766, 1782, 1811, 2749, 2784, 2790, 2805, 2976, 3128, 3129, 3146, 3150, and 3151.

- 7. The library of claim 1, wherein the library comprises a polynucleotide corresponding to a gene differentially expressed in normal human prostate cells relative to human prostate cancer cells, wherein the expression is greater in normal cells than cancer cells, and wherein the sequence is selected from the group consisting of SEQ ID NOs:53, 446, 1410, 1754, 1801, 1845, 2060, 2143, 2632, 2899, and 3338.
- 8. The library of claim 1, wherein the library comprises a polynucleotide corresponding to a gene differentially expressed in normal human prostate cells relative to human prostate cancer cells, wherein the expression is greater in cancer cells than normal cells, and wherein the sequence is selected from the group consisting of SEQ ID NOs:86, 93, 687, 1269, 1581, 1647, 1649, 1710, 1717, 1772, 1960, 2987, 3128, 3132, 3150, 3222, and 3268.
- 9. An isolated polynucleotide comprising a nucleotide sequence having at least 90% sequence identity to an identifying sequence of SEQ ID NOs:1-3351 or a degenerate variant or fragment thereof.
 - 10. A recombinant host cell containing the polynucleotide of claim 9.
 - 11. An isolated polypeptide encoded by the polynucleotide of claim 9.
 - 12. An antibody that specifically binds a polypeptide of claim 11.
 - 13. A vector comprising the polynucleotide of claim 9.
- 14. A method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, the method comprising the step of:

detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, wherein the gene product is encoded by a

gene corresponding to a sequence of at least one of SEQ ID NOs: 14, 137, 151, 152, 171, 200, 254, 262, 271, 348, 412, 472, 507, 520, 530, 588, 623, 637, 660, 678, 680, 700, 714, 774, 812, 834, 901, 937, 976, 1168, 1333, 1352, 1520, 1524, 1546, 1550, 1574, 1580, 1590, 1599, 1607, 1622, 1706, 1752, 1768, 1769, 1780, 1781, 1799, 1803, 1811, 1851, 1856, 1867, 1872, 1875, 1884, 1919, 1923, 1939, 1975, 2024, 2045, 2060, 2071, 2118, 2119, 2128, 2135, 2177, 2181, 2184, 2185, 2190, 2193, 2232, 2239, 2283, 2311, 2314, 2338, 2378, 2393, 2394, 2395, 2398, 2460, 2490, 2505, 2514, 2540, 2542, 2597, 2607, 2640, 2657, 2669, 2670, 2674, 2679, 2684, 2707, 2724, 2757, 2776, 2804, 2818, 2906, 2959, 2964, 2968, 2976, 2980, 2987, 3010, 3043, 3047, 3050, 3071, 3072, 3092, 3095, 3097, 3140, 3157, 3173, 3187, 3203, 3210, 3212, 3220, 3236, 3249, 3264, 3284, 3288, 3305, 3309, 3318, 3330, 3331, and 3335.

wherein detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived.

15. A method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, the method comprising the step of:

detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, wherein the gene product is encoded by a gene corresponding to a sequence of at least one of SEQ ID NOs:7, 164, 734, 836, 928, 965, 987, 1026, 1044, 1119, 1226, 1227, 1251, 1316, 1429, 1442, 1540, 1553, 1560, 1577, 1588, 1610, 1620, 1626, 1673, 1960, 2416, 2749, 2976, 2987, 3128, 3129, 3132, 3150, 3222, and 3268.

wherein detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived.